

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2004, 15:01:21 ; Search time 343 Seconds  
(without alignments)  
5982.887 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257  
Perfect score: 6089  
Sequence: 1 atgccggccatgcggggcct.....aagaaggcacaggggtctga 3252

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US09965830/runat\_01092004\_160110\_4801/app\_query.fasta\_1.3399  
-DB=SPTREMBL 25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09965830 @CGN\_1\_1\_536 @runat\_01092004\_160110\_4801 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2489	40.9	1097	11 Q8BX82	Q8bx82 mus musculu

2	1909	31.4	351	4	Q8N500	Q8n500 homo sapien
3	1901	31.2	1284	5	Q9V899	Q9v899 drosophila
4	1901	31.2	1284	5	Q23974	Q23974 drosophila
5	1537.5	25.3	1117	11	Q80XE8	Q80xe8 mus musculu
6	1511.5	24.8	1058	4	Q8IZI2	Q8izi2 homo sapien
7	1416	23.3	1011	5	Q7YW98	Q7yw98 manduca sex
8	1405.5	23.1	1186	13	Q8JH78	Q8jh78 brachydanio
9	1387	22.8	1174	5	Q9VXZ6	Q9vxz6 drosophila
10	1342.5	22.0	988	11	Q8CX35	Q8cx35 mus musculu
11	1261.5	20.7	956	5	Q9XYX7	Q9xyx7 caenorhabdi
12	1259.5	20.7	956	5	O44164	O44164 caenorhabdi
13	1185.5	19.5	772	4	Q86U57	Q86u57 homo sapien
14	1084	17.8	791	5	Q18325	Q18325 caenorhabdi
15	1075.5	17.7	732	4	Q8IV15	Q8iv15 homo sapien
16	1046	17.2	855	5	O02497	O02497 drosophila
17	720.5	11.8	422	4	Q86XI1	Q86xi1 homo sapien
18	537.5	8.8	515	11	Q8C782	Q8c782 mus musculu
19	534	8.8	522	11	Q8CC38	Q8cc38 mus musculu
20	507	8.3	395	11	Q8BYS2	Q8bys2 mus musculu
21	474.5	7.8	774	4	Q86WJ5	Q86wj5 homo sapien
22	474	7.8	890	4	Q86WJ6	Q86wj6 homo sapien
23	449	7.4	678	5	O96777	O96777 heliothis v
24	443	7.3	5146	6	Q8SPM4	Q8spm4 bos taurus
25	439	7.2	1463	5	Q9U5E2	Q9u5e2 drosophila
26	434	7.1	767	5	O76977	O76977 strongyloce
27	431	7.1	945	5	Q9Y1J9	Q9y1j9 drosophila
28	431	7.1	1327	5	Q9V702	Q9v702 drosophila
29	430	7.1	1324	5	Q8IR35	Q8ir35 drosophila
30	429.5	7.1	1696	5	Q9VXV8	Q9vxv8 drosophila
31	428.5	7.0	632	11	Q9ER32	Q9er32 rattus norv
32	420	6.9	631	11	Q8CFV6	Q8cfv6 mus musculu
33	417.5	6.9	670	11	Q9ER33	Q9er33 rattus norv
34	415.5	6.8	611	11	Q9QWN7	Q9qwn7 rattus norv
35	414	6.8	907	10	Q8H569	Q8h569 oryza sativ
36	413.5	6.8	900	5	Q97119	Q97119 limulus pol
37	413	6.8	686	6	Q9N0H4	Q9n0h4 sus scrofa
38	411	6.7	849	10	Q9SML2	Q9sm12 zea mays (m
39	401	6.6	664	11	Q80XH6	Q80xh6 mus musculu
40	401	6.6	1414	5	Q26634	Q26634 strongyloce
41	397	6.5	1218	5	Q9W201	Q9w201 drosophila
42	396	6.5	1461	4	O76045	O76045 homo sapien
43	395.5	6.5	1953	5	Q9BIT7	Q9bit7 nephila ina
44	394.5	6.5	1464	4	Q8N473	Q8n473 homo sapien
45	391	6.4	1453	11	Q810J9	Q810j9 mus musculu

ALIGNMENTS

RESULT 1  
Q8BX82  
ID Q8BX82 PRELIMINARY; PRT; 1097 AA.  
AC Q8BX82;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE ELK channel 3 (Fragment).  
GN CL30090D05RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
DR EMBL; AK048629; BAC33401.1; -.  
DR PIR; PT0566; PT0566.  
DR PIR; PT0633; PT0633.

DR MGD; MGI:2445160; C130090D05R1k.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.  
DR InterPro; IPR000595; cNMP\_binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc\_C.  
DR InterPro; IPR000014; PAS\_domain.  
DR Pfam; PF00027; cNMP\_binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; cNMP; 1.  
DR SMART; SM00086; PAC; 1.  
DR TIGRFAMs; TIGR00229; sensory\_box; 1.  
DR PROSITE; PS50042; cNMP\_BINDING\_3; 1.  
DR PROSITE; PS50113; PAC; 1.  
FT NON TER 1  
SQ SEQUENCE 1097 AA; 122704 MW; D7E37630C1E93B5F CRC64;

Alignment Scores:

Pred. No.: 1.14e-132 Length: 1097  
Score: 2489.00 Matches: 550  
Percent Similarity: 61.63% Conservative: 147  
Best Local Similarity: 48.63% Mismatches: 286  
Query Match: 40.88% Indels: 148  
DB: 11 Gaps: 26

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x Q8BX82 (1-1097)

QY 16 GGCCTCTCGCGCTCAGAACACCTTCCTGGACACCATCGCTACGGCTTCGACGGCAGC 75  
Db 1 GlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThrArgPheAspGlyThr 20  
QY 76 CACAGTAACTTCGTGGGCAACGCCAGGTGGCGGGCTCTTCCCGTGGTCTACTGC 135  
Db 21 HisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPheProIleValTyrCys 40  
QY 136 TCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGCTGAGGTATGACGCGGGCTGT 195  
Db 41 SerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluValMetGlnLysSerCys 60  
QY 196 GCCTGTCTCTTATGGGCCAGACACAGTAGCTCGTCCGCCAACAGATCCGCAAG 255  
Db 61 SerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMetLeuGlnIleGluLys 80  
QY 256 GCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTACCGGAAGAGCGGGCTC 315  
Db 81 SerLeuGluGluLysValGluPheLysGlyGluIleMetPheTyrLysLysAsnGlyAla 100  
QY 316 CCGTCTCTGTCTCTCGATGTGATACCCATAAAGAATGAGAAAGGGAGGTGGCTCTC 375  
Db 101 PropheTrpCysLeuLeuAspIleValProIleLysAsnGluLysGlyAspValValLeu 120  
QY 376 TTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGACCGAGGGGGCCCGACAGATGG 435  
Db 121 PheLeuAlaSerPheLysAspIleThrAspThrLysValLysIleThrSerGluAspLys 140  
QY 436 AAGGAGACAGGTGGTGGCGGCCCGGATATGGCGGGCACGATCC---AAAGGTTCAAT 492  
Db 141 LysGluAsp-----ArgThrLysGlyArgSerArgAlaGlySerHisPheAsp 156  
QY 493 GCCAACCGGCGGAGCGGGCCGTGCTCTACCACTGTCCGGGCACCTGCAGAAGCAG 552  
Db 157 SerAlaArgArgSerArgAlaValLeuTyrHisIleSerGlyHisLeuGlnArgArg 176

QY 553 CCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTGGGGAGAAACCAAACTTGCTGTGAG 612  
Db 177 GluLysAsnLysLeuLysIleAsnAsnValPheValAspLysProAlaPheProGlu 196  
QY 613 TACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACCTGTGGGGCACTGAGA 672  
Db 197 TyrLysAlaSerAspAlaLysLysSerLysPheIleLeuLeuHisPheSerThrPheLys 216  
QY 673 GCCACCTGGGATGGCTTCATCCTGCTCGGCACACTCTATGTGGTGTCACTGTGCCCTAC 732  
Db 217 AlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAlaValThrValProTyr 236  
QY 733 AGCGTGTGTGAGCACAGCACGGGAGCCAGTCGCCCGCGCGGCCGCCAGCGTCTGT 792  
Db 237 AsnValCysPheIleGlyAsnGluAspLeuSerThrThrArgSer---ThrThrValSer 255  
QY 793 GACCTGGCGGTGAGGTCTCTTCATCCTTGACATTTGTGTGAATTTCCGTACCATTC 852  
Db 256 AspIleAlaValGluIleLeuPheIleAspIleLeuAsnPheArgThrThrTyr 275  
QY 853 GTGTCCAAGTCGGGCCAGGTGGTGTGGTGGCCCAAGTCCATTTGCCCTCCACTACGTCACC 912  
Db 276 ValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCysIleHisTyrValThr 295  
QY 913 ACCTGGTTCCTGTGGATGTCATCGCAGCGTGCCTTTGACCTGCTACATGCTTCAAG 972  
Db 296 ThrTrpPheIleIleAspLeuIleAlaLeuProPheAspLeuLeuTyrAlaPheAsn 315  
QY 973 GTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCCTGTGCGCCTGTGCGC 1032  
Db 316 ValThrValValSerLeuValHisLeuLysThrValArgLeuLeuArgLeuLeuArg 335  
QY 1033 CTGCTTCCGGCGTGGACCGGTACTCGCAGTACAGCGCGTGGTGTGCTGACACTGCTCATG 1092  
Db 336 LeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleValLeuThrLeuLeuMet 355  
QY 1093 GCCGTGTTCCGCTCTCGCGCACTGGGTGGCTGCTGCTGGTTTACATTTGCGCAGCGG 1152  
Db 356 SerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleTrpTyrIleIleGlyLysMet 375  
QY 1153 GAGATCGAGAGCAGCGAATCCGAGCTGCCTGCATGGTGGCTGCAGGAGCTGGCCCCGC 1212  
Db 376 GluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeuHisGluLeuGlyLys 395  
QY 1213 CGACTGGAGACTCCCTACTACTGTTGGTGGCGGAGGCCAGCTGGAGGGAACAGCTCCGGC 1272  
Db 396 ArgLeuGluSerProTyrTyr-----GlyAsnAsnThr--- 406  
QY 1273 CAGAGTGACAACTGACAGCAGCAGCAGCGAGGCGCAACGGGCTGGAGCTGCTGGGC 1332  
Db 407 -----LeuGly 408  
QY 1333 GGCCCGTCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAGCAGCTCACC 1392  
Db 409 GlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThrLeuSerSerLeuThr 428  
QY 1393 AGCGTGGGCTTCGGCAACGTGTCCGCCCAACACGGACACCGAGAGATCTTCCATCTGC 1452  
Db 429 SerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLysIlePheSerIleCys 448  
QY 1453 ACCATGCTCATCGGCGCCTGATGCACCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1512  
Db 449 ThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsnValThrAlaIle 468  
QY 1513 CAGCGCATGTACGCCCGCGCTTCTGTACCAAGCGCGCACCGCGCGCGCGCGCGCGCTAC 1572  
Db 469 GlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLysAspLeuLysAspPhe 488  
QY 1573 ATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCC 1632  
Db 489 IleArgValHisHisLeuProGlnGlnLeuLysGlnArgMetLeuGluTyrPheGlnThr 508  
QY 1633 ACCTGGCGGTGAACATGGCATCGACACCACCGAGCTGTGACAGCGCTCCCTGACGAG 1692





Query Match:	31.35%	Indels:	0
DB:	4	Gaps:	0
US-09-965-830-1_COPY_6_3257 (1-3252) x Q8N500 (1-351)			
QY	2197	ACAGATGGGAGCAGGGCCCGCCACGGTCTCTCCCGAGCCCGCCAGCTGATGAGCCCTCCAGCCCC	2256
Db	1	ThrAspGlyGluGlnGlyProThrValSerProAlaProAlaAspGluProSerSerPro	20
QY	2257	CTGCTGTCCCTGGCTGCACCTCCTCATCTCTCAGCTGCCAAGCTGTATCCCCACGTGGA	2316
Db	21	LeuLeuSerProGlyCysThrSerSerSerAlaAlaLysLeuLeuSerProArgArg	40
QY	2317	ACAGCACCCCGGCTCGTCTAGTGGCAGAGGAGGCCAGGCAGGGCGGCTTTGAAG	2376
Db	41	ThrAlaProArgProArgLeuGlyGlyArgGlyArgProGlyArgAlaGlyAlaLeuLys	60
QY	2377	GCTGAGGTGGCCCTCTGCTCCCGCCCGGCTAGAGGGCTACGGCTGCCCCCATG	2436
Db	61	AlaGluAlaGlyProSerAlaProProArgAlaLeuGluGlyLeuArgLeuProProMet	80
QY	2437	CCATGGATGTGCCCCCAGATCTGAGCCCGAGGTAGTAGTGGCATTTGAAGACGGCTGT	2496
Db	81	ProTrpAsnValProProAspLeuSerProArgValValAspGlyIleGluAspGlyCys	100
QY	2497	GGCTCGGACCGAGCCCAAGTTCTCTTTCGGGTGGCCAGTCTGGCCCGGAATGTAGCAGC	2556
Db	101	GlySerAspGlnProLysPheSerPheArgValGlyGlnSerGlyProGluCysSerSer	120
QY	2557	AGCCCTCCCTGGACCGAGAGCGGCTGCTCACTGTTCCCGATGGGCCCGAGGAGCA	2616
Db	121	SerProSerProGlyProGluSerGlyLeuLeuThrValProHisGlyProSerGluAla	140
QY	2617	AGGAACACAGACACTGGACAAGCTTCGGCAGGCGGTGACAGAGCTGTCTCAGACAGGTG	2676
Db	141	ArgAsnThrAspThrLeuAspLysLeuArgGlnAlaValThrGluLeuSerGluGlnVal	160
QY	2677	CTGCAGATGGGGAAGGACTGCAGTCACTTCGCCAGGCTGTGCAGCTGTCTGGCGCCC	2736
Db	161	LeuGlnMetArgGluGlyLeuGlnSerLeuArgGlnAlaValGlnLeuValLeuAlaPro	180
QY	2737	CACAGGAGGTCCGTCCCTCGGSCATCGGAGAGGGCGCGTCCCGAGCCAGCACCTCC	2796
Db	181	HisArgGluGlyProCysProArgAlaSerGlyGluGlyProCysProAlaSerThrSer	200
QY	2797	GGGCTCTGCAGCCTCTGTGTGGACACTGGGGCATCCTCCTACTGCTGCAGCCCCCA	2856
Db	201	GlyLeuLeuGlnProLeuCysValAspThrGlyAlaSerSerTyrCysLeuGlnProPro	220
QY	2857	GCTGGCTCTGTGTAGTGGGACTTGGCCCGCCACCTCGTCGCGGGGCTCTCCCTCATG	2916
Db	221	AlaGlySerValLeuSerGlyThrTrpProHisProArgProGlyProProLeuMet	240
QY	2917	GCACCTGGCCCTGGGTCCCGAGCTGTCTCAGAGCTCCCGCTGGCTCGAGCCACAGCT	2976
Db	241	AlaProTrpProTrpGlyProProAlaSerGlnSerSerProTrpProArgAlaThrAla	260
QY	2977	TTCTGGACCTCCACCTCAGACTCAGAGCCCGCTGCCTCAGGAGACCTCTGCTGAGCCC	3036
Db	261	PheTrpThrSerThrSerAspSerGluProProAlaSerGlyAspLeuCysSerGluPro	280
QY	3037	AGCACCCCTGCTCCCTCCTCTCTGAGGAAGGGGTAGGACTGGGCGCCGAGAGCCT	3096
Db	281	SerThrProAlaSerProProProSerGluGluGlyAlaArgThrGlyProAlaGluPro	300
QY	3097	GTGAGCCAGGCTGAGGCTACCGACCTGGAGAGCCCCCACCAGGCTCAGGGGCGCTGGCC	3156
Db	301	ValSerGlnAlaGluAlaThrSerThrGlyGluProProProGlySerGlyGlyLeuAla	320
QY	3157	TTGCCCTGGGACCCCGACAGCCTGGAGATGGTGTATTGGCTGCCATGGCTCTGGCACA	3216
Db	321	LeuProTrpAspProHisSerLeuGluMetValLeuIleGlyCysHisGlySerGlyThr	340

QY	3217	GTCCAGTGGACCCAGGAAGACAGGCACAGGGGTC	3249
Db	341	ValGlnTrpThrGlnGluGluGlyThrGlyVal	351
RESULT 3			
QYV899		PRELIMINARY;	PRT; 1284 AA.
ID	Q9V899		
AC	Q9V899;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	CG5076 protein.		
GN	ELK OR CG5076.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Berkeley;		
RX	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,		
RA	Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,		
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;		
RT	"The genome sequence of Drosophila melanogaster.";		
RL	Science 287:2185-2195(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Amanatides P.G., Brandon R.C., Rogers Y., An H., Baldwin D.,		
RA	Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A.,		
RA	Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V.,		
RA	Doup L.E., Doyle C., Dresnek D., Farfan D., Ferreira S., Frise E.,		
RA	Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J.,		
RA	Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M.,		
RA	Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M.,		
RA	Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V.,		
RA	Park S., Patel S., Pfeiffer B., Phouanavong S., Pittman G.S.,		
RA	Puri V., Richards S., Scheeler F., Stapleton M., Strong R.,		
RA	Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S.,		

RA Smith H.O., Venter J.C., Rubin G.M.;  
RT "Sequencing of Drosophila melanogaster genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,  
RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,  
RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,  
RA Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,  
RA Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Mungall C.J., Lewis S.E.;  
RT "Annotation of Drosophila melanogaster genome.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003801; AAF5772.2; -.  
DR FlyBase; FBgn0011589; elk.  
DR GO; GO:0008076; C:voltage-gated potassium channel complex; NAS.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; NAS.  
DR GO; GO:0006813; P:potassium ion transport; NAS.  
DR InterPro; IPR000595; cNMP\_binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc\_C.  
DR InterPro; IPR000014; PAS\_domain.  
DR Pfam; PF00027; cNMP\_binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; cNMP; 1.  
DR SMART; SM00086; PAC; 1.  
DR TIGRFAMS; TIGR00229; sensory\_box; 1.  
DR PROSITE; PS50042; cNMP\_BINDING\_3; 1.  
DR PROSITE; PS50113; PAC; 1.  
DR PROSITE; PS50112; PAS; 1.  
KW Ionic channel; Transmembrane.  
SQ SEQUENCE 1284 AA; 141378 MW; C6EC31891E4B6D24 CRC64;

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QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTGCTGGGCAACGCCACGAGTGCGGGCTCTTC 120  
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QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCAAGAGATTCAAGGCTGAGCTGATCCTGTAC 300  
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Db 100 LysLysGluGlyAlaProPheTrpCysLeuPheAspIleValProIleLysAsnGluLys 119  
QY 361 GGGGAGGTGGCTCTCTTCTAGTCTCTCACAAAGGACATCAGCGAAACCAAG----- 411  
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QY 411 ----- 411  
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QY 421 GGCCTC-----GACAGATGGAAGGAGACAGGTGTGTGGCGCGCGCATATGGCCGG 471  
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Db 200 Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValLeuTyrGlnLeu 216  
QY 532 TCCGGGCACCTGCAGAAGCAGCCCAAGGGC---AAGCACAAAGTCAATAAGGGG----- 582  
Db 217 SerGlyHisTyrLysProGluLysGlyGlyValLysThrLysLeuLysLeuGlyAsnAsn 236  
QY 583 --GTGTTTGGGAGAAACCAACTTGCCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCG 639  
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QY 640 CCCTTCATCCTGTTGCACTGTGGGCACTGAGAGCCACCTGGATGGCTTCATCCTGCTC 699  
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QY 700 GCCACACTCTATGTGGTGTCACTGTGCCCTACAGCGTGTGTGAGCAGCAGCAGCGGAG 759  
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QY 991 ---GCCCATCTGCTGAAGACGGTGGCGCTGCTGCGCTGTGCGCTGCTTCCGCGGCTG 1047  
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Db 427 -----TrpPheProGluSerAsnIleGlyTrpLeuGlnLeuLeuAlaGluArg----- 442  
QY 1222 ACTCCCTACTACCTGGTGGCGCGAGGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGAC 1281  
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Db	443	-----LysAsnAlaSerValAlaIleLeuThrThrAlaGlu-----	454
QY	1342	CTGGCGAGCCCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTCACCAGCGTGGGC	1401
Db	455	-----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly	471
QY	1402	TTCGGCAACGTGTCGGCCAAACACGACACCGAGAGATCTTCTCCATCTGCACCATGCTC	1461
Db	472	PheGlyAsnValSerAlaAsnThrThrAlaGluLysValPheThrIleIleMetMetLeu	491
QY	1462	ATCGGCGCCCTGATGACGCGGTGGTGTGGGAACGTGACGGCCATCATCCAGCGCATG	1521
Db	492	IleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMet	511
QY	1522	TACGCGCGCCGCTTCTGTACACAGCGCACGCGGACCTGCGGACTACATCCGCATC	1581
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QY	1582	CACCGTATCCCAAGCCCTCAAGCAGCGCATGTGGAGTACTTCCAGGCCACTGGGGCG	1641
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QY	1642	GTGAACAATGGATCGACACACCGAGCTGTCGACAGAGCTCCCTGACGAGCTGGCGCA	1701
Db	552	LeuSerHisGlyIleAspIleTyrGluThrLeuArgGluPheProGluGluLeuArgGly	571
QY	1702	GACATCGCCATGACCTGCACAAGGAGTCTTGAGCTGCCACTGTTTGGCGGCCAGC	1761
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QY	1762	CGCGGTGCTGCGGCACTGTCTCTGGCCCTGGGCCCCGCTTCTGCACGCGGCGCGAG	1821
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QY	1822	TACCTCATCCCAAGCGGATGCCCTGCAGGCCCTCTACTTTGTCTGCTGGCTCCATG	1881
Db	612	TyrLeuIleHisLysGlyAspAlaLeuAsnTyrIleTyrTyrLeuCysAsnGlySerMet	631
QY	1882	GAGGTGCTCAAGGTGGCACCGTGTCTCGCCATCTCTAGGAAGGCGACCTGATCGGTGT	1941
Db	632	GluValIleLysAspMetValValAlaIleLeuGlyLysGlyAspLeuValGlySer	651
QY	1942	GAGCTG-----	1947
Db	652	AspIleAsnValHisLeuValAlaThrSerAsnGlyGlnMetThrAlaThrThrAsnSer	671
QY	1948	CCCCGGCGGAGAGGTGGTAAAGGCCAATGCCAGCGTGAAGGGCTGACGTACTGCGTC	2007
Db	672	AlaGlyGlnAspValValValArgSerSerSerAspIleLysAlaLeuThrTyrCysAsp	691
QY	2008	CTGCAGTGTCTGCAGCTGGCTGGCCCTGCACGACAGCCTGCGCTGTACCCCGAGTTGCC	2067
Db	692	LeuLysCysIleHisMetGlyGlyLeuValGluValLeuArgLeuTyrProGluTyrGln	711
QY	2068	CCGCGCTTCAGTCTGCTGCCCTCCGAGGGGAGCTCAGCTACAACCTGGGTGCTGGGGAGGC	2127
Db	712	GlnGlnPheAlaAsnAspIleGlnHisAspLeuThrCysAsnLeuArgGluGlyTyrGlu	731
QY	2128	TCTGCAGAGGTGGACACCAGC-----TCCCTGAGCGGCGACAATACC	2169
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QY	2170	CTTATGTCCACGCTGGAG-----GAGAAGGAGACAGATGGGGAGCAGGGC	2214
Db	752	AsnArgGluGluAlaGluGluGlyGlyLysGlyGluLysGluAsnGlyGly-----Gly	769
QY	2215	CCC-----ACGTCCTCCAGCCCCAGCTGATGAGCCCTCC	2250
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790 SerProLeuLeuGlyMetGly-----SerPro 798

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808 -----ArgSerLeuIleThrLeuArg----- 814

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900 ProProAlaArgSerIleProAsnIleSerGly--ValAlaGlyThrArgSerGlyVala 919

2905 CCTCCCCCTCATGGACACCCTGGCCCTGGGGTCCCCCAGCGTCTCAGAGCTCCCCCTGGCCT 2964
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957 rAsnThrAlaSerSerLysAlaProSerProValGluPro 970

RESULT 4
Q23974
ID Q23974 PRELIMINARY; PRT; 1284 AA.
AC Q23974;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative potassium channel subunit (EAG-like K[+] channel protein).
GN ELK OR CG5076.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R; TISSUE=Head;

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SEQUENCE FROM N.R.  
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QY 1702 GACATCGCCATGCACCTGCACAAGGAGTGCTGTCAGCTGCCACTGTTTGAAGCGGCCAGC 1761  
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Db 672 AlaGlyGlnAspValValArgSerSerSerAspIleLysAlaLeuThrTyrCysAsp 691  
QY 2008 CTGCAGTGTCTGCAGTGGCTGGCCTGCACGACAGCCTTGCCTGTATCCCGAGTTTGCC 2067  
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QY 2068 CCGCGCTTCAGTCTGTCGCTCCGAGGGGAGCTCAGCTACAACCTGGTGTGGGGAGGC 2127  
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QY 2311 CGTCGAACAGCACCCCGGCTCTGCTVAGGTGGCAGAGGAGGCCAGGGCAGGGCT 2370  
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QY 2965 CGAGCCACAGCTTTCTGGACCTCCACCT-----CAGACTCAGAGCCCCCTGCC 3012  
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Db 957 rAsnThrAlaSerSerLysAlaProSerProValGluPro 970



RESULT 5  
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ID Q80XE8 PRELIMINARY; PRT; 1117 AA.  
AC Q80XE8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to potassium voltage-gated channel, subfamily H (Bag-related),  
DE member 2 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Olfactory epithelium;  
RA Strausberg R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC051016; AAH51016.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.  
DR InterPro; IPR000595; CNMP binding.  
DR InterPro; IPR003967; Erg\_Channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc\_C.  
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DR Pfam; PF00027; cNMP\_binding; 1.  
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DR SMART; SM00100; CNMP; 1.  
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DR PROSITE; PS50042; CNMP\_BINDING\_3; 1.  
DR PROSITE; PS50113; PAC; 1.  
DR PROSITE; PS50112; PAS; 1.  
FT NON TER 1117 1117  
SQ SEQUENCE 1117 AA; 122263 MW; 4E51C18D3C49D2FA CRC64;  
  
Alignment Scores:  
Pred. No.: 7.91e-79 Length: 1117  
Score: 1537.50 Matches: 395  
Percent Similarity: 45.37% Conservative: 139  
Best Local Similarity: 33.56% Mismatches: 322  
Query Match: 25.25% Indels: 321  
DB: 11 Gaps: 28  
  
US-09-965-830-1\_COPY\_6\_3257 (1-3252) x Q80XE8 (1-1117)  
  
QY 1 ATGCCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCTCTGGACACCATCGCTACG 60  
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleArg 20  
  
QY 61 CGCTTCGACGCGCACGACAGTAACCTTCGTGCTGGGCAACGCCAGTGCGGGGCTCTTC 120  
Db 21 LysPheGluGlyGlnSerArgLysPheIleAlaAsnAlaArgValGluAsnCys--- 39  
  
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59  
  
QY 181 ATGCAGCGGGGTGTGCTGCTCTCTTCCTTTATGGCCAGACACACGATGAGTCTCGCCG 240  
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAala 79  
  
QY 241 CAACAGATCCGAAGGCCCTGGACGAGCAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 1117 AA; 122263 MW; 4E51C18D3C49D2FA CRC64;  
  
80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99  
301 CGGAAGAGCGGGCTCCCGTTCTGTGCTCTCTGGATGTATACCCATAAAGAAATGAGAAA 360  
100 ArgLysAspGlySerCysPheLeuCysLeuValAspValValProValLysAsnGluAsp 119  
361 GGGAGGTGCTCTCTTCTTA-----GTCTCTCACAAAGGACATC----- 399  
120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139  
400 -----AGCGAAACCAAGAACCGAGGGGGCCCGACAGATGGAGGAGACAGGT--- 447  
140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerTrpLeuAlaSerGlyArg 159  
447 ----- 447  
160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179  
448 -----GGTGGCCGGCGCCGATATGGC----- 468  
180 ValArgThrGlySerMetArgSerAlaGlyAlaProGlyAlaValValAspValAsp 199  
468 ----- 468  
200 LeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValSerAlaMetAsp 219  
468 ----- 468  
220 AsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProGlySer 239  
468 ----- 468  
240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnSerLeuAsn 259  
469 -----CGGACACGATCCAAAGGCTTCAATGCC 495  
260 ProAspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAla 279  
496 AACCGCGCGGAGCCGGGCC-----GTGCTCTACCACTGTCGGGACCTGCAG 546  
280 SerValArgArgAlaSerSerAlaAspIleGluAlaMetArgAlaGlyAlaLeuPro 299  
547 AAGCAGCCCAAG-----GCCAAGCACAGCTCAATAAGGGGTGTTGGG 591  
300 ProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn 319  
592 GAGAAACCAAAAC----- 603  
320 SerThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThr 339  
603 ----- 603  
340 LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu 359  
603 ----- 603  
360 IleIleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnVal 379  
604 -----TTGCCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCC 642  
380 LeuSerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArg 399  
643 TTCATCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702  
400 TrpThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuLeu 419  
703 ACACCTATGTGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744  
420 ValIleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLysGluThrGlu 439  
745 -----AGCACAGCAGCGGAGCCAGTGCCTGCGCCCGCGCGCGCGCGCGCGCGCGCG 798  
440 AspGlySerGlnAlaProAspCysGlyTyrAlaCysGlnProLeuAlaValValAspLeu 459



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Q8IZI2
ID Q8IZI2 PRELIMINARY; PRT; 1058 AA.
AC Q8IZI2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ether-a-go-go related potassium channel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Shoen F., Malykhina A.P., Akbarali H.I.;
RT "HERG potassium channel from human colon.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY130462; AAN05415.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. .; IEA.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR003967; Erg_channel.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR01470; ERGCHANNEL.
DR SMART; SM00100; cNMP; 1.
DR SMART; SM00086; PAC; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
DR PROSITE; PS50113; PAC; 1.
DR PROSITE; PS50112; PAS; 1.
KW Ionic channel.
SQ SEQUENCE 1058 AA; 116000 MW; 70F37F537AAFE084 CRC64;

Alignment Scores:
Pred. No.: 2.31e-77 Length: 1058
Score: 1511.50 Matches: 384
Percent Similarity: 45.62% Conservative: 131
Best Local Similarity: 34.01% Mismatches: 299
Query Match: 24.82% Indels: 315
DB: 4 Gaps: 28

US-09-965-830-1_COPY_6_3257 (1-3252) x Q8IZI2 (1-1058)

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Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg 20
QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTGGGCAACGCCAGGTGGCGGGCTCTTC 120
Db 21 LysPheGluGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys--- 39
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCCTCCGGGTGAGGTC 180
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59
QY 181 ATGCAGCGGGGTGCTGCTCTCCTTCCTTTATGGCCAGACACCATGAGCTCGTCCGC 240
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
QY 241 CAACAGATCCGCAAGGCCCTGGACGACGACAAAGGATTCAAGGCTGACGTGATCCTGTAC 300
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluArgLysValGluIleAlaPheTyr 99
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QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTCTGGATGTATACCCATAAAGAATGAGAAA 360
Db 100 ArgLysAspGlySerCysPheLeuCysLeuValGlyValValProValLysAsnGluAsp 119
QY 361 GGGAGAGTGGCTCTCTTC-----CTAGTCTCTCACAAAGACATC----- 399
Db 120 GlyAlaValIleMetPheValLeuAsnPheGluValValMetGluLysAspMetValGly 139
QY 400 -----AGCGAAACCAAGAACCGAGGGGCCCCGACAGATGGAAGGACAGGT--- 447
Db 140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerTrpLeuAlaSerGlyArg 159
QY 447 ----- 447
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
QY 448 -----GGTGGCGGCGCGCCGATATGGC----- 468
Db 180 ValArgThrGlySerMetArgSerAlaGlyAlaProGlyAlaValValValAspAlaAsp 199
QY 468 ----- 468
Db 200 LeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGlyValSerAlaMetAsp 219
QY 469 -----CGGCGA----- 474
Db 220 AsnHisValAlaGlyLeuGlyProAlaGluGluArgAlaLeuValGlyProGlySer 239
QY 475 -----CGATCCAAAGGCTTCAAT 492
Db 240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnGlyLeuAsn 259
QY 493 GCCAAC-----CGCGCGCGGAGCGCGCGGTGCTCTAC 525
Db 260 ProAspAlaSerGlySerSerCysSerProAlaArgThrArgSerArgGluSerCysAla 279
QY 526 CACCTG-----TCCGGGCGACCTGCAG 546
Db 280 SerValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyAlaLeuPro 299
QY 547 AAGCAGCCCAAG-----GGCAAGCACAAAGCTCAATAAGGGGGTGTGGG 591
Db 300 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn 319
QY 592 GAGAAACCAAAAC----- 603
Db 320 SerThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnThrThr 339
QY 603 ----- 603
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QY 603 ----- 603
Db 360 IleIleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnVal 379
QY 604 -----TTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCC 642
Db 380 LeuSerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProLysIleHisArg 399
QY 643 TTCATCCTGTGCACTGTGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCC 702
Db 400 TrpThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeu 419
QY 703 ACACCTCTATGTGGCTGCTCACTGTGCCCTACAGCGTGTGTGTG----- 744
Db 420 ValIleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGlu 439
QY 745 -----AGCACAGCACGGGAGCCAGTGCCTCCCGCGCGCGCCAGCGTCTGTGACCTG 798
Db 440 AspGlySerGlnAlaProAspCysGlyTyrAlaCysGlnProLeuAlaValValAspLeu 459
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Db 561 LeuAlaSerAspGlyCysLeuArgAlaLeuAlaMetHisPheGlnMetSerHisSerAla 580  
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Db 581 ProGlyAspLeuLeuTyrHisThrGlyGluSerIleAspSerLeuCysPheIleValThr 600  
QY 1873 GGCTCCATGAGGTGCTCAAGGGTGGCACCGTGTCCCATCTCTAGGGAAGGGCGACCTG 1932  
Db 601 GlySerLeuGluValIleGlnAspGluValValAlaIleLeuGlyLysGlyAspVal 620  
QY 1933 ATCGGCTGTGAGTGCCTCCCGGGGAGCAGGTGGTAAAGGCCAATGCCGACGTGAAGGG 1992  
Db 621 PheGlyAspSerPheTrpLysAspSerAlaValGlyGlnSerAlaAlaAsnValArgAla 640  
QY 1993 CTGACGTACTGCTCCTGCAGTGTCTGCAGCTGGCTGGCTGCACGACAGCCTTGGCTG 2052  
Db 641 LeuThrTyrCysAspLeuHisThrIleLysArgAspArgLeuLeuGluValLeuAspPhe 660  
QY 2053 TACCCCGAGTTGCCCGCGCTTCAGTCGTGGCTCCGAGGGGAGCTCAGCTACAACCTG 2112  
Db 661 TyrGlnAlaPheAlaAsnSerPheAlaArgAsnLeu-----ThrLeuThrTyrAsnLeu 678  
QY 2113 GGTGCTGGGGAGGCTCTGCAGAGGTGGACACAGCTCCCTGAGCGGGCGACAATACCTT 2172  
Db 679 ArgHisArgLeuIlePheArgLysVal-----AlaAspValArgArgGluArgGluLeu 696  
QY 2173 ATGTCC-----ACGCTGGAGAGAAGGAGACAGAT----- 2202  
Db 697 MetGluArgArgLysArgGluProGlnLeuGluGlnAlaGlnAspHisLeuValArgLys 716  
QY 2203 -----GGGGAGCAGGGCCCCCAGGTCTCCCCAGCCCCCAGCTGATGAG 2244  
Db 717 IlePheSerArgPheArgArgGluArgSerValAlaAlaAlaProAlaProAlaProAla 736  
QY 2245 CCCTCCAGCCCCCTGTGTCCCTGGCTGCACCTCCTCATCTCAGCTGCCAAGCTGCTA 2304  
Db 737 ArgAlaSerPro-----AlaProProAlaThrAlaValAlaThrAlaAlaAlaPro 754  
QY 2305 -----TCCCCACGTGGAACAGCACCCCGCCT-----CGTCTAGGT 2340  
Db 755 ProAlaSerAspAlaGluArgGlyAspAlaProGlnProProProAlaValAlaAlaPro 774  
QY 2341 GGCAGAGGAGGCCAGGCAGG-----GCAGGGCTTTGAAGGCTGAGGCTGGGCCCC 2391  
Db 775 AlaArgGlyLysTrpGlyArgLeuLeuAlaGlyGlySerLeu-----AspAlaGlyGln 792  
QY 2392 TCTGCTCCCCCAGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCC 2451  
Db 793 AlaAspThrProArgGlyAla-----PheSer 801  
QY 2452 CCAGATCTGAGCCCCCAGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACGAGCCC 2511  
Db 802 ArgSerLeuSerAlaArg-----AspArgPro 810  
QY 2512 AAGTTCTCTTCCGCGTGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCCTCC---CCT 2568  
Db 811 Pro-----ProSerGlyThrAspAlaThrAlaGlnAlaSerAlaAla 824  
QY 2569 GGACCAGAGAGCGGCTGCTCACTGTTCCCATGGGCCCGCAGGAGGCAAGGAACACAGAC 2628  
Db 825 GlyAlaValThrSerAlaLeuSerLeuLysAlaSerPheAlaLysAlaArgSerAlaSer 844  
QY 2629 ACACGTG-----GACAAGCTTCGGCAGGCGGTGACAGAGCTGTACAGAGCGGTG 2676  
Db 845 AlaLeuGlyValGlyThrGlySerAlaArgGlnAspThrIleGlu----- 859  
QY 2677 CTGCAGATCGGGAAGGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCGCGGCC 2736  
Db 860 -----GluGluLeuGluGluArg-----ProPro 868  
QY 2737 CACAGGAGGTTCCGTGCCCTCGGCATCGGGAGAGGGCGCTGCCAGCCAGCACCC--- 2793  
Db 869 AlaLeuProAlaProProProValThrProAlaProThrProAlaProValSerThrHis 888

QY 2794 TCCGGGCTTCTGTGAGCCTCTGTGTGTGTGACACTGGGGCATCTCTCTACTGCTGCAGCCC 2853  
Db 889 AspAlaAlaLeuAlaGluLeuArgArgAspValArgAsnGluValGlnArgLeuGlnGln 908  
QY 2854 CCAGCTGGCTCTGTCTTGAGT-----GGGACTTGGCCC 2886  
Db 909 LysLeuGlyArgValGluGluLeuLeuThrMetLeuAlaAlaArgLeuGlyAlaGluPro 928  
QY 2887 CACCCCTCGTCCGGGGCCTCTCCCTCATGTGCACCCCTGGCCCTGGGGTCCCCCAGCGTCT 2946  
Db 929 GlyAspSerProGlyGlyAlaAla-----GlyAlaAlaSerAla 941  
QY 2947 CAGAGCTCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCC 3006  
Db 942 AlaGlyAlaAspGluProArgAlaProAla-----AlaPro 953  
QY 3007 CCTGCCTCAGGAGACCTCTGTCTGTAGCCAGCAGCCCTGCCTCCCTCTCTCTCTGAG 3066  
Db 954 ProAla-----AspLeuAlaAlaLeuThrArgLysArgArgSerLysAlaArgSerLys 971  
QY 3067 GAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGTGAGCCAGGCTGAGGCTACCAGCACTGGA 3126  
Db 972 GlyAlaAlaProGlnAlaProThr---ProThrThrProGlyAspAlaProSerSer--- 989  
QY 3127 GAGCCCCCAGGCTCAGGGGCGCTGGCC 3156  
Db 990 ---ProProGlyGlySerAlaGlyValAla 998  
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Q8JH78 PRELIMINARY; PRT; 1186 AA.  
AC Q8JH78;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
DE Erg K+ channel.  
GN ERG.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Langheinrich U., Wagner T.;  
RT "Zerg function in zebrafish."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF532865; AAM95975.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR000595; CNMP binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR Pfam; PF00027; CNMP binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; CNMP; 1.  
DR PROSITE; PS50042; CNMP\_BINDING\_3; 1.  
KW Ionic channel; Transmembrane.  
SQ SEQUENCE 1186 AA; 132279 MW; BCFF3F23551A8BD3 CRC64;

Alignment Scores: 2.36e-71 Length: 1186  
Pred. No.: 1405.50 Matches: 396  
Score:



Percent Similarity: 43.59% Conservative: 168			
Best Local Similarity: 30.60% Mismatches: 394			
Query Match: 23.08% Indels: 337			
DB: 13 Gaps: 36			
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Db	1	MetProValArgArgGlyHisValAlaLeuGlnAsnThrTyrrLeuAspThrIleileArg	20
QY	61	CGCTTCGACGGCACAGTAACCTTCGTGGCAACGCCAGGTGGCGGCTCTTC	120
Db	21	LysPheAspGlyGlnAsnArgLysPheLeuIleAlaAsnAlaGlnMetLysAsnCys--	39
QY	121	CCCGTGGTCTACTGCTGTATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC	180
Db	40	GlyIleileTyrCysAsnGluGlyPheCysGlnMetPheGlyPheSerArgAlaGluile	59
QY	181	ATGCAGCGGGCTGTCCCTGCTCCTCTTATGSGCCACACACAGTGAGCTCGTCCGC	240
Db	60	MetGlnGlnSerCysThrCysGlnPheLeuValGlyProGlyThrMetLysSerAlaLeu	79
QY	241	CAACAGATCCGCAAGCCCTGGACGAGCACAAAGGAGTTCAAGGCTGAGCTGATCCTGTAC	300
Db	80	GlyGlnLeuAlaGlnAlaLeuGlySerGluGluArgLysValGluileLeuTyrrTyrr	99
QY	301	CGGAAGAGCGGGCTCCCGTTCTGTGTCTCTCAGAGGATGATACCCATAAAGAAATGAGAAA	360
Db	100	SerLysGluGlyThrCysArgProCysLeuileAspValileProValLysAsnGluGlu	119
QY	361	GGGAGGTGGTCTCTTCTCTAGTCTCTCACAAAGGACATCAGCGAA--ACCAAGAACCGA	417
Db	120	GlyValValileMetPheileLeuAsnPheGlnGluLeuAspProSerMetLysLys	139
QY	418	GGGGC-----CCCACAGATGGAAGGAGACAGGTGGTGGCCGGCGCCGA	462
Db	140	GlyGlyLeuLysGlnArgMetAlaAsnSerTrpLeuArgAlaGlyGlnArgArgMet	159
QY	463	TATGGCCGGCACGATCCAA-AGGCTTCAATGCCAACCGGG--	503
Db	160	HisLeuArgMetProSerLeuArgVallysArgGlnProSerLeuProLysAspHisPhe	179
QY	503	-----	503
Db	180	GluGlyValValaspTyrrLeuGlnProSerHisGluGluValAlaLeuLysAspLeu	199
QY	503	-----	503
Db	200	GlnMetSerProAspSerCysLeuLysSerGluThrGlnAlaLeuIleGlnGlnThrPro	219
QY	504	-----GCGGAGCGGGCCGTGCTCTACCACTGTCCGG	536
Db	220	SerSerCysGluLeuSerProProSerArgProSerAspArgLeuGluPro-SerGl	239
QY	537	GCACCTGCAGAGCAGCCCAAGGCAAG-----CACAAAGCTCAATAAGGG--	582
Db	239	yProLeuLeuLysHisSerHisSerArgGluSerMetHisSerLeuArgArgAlaSerSe	259
QY	582	-----	582
Db	259	rLeuHisAspIleaspGlyMetArgAspGlnTrpSerAspLeuLysProSerAsnLeuAs	279
QY	583	-----GTGTTTGGGAGAAACCAAAC-----	603
Db	279	nSerThrSerAspSerAspLeuMetArgHisArgThrIleGlyArgIleProGlnValTh	299
QY	603	-----	603
Db	299	rIleSerPheGlySerAspArgLeuArgProProSerProThrGluileGluileAl	319
QY	603	-----	603

Db	319	aProSerLysIleLysAspArgSerGlnAsnValSerGluLysValThrGlnValThrGl	339
QY	604	-----TTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTC	638
Db	339	nValLeuSerLeuGlyAlaAspValLeuProGluTyrrLysLeuGlnAlaProArgIleHi	359
QY	639	GCCCTTCATCCTGTTGCACGTGGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCT	698
Db	359	sLysTrpThrIleLeuHisTyrrSerProPheLysAlaValTrpAspTrpIleileLeuLe	379
QY	699	CGCCACACTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGACGGGA	758
Db	379	uLeuValLeuTyrrThrAlaValPheThrProTyrrSerAlaAlaPheLeuLeuAsnGluGl	399
QY	759	GCCAGTCCGCCCGC-----GGCCCGCCCGCTCTGTGACCT	797
Db	399	nGluAspGluArgArgArgThrCysGlyTyrrThrCysAsnProLeuAsnValValAspLe	419
QY	798	GGCCGTGGAGGTCTCTTCATCCTTGACATTTGTGCTGAATTTCCGTACCACATTCGTGTC	857
Db	419	uValValAspValMetPheileileAspIleLeuileAsnPheArgThrThrTyrrValas	439
QY	858	CAAGTCGGCCAGGTGTTTGGCCCCAAAAGTCCATTTGCCTCCACTACCTACCCACCTG	917
Db	439	nHisAsnAspGluValValSerAsnProAlaArgIleAlaGlnHisTyrrPheLysGlyTr	459
QY	918	GTTCTGTGGATGTATCGCAGCGCTGCCCTTTGACCTGTACATGCCTTCAAG-----	972
Db	459	pPheLeuIleAspIleValAlaAlaIleProPheAspLeuLeu---IlePheArgSerGl	478
QY	973	-----GTCAACGTGTACTTCGGGGGCCCATCTGTGAAGACGGTGGCCCT	1016
Db	478	ySerAspGluProGlnThrThrThrLeuIleGly-----LeuLeuLysThrAlaArgLe	496
QY	1017	GCTGCGCCTGCTGCGCCTGCTTCCGCGGTGGACCGGTACTCGCAGTACAGCGCGGTGGT	1076
Db	496	uLeuArgLeuValArgValAlaArgLysLeuAspArgTyrrSerGluTyrrGlyAlaAlaVa	516
QY	1077	GCTGACACTGCTCATGGCCGTGTTTCGCCCTGCTCGCGCACTGGGTGCGCTGCTGGTT	1136
Db	516	lLeuPheLeuLeuMetCysThrPheAlaLeuileAlaHisTrpLeuAlaCysIleTrpTy	536
QY	1137	TTACATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTG-----CCTGAGATTGG	1190
Db	536	rAlaIleGlyAsnMetGlu--ArgThrSerSerAlaArgIleGlyGlyMetLysIleGl	555
QY	1191	CTGGCTGCAGGAGTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGCGGAGGCC	1250
Db	555	yTrpLeuAspAsnLeuAlaAspGlnIle-----	564
QY	1251	AGCTGGAGGAACAGCTCCGGCCAGAGTGCACAACTGCAGCAGCAGCGAGGCCAACGG	1310
Db	565	-----GlyLysGlnTyrrAsnAspSerAsnSer-----	573
QY	1311	GACGGGCTGGAGCTGCTGGCGGCCCGTCTGCTGCGCAGCGCTACATCACCCTCCTCTA	1370
Db	574	-----PheSerGlyProSerIleLysAspLysTyrrValThrAlaLeuTy	588
QY	1371	CTTCGCACTCAGCAGCCTCACCAGCGTGGCTTCGGCAACGTGTCCGCCAACACGGACAC	1430
Db	588	rPheThrPheSerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnPr	608
QY	1431	CGAGAAGATCTTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACGCGGTGGTGT	1490
Db	608	oGluLysIlePheSerIleCysValMetLeuileGlySerLeuMetTyrrAlaSerIlePh	628
QY	1491	TGGGAACGTGACGGCCATCATCCAGCGCATGTACCCCGCTTCTGTGTACCACAGCCG	1550
Db	628	eGlyAsnValSerAlaIleileGlnArgLeuTyrrSerGlyThrAlaArgTyrrHisThrGl	648
QY	1551	CACGCGGACCTGCGCGACTACATCCGCATCCACCGTATCCCCAACGCCCTCAAGCAGCG	1610
Db	648	nMetLeuArgValLysGluPheileArgPheHisGlnIleProGlyGlyLeuArgGlnAr	668







Db 360 LysLeuAspArgTyrLeuGluTyrGlyAlaAlaMetLeuIleLeuLeuLeuCysPheTyr 379  
QY 1102 GCCCTGCTCGCGCACTGGTGCCTCGCTCGCTTACATTGGCCAGCGGAGATCGAG 1161  
Db 380 MetLeuValAlaHisTrpLeuAlaCysIleTrpTyrSerIleGlyArgSerAspAlaAsp 399  
QY 1162 AGCAGCGAATCCGAGCTGCCTGAGATTGGCTGCAGGAGCTGGCCCGCGACTGGAG 1221  
Db 400 AsnGly-----IleGlnTyrSerTrpLeuTrpLysLeuAlaAsnValThrGln 415  
QY 1222 ACTCCCTACTACCTGGTGGCGGAGGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGAC 1281  
Db 416 SerProTyrSerTyrIleTrp----- 422  
QY 1282 AACTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGGCTGGAGCTGCTGGCGGCGCCGCTCG 1341  
Db 423 -----SerAsnAspThrGlyProGluLeuValAsnGlyProSer 435  
QY 1342 CTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTCACGCGTGGGC 1401  
Db 436 ArgLysSerMetTyrValThrAlaLeuTyrPheThrMetThrCysMetThrSerValGly 455  
QY 1402 TTCGGCAACGTGTCGCGCAACACCGGACACCGAGAGATCTTCTCCATCTGCACCATGCTC 1461  
Db 456 PheGlyAsnValAlaAlaGluThrAspAsnGluLysValPheThrIleCysMetMetIle 475  
QY 1462 ATCGGCGCCCTGATGCACGCGGTGGTGTGTTGGGAACGTGACGGCCATCATCCAGCGCATG 1521  
Db 476 IleAlaAlaLeuLeuTyrAlaThrIlePheGlyHisValThrThrIleIleGlnMet 495  
QY 1522 TAGCGCGCGCTTCTGTACCAACAGCGCGCACCTGGCGACCTACATCCGCATC 1581  
Db 496 ThrSerAlaThrAlaLysTyrHisAspMetLeuAsnAsnValArgGluPheMetLysLeu 515  
QY 1582 CACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACTGGGCG 1641  
Db 516 HisGluValProLysAlaLeuSerGluArgValMetAspTyrValValSerThrTrpAla 535  
QY 1642 GTGAACAATGGCATCGACACCAACCGAGCTGTGTCAGAGCCTCCCTGACGAGCTGGCGCA 1701  
Db 536 MetThrLysGlyLeuAspThrGluLysValLeuAsnTyrCysProLysAspMetLysAla 555  
QY 1702 GACATCGCCATGCACCTGCACAAGGAGGTCTG-----CAGCTGCCACTGTTTGGCGGCC 1758  
Db 556 AspIleCysValHisLeuAsnArgLysValPheAsnGluHisProAlaPheArgLeuAla 575  
QY 1759 AGCGCGGCTGCCTGGCGCACTGTCTCTGCGCCCTGCGGCCCGCTTCTGACGCGCGGC 1818  
Db 576 SerAspGlyCysLeuArgAlaLeuAlaMetHisPheMetMetSerHisSerAlaProGly 595  
QY 1819 GAGTACCTCATCCACCAAGCGATGCCCTGCAGGCCCTCTACTTTGTCTGCTGGCTCC 1878  
Db 596 AspLeuLeuTyrHisThrGlyGluSerIleAspSerLeuCysPheIleValThrGlySer 615  
QY 1879 ATGGAGGTGCTCAAGGTGGCACCGTGTCTGCCATCTAGGGAAGGCGACCTGATCGGC 1938  
Db 616 LeuGluValIleGlnAspAspGluValValAlaIleLeuGlyLysGlyAspValPheGly 635  
QY 1939 TGTGAGCTGCCCGGCGGAGCAGGTGGTAAAGGCCAATGCCGACGTGAAGGGGCTGACG 1998  
Db 636 AspGlnPheTrpLysAspSerAlaValGlyGlnSerAlaAlaAsnValArgAlaLeuThr 655  
QY 1999 TACTGCGTCTGCAGTGTCTGCAGTGGCTGGCTGGCCCTGCACGACGCTTGGCTGTACCCC 2058  
Db 656 TyrCysAspLeuHisAlaIleLysArgAspLysLeuLeuGluValLeuAspPheTyrSer 675  
QY 2059 GAGTTTGGCCCGCTTCACTGCTGGCCCTCCGAGGGGAGCTCAGCTACAACTGGGTGCT 2118  
Db 676 AlaPheAlaAsnSerPheAlaArgAsnLeu-----ValLeuThrTyrAsnLeu 691  
QY 2119 GGGGAGGCTCTGCAGAGGTGGACACCGAGCTCCCTGAGCGGCGACAATACCCTTATGTCC 2178

Db 692 -----ArgHisArg 694  
QY 2179 ACGTGGAGGAAGAGACAGATGGGGAGCAGGGCCCCACGGTCTCCCCAGCCCCAGCT 2238  
Db 695 LeuIlePheArgLysValAlaAspValLysArgGluLysGluLeuAlaGluArgArgLys 714  
QY 2239 GATGAGCCCTCCAGCCCCCTGCTGTCCCTGGCTGCACCTCCTCATCCTCAGTGCCTAAG 2298  
Db 715 AsnGluProGlnLeuProGln-----AsnGlnAspHisLeuValArgLys 729  
QY 2299 CTGCTATCCCCACGTCGAACAGCACCCCGGCTCGTCTAGGTGGCAGAGGAGGCCAGGC 2358  
Db 730 IlePheSerLysPheArgArgThrProGlnValGlnAlaGlySerLysGluLeuValGly 749  
QY 2359 AGGCGAGGGCTTTGAAGGCTGAGGCTGGC----- 2388  
Db 750 GlySerGlyGlnSerAspValGluLysGlyAspGlyGluValGluArgThrLysValPhe 769  
QY 2389 CCCTCTGCTCCCCACCGGCCCTAGAGGGGTACGGCTGCCCCCATGCCATGG----- 2442  
Db 770 ProLysAlaProLysLeuGlnAlaSerGlnAlaThrLeuAlaArgGlnAspThrIleAsp 789  
QY 2443 -----AATGTGCCCCCAGATCTGAGCCCCAGGGTAGTAGTGGCATT 2484  
Db 790 GluGlyGlyGluValAspSerSerProProSerArgAspSerArgValVal-----Ile 807  
QY 2485 GAAGACGGCTGTGGCTCGGACCGCCAAAGTTCTTCTCCGCGTGGGCCAGTCTGGCCCG 2544  
Db 808 GluGlyAlaAlaValSer-----SerAlaThrValGlyProSerProPro 822  
QY 2545 GAATGTAGCAGCAGCCCC-----TCCCTGGACACAGAGCGGC 2583  
Db 823 ValAlaThrThrSerSerAlaAlaAlaGlyAlaGlyValSerGlyProGlySerGly 842  
QY 2584 -----CTGCTCACT----- 2592  
Db 843 GlyThrValValAlaIleValThrLysAlaAspArgAsnLeuAlaLeuGluArgGluArg 862  
QY 2593 ---GTTCCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG---CTTCGG 2646  
Db 863 GlnIleGluMetAlaSerSerArgAlaThrThrSerAspThrTyrAspThrGlyLeuArg 882  
QY 2647 CAGGCGGTGACAGAGCTGTGACAGCAG-----GTGCTGCAGATG----- 2685  
Db 883 GluThrProProThrLeuAlaGlnArgAspLeuIleAlaThrValLeuAspMetLysVal 902  
QY 2686 -----CGGAAGACTGCAGTCACTTCGCCAGGCTGTGCA----- 2720  
Db 903 AspValArgLeuGluLeuGlnArgMetGlnGlnArgIleGlyArgIleGluAspLeuLeu 922  
QY 2721 -----GCTTGTCTGGCGCCCCACAGGGAGGTCCGTGCCCTCG--- 2759  
Db 923 GlyGluLeuValLysArgLeuAlaProGlyAlaGlySerGlyGlyAsnAlaProAspAsn 942  
QY 2760 -----GGCATCGGAGAGGG 2774  
Db 943 SerSerGlyGlnThrThrProGlyAspGluIleCysAlaGlyCysGlyAlaGlyGlyGly 962  
QY 2775 GCCGTGCCCGCCAGC-----ACCTCCGGGCTTCTGCAGCCTCTGTGTGTGGA 2822  
Db 963 GlyThrProThr-ThrGlnAlaProProThrSerAlaValThrSerPro-----ValAs 980  
QY 2823 CACT----- 2826  
Db 980 pThrValIleThrIleSerSerProGlyAlaSerGlySerGlyThrGlyAlaGln 1000  
QY 2827 -----GGGGCATCCTCCTACTGCTGCAGCCCCCAGCTGGCTCTGT 2867  
Db 1000 yAlaGlySerAlaValAlaGlyAlaGlyGlyAlaGlyLeuLeuAsnProGlyAlaThrVa 1020  
QY 2868 CTTGAGTGGGACTTGGCCCCACCTCGTCCGGGGCCTCCTCCCTCATG----- 2916  
Db 1020 lValSerSerAlaGlyGlyAsn-----GlyLeuGlyProLeuMetLeuLysLysAr 1037







Q9XXY7  
AC Q9XXY7; PRELIMINARY; PRT; 956 AA.  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE EAG K+ channel EGL-2.  
GN EGL-2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N2;  
RA Weinshenker D., Wei A., Salkoff L., Thomas J.H.;  
RT "Regulation of cell excitability by egl-2, an EAG-like K+ channel  
RT blocked by a tricyclic antidepressant in Caenorhabditis elegans.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF130443; AAD28468.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004601; F:peroxidase activity; IEA.  
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR GO; GO:0006979; P:response to oxidative stress; IEA.  
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.  
DR InterPro; IPR000595; cNMP binding.  
DR InterPro; IPR003967; Erg channel.  
DR InterPro; IPR005821; Ion trans.  
DR InterPro; IPR001622; K+channel pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc C.  
DR InterPro; IPR000014; PAS domain.  
DR InterPro; IPR002016; Peroxidase.  
DR Pfam; PF00027; cNMP binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; cNMP; 1.  
DR SMART; SM00086; PAC; 1.  
DR SMART; SM00091; PAS; 1.  
DR TIGRFAMs; TIGR00229; sensory box; 1.  
DR PROSITE; PS50042; cNMP BINDING\_3; 1.  
DR PROSITE; PS50113; PAC; 1.  
DR PROSITE; PS50112; PAS; 1.  
DR PROSITE; PS00435; PEROXIDASE\_1; 1.  
KW Ionic channel; Transmembrane.  
SQ SEQUENCE 956 AA; 108091 MW; E998B7F212805273 CRC64;  
  
Alignment Scores:  
Pred. No.: 3.16e-63 Length: 956  
Score: 1261.50 Matches: 342  
Percent Similarity: 47.51% Conservative: 182  
Best Local Similarity: 31.01% Mismatches: 357  
Query Match: 20.72% Indels: 222  
DB: 5 Gaps: 35  
  
US-09-965-830-1\_COPY\_6\_3257 (1-3252) x Q9XXY7 (1-956)  
  
QY 1 ATGCCG---GCCATGGGGGCTCTCTGGCGCTCAGAACACCTTCTCGGACACCATCGCT 57  
Db 1 MetProValGlyLysArgGlyLeuValAlaProGlnAsnThrPheLeuGluAsnValile 20  
  
QY 58 ACGCGCTTCAGCGGCACGCACAGTAACCTTCGTGGGCAACGCCAGGTGGCGGGCTC 117  
Db 21 ArgArgCysAsnAsnAlaAspThrSerPheilleLeuAlaAsnAlaGlnValValAsp--- 39  
  
QY 118 TTCCCCGCTGCTACTGCTCTGATGGCTTCTGTGACCTCAGGGGTTCTCCGGGCTGAG 177  
Db 40 TyrProilleValTyrCysAsnAspGlyPheSerLysLeuValGlyTyrThrArgAlaGlu 59

QY 178 GTCATGCAGCGGGGCTGTGCCTGCTCCTTCCCTTTATGGGCACACACAGTGAGCTCGTC 237  
Db 60 IleMetGlnLysProCysSerLeuAlaPheMetHisGlyGluHisGlyGluValGlySer 79  
  
QY 238 CGCAACAGATCCGCAAGGCGCTGGACGAGCACAAAGGAGTTCAAGGCTGAGCTGATCCTG 297  
Db 80 LeuGlnLysMetGlnGluAlaLeuGluAsnAlaArgThrGluGlnAlaGluileGlyLeu 99  
  
QY 298 TACCGGAAGAGCGGGCTCCCGTCTTGGTGTCTCCTGGATGTATACCCATAAAGAATGAG 357  
Db 100 CysLysLysAsnLysThrProilleTrpLeuLeuValHisLeuAlaProilleLysAsnHis 119  
  
QY 358 AAAGGGAGGTGGCTCTCTCTTAGTCTCTCACAGGACATCAGCGAAACCAAG----- 411  
Db 120 LysAspAlaValvalLeuTyrLeuCysGlnPheLysAspilleThrProLeuLysGlnPro 139  
  
QY 412 -----AACCGAGGGGGCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGC 459  
Db 140 LeuAspAspGluAsnAsnLysGlyLeuSerArgilleLeuGlnileAla----- 155  
  
QY 460 CGATATGGCGGCACGATCCAAAGGCTTCAATGCCAACCCGGCGGAGCGCGGCGCTG 519  
Db 156 ArgilleAlaLysSerLysGlnGln---PheAsnGlnilleGluThrLysAsp----- 171  
  
QY 520 CTCTACCACCTGTCCGGGCACCTGCAGAAGCAGCGCCAAAGGCAAGCACAAAGCTCAATAAG 579  
Db 172 -----LeuHisLysSerPro---GlyAsnThrSerSerAsn--- 182  
  
QY 580 GGGGTGTTTGGGGAGAAACCAAC-----TTGCTGAGTACAAAGTAGCC 624  
Db 183 -----PheAsnGlnValMetAsnLeuGlyGlyAspMetLeuProGlnTyrArgGlnGlu 200  
  
QY 625 GCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGCACGTGAGAGCCACCTGGAT 684  
Db 201 ThrProLysThrSerProHisilleLeuHisTyrSerSerPheLysThrileTyrAsp 220  
  
QY 685 GGCTTCATCCTGCTGCCACACTCTATGTGGTGTCTACTGTGCCCTACAGCGTGTGT--- 741  
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QY 742 -----GTGACACAGCAGCGGAGCCCGAGTCCCGCGCGC 774  
Db 241 LysAsnSerLeuArgPropheTyrLeuilleSerSerArgGluAsnProGlyGlyIle 260  
  
QY 775 GGCGCGCGCGCTGTGTGACCTGGCGCTGGAGGTCCTCTTCATCCTTCACATTGTGCTG 834  
Db 261 AspSerValAlaLeuMetAspSerilleValAspValillePhePheAlaAspilleLeu 280  
  
QY 835 AATTTCCGTACACATTCGTGTCCAAGTCGGCGCCAGGTGGTGTTCGCCCAAAGTCCATT 894  
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QY 895 TGCCTCCACTACGTACACACCTGGTTCCTGCTGGATGTATCGCAGCGCTGCCCTTTGAC 954  
Db 301 ArgGlnAsnTyrPheLysSerTrpPheuilleAspLeuLeuSerCysLeuProTyrAsp 320  
  
QY 955 CTGCTACATGCGCTTCAAG-----GTCAACGTGTACTTCGGGGCCCATCTG 999  
Db 321 IlePheTyrMetPheLysArgAspAspGluArgilleGlySerLeuPheSerAla----- 338  
  
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Db 359 GluTyrGlyAlaAlaThrLeuLeuLeuLeuCysAlaTyrValilleValAlaHistrp 378  
  
QY 1120 GTCGCTCGCTCTGGTTTTACATTTGGCCAGCGGGAGATC-----GAGAGCAGCGAATCC 1173  
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QY	1174	GAGCTGCTGAGATTGGCTGGCTGCAGGAGCTGGCCCGCGACTGGAGACTCCCTACTAC	1233
Db	399	AlaLeuProAsp---GlyTrpLeuTrpLysLeuSerAsnAspLeuArgGlnHisTyr---	416
QY	1234	CTGGTGGCCGAGGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGAACAATGCAGCAGC	1293
Db	417	-----AsnIleProLeu	420
QY	1294	AGCAGCGAGGCCAACGGACCGGGCTGGAGCTGCTGGGGCGCCCGCTGCGCAGCGCC	1353
Db	421	SerAsnLysThrThr-----LeuValGlyGlyProSerArgThrSerAla	435
QY	1354	TACATCACCTCCTCTACTTTCGCACTCAGCAGCCTCACACGCGTGGGCTTCGGCAACGTG	1413
Db	436	TyrIleSerSerLeuTyrTyrThrMetSerCysMetSerThrValGlyPheGlyAsnIle	455
QY	1414	TCCGCCAACACGGACACCGAGAAGATCTTTCATCTGCACCATGTCATCGCGGCCCTG	1473
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QY	1474	ATGCACGCGGTGGTGTGGGAACGTGACGGCCATCATCCAGCGCATGTFACGCCCGCCG	1533
Db	476	LeuTyrAlaAlaIlePheGlyHisMetThrThrIleIleGlnGlnMetThrSerSerThr	495
QY	1534	TTTCTGTACCACGCGCACGCGCGACCTGCGCGACTACATCCGCATCCACCGTATCCCC	1593
Db	496	ValArgTyrHisGluMetIleSerAsnValArgGluPheIleLysLeuGlnGluIlePro	515
QY	1594	AAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGGGCGGTGAACAATGGC	1653
Db	516	LysGluLeuAlaGluArgValMetAspTyrValValSerThrTrpAlaMetThrLysGly	535
QY	1654	ATCGACACCACCGAGCTGCTGCAGAGCCCTCCCTGACGAGCTGCGCGCAGACATCGCCATG	1713
Db	536	IleAspThrAlaLysValLeuGlyTyrCysProLysAspMetLysAlaAspIleCysVal	555
QY	1714	CACCTGCACAAGGAGGTCTCTG---CAGCTGCCACTGTTTGAGCGCGCCAGCGCGGTGC	1770
Db	556	HisLeuAsnArgLysValPheAsnGluHisSerCysPheArgLeuAlaSerAspGlyCys	575
QY	1771	CTGCGGGCACTGTCTCTGGCCCTGCGGCCCGCCCTTCTGCACGCCGGCGGAGTACCTCATC	1830
Db	576	LeuArgSerLeuAlaMetPheLeuGluLeuAsnHisAlaAlaProGlyAspLeuLeuTyr	595
QY	1831	CACCAAGCGCATGCCCTGCAGGCCCTCTACTTTGTCTGCTCTGGCTCCATGAGGTGCTC	1890
Db	596	HisThrGlyGluSerValAspAlaLeuTrpPheValValSerGlySerLeuGluValIle	615
QY	1891	AAGGTGGCACCGTGTCTGCCATCTTAGGGAAGGCGGACCTGATCGGCTGTGAGCTGCC	1950
Db	616	GlnAspAspGluValValAlaIleLeuGlyLysGlyAspValPheGly-----	631
QY	1951	CGCGCGGAGCAGGTGGTAAGGCCAAT-----GCGGACGTGAAG	1989
Db	632	-----AspGluPheTrpLysAlaAsnGlySerThrGlyGlnSerAlaAlaAsnValArg	649
QY	1990	GGGTGACGTACTGCGTCCGTGAGTGTCTGCAGCTGGCTGCGCAGCAGCGCTTGGC	2049
Db	650	AlaLeuThrTyrSerAspLeuHisMetIleLysLysAspLysLeuMetAspValLeuAsp	669
QY	2050	CTGTACCCCGAGTTTGCCCGCGCTTCAGTGTGGCTCCGAGGGGAGCTCAGCTACAAC	2109
Db	670	PheTyrLysAlaPheAlaAsnSerPheAlaArgAsnMet-----ThrLeuThrTyrAsn	687
QY	2110	CTGGGTGTGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGCGCGCACAATACC	2169
Db	688	Leu-----ThrHisArgMetLysPheArgLys	696
QY	2170	CTTATGTCCACGCTGGAGGAGACGACAGATGGGAGCAG-----	2211
Db	697	ValAlaAspValLysArgGluLysGluLeuAspAlaLysArgLysAsnGluLysLeuThr	716
QY	2212	-----GGCCCC	2217

Db		717	LeuProAsnAspHisProIleArgLysLeuLeuPheArgMetArgGluArgHisGlyPro	736
QY		2218	ACGGTCTCCAGCCCCCA-----GCTGATGAGCCTCCAGCCCCCTGTGTCTCCCTGGC	2271
Db		737	ArgIlePheProSerProMetPheAlaAsp-	750
QY		2272	TGCACCTCTCATCTCAGCTGCCAAGTGCTATCCCACGTCGAACAGCACCCCGGCCT	2331
Db		751	LeuLysLysSerThrGluIleSerArgIleSerSerLeuHisSerMetIle-	767
QY		2332	CGTCTAGGTGGCAGAGGGAGGCCAGGCAGGGCAGGGCTTTGAAGGCTGAGGTGGCCCC	2391
Db		768	-----AspGluThrGlyGlyGlySerSerTyrValLysSerProArg	782
QY		2392	TCTGTCTCCCCCAGGGCCCTAGAGGGGCTACGGGTGCCCCCATGCCATGGAATGTGCC	2451
Db		783	SerLysProLysArg-	788
QY		2452	CCAGATCTGAGCCCCCAGGGTAGTAGATGGCATTTGAAGCGGTGTGGCTCGGACCAGC--	2509
Db		789	ProLeuMetLysArgGlnThrValAsp-----GluAsp-AlaLeuSerArgThrSerTr	806
QY		2510	-----CCAAGTTCTCTTCCGGGTGGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCC	2562
Db		806	pGlyMetAspLysLysAspArgGluTrpSerSerLeuSerAsn-	820
QY		2563	TCCCCTGGACCAGAGAGCGGCTGCTCACTGTTCCTCCATGGGCCCCAGCGAGGCAAGAAAC	2622
Db		821	-----IleLysThrGluMe	825
QY		2623	ACAGACACACTGGACAAGCTTCGGCAGGCGG-----TGACAGAGCTGTACAGAGAG	2673
Db		825	tlysSerLysPheAspilelleGlyGluArgLeuThrIlelleGluGlnIleAsnSerAr	845
QY		2674	GTGCTGCAGATGCGGGAAGCACTGCAGTCACCTTCGCCAGGCTGTGCAGCTTGTCTCTGGCG	2733
Db		845	g-LeuAlaLeuLeuGluArgValLeuIleGlyAsnAsnGly-	858
QY		2734	CCCCACAGGAGGTCCTGTCCTCGGGCATCGGGAGAGGGCCGTGCCAGCCAGCACC	2793
Db		859	-----GlyAlaAsnThrProSerThrMetProValGlySerPhe-	871
QY		2794	TCCGGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGGCATCTCTACTGCTGCAGCCC	2853
Db		872	-----SerAlaLeuAsnGluSerGlyAsn-----ArgLeuThrLeuAspAlaAlap	887
QY		2854	CCAGCTGGCTCTGTCTTGTAGTGGGACTTGGCCCCACCCCTCGTCGGGGCCCTCCTCCCCCTC	2913
Db		887	roValAlaArgSerValSerTrp-----SerGluGlnHisGlnProH	901
QY		2914	ATGGCACCCCTGGCCCTGGGGTCCCCCAGCGTCTCAGAGCTCCCCCTGGCCTCGAGCCACA	2973
Db		901	iSTrpGlnArgThrSerThrValProProLeuArgGluLeuGluAlaGlyGluTrpGlu-	920
QY		2974	GCTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAG	3033
Db		921	-----ProProIleArgGluPro-ThrProAsn	929
QY		3034	CCCAGCACCCCTGCCTCCCCCTCTCTCTCTGTGAGGAAGGGCTAGGACTGGGCCCGCAGAG	3093
Db		930	ProSerThrSerSerSerArgValProHisIleGlnAsnAspGluAspGlyGluAlaArg	949
QY		3094	CCT 3096	
Db		950	Pro 950	
 RESULT 12 O44164 PRELIMINARY; PRT; 956 AA.				
ID	O44164			
AC	O44164;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)			





Db 339 LeuLysValValArgLeuLeuArgLeuGlyArgValAlaAlaArgLysLeuAspAsnTyrLeu 358  
QY 1060 CAGTACAGCGCGTGGTGTGCTGACACTGCTCATGGCCGTGTTGCGCCTGCTCGCGCACTGG 1119  
Db 359 GluTyrGlyAlaAlaThrLeuLeuLeuLeuLeuCysAlaTyrValIleValAlaHisTrp 378  
QY 1120 GTCGCTGCTGCTGTTTACATTGGCCAGCGGAGATC-----GAGAGCAGCGAATCC 1173  
Db 379 LeuAlaCysValTrpPheTrpIleGlyAspSerGluValArgLeuLysMetAspAsnLeu 398  
QY 1174 GAGCTGCCTGAGATTGGCTGGCTGCAGGAGTGGCCCGCGACTGGAGACTCCCTACTAC 1233  
Db 399 AlaLeuProAsp---GlyTrpLeuTrpLysLeuSerAsnAspLeuArgGlnHisTyr--- 416  
QY 1234 CTGGTGGCGCGAGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGC 1293  
Db 417 -----AsnIleProLeu 420  
QY 1294 AGCAGCGAGGCCAACGGGACGGGGCTGGAGCTGTGGGGCGGCCGTGCGTGCGCAGCGCC 1353  
Db 421 SerAsnLysThrThr-----LeuValGlyGlyProSerArgThrSerAla 435  
QY 1354 TACATCACCTCCCTCTACTTCGCACCTCAGCAGCCTCACGAGCGTGGGCTCGGCAACGTG 1413  
Db 436 TyrIleSerSerLeuTyrTyrThrMetSerCysMetSerThrValGlyPheGlyAsnIle 455  
QY 1414 TCCGCCAACACGGACACCGAGAGATCTTCTCCATCTGCACCATGTCTATCGGCGCCCTG 1473  
Db 456 AlaSerAsnThrAspAsnGluLysIlePheGlyValCysMetMetIleIleSerAlaLeu 475  
QY 1474 ATGCACGCGGTGGTGTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCGC 1533  
Db 476 LeuTyrAlaAlaIlePheGlyHisMetThrThrIleIleGlnGlnMetThrSerSerThr 495  
QY 1534 TTTCTGTACACAGCGCGCAGCGGACCTGGCGGCACTACATCCGCATCCACCGTATCCCC 1593  
Db 496 ValArgTyrHisGluMetIleSerAsnValArgGluPheIleLysLeuGlnGluIlePro 515  
QY 1594 AAGCCCTCAAGCAGCGCATGCTGGAGTACTTCAGGCCACCTGGGCGGTGAACAATGGC 1653  
Db 516 LysGluLeuAlaGluArgValMetAspTyrValValSerThrTrpAlaMetThrLysGly 535  
QY 1654 ATCGACACCCAGCTGTGTGAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATG 1713  
Db 536 IleAspThrAlaLysValLeuGlyTyrCysProLysAspMetLysAlaAspIleCysVal 555  
QY 1714 CACCTGCACAAGGAGTCTGTG---CAGCTGCCACTGTTGAGCGCGCCAGCGCGGCTGC 1770  
Db 556 HisLeuAsnArgLysValPheAsnGluHisSerCysPheArgLeuAlaSerAspGlyCys 575  
QY 1771 CTGCGGGCACTGTCTCTGCGCCCTGCGGCCCGCCCTTCTGCACGCCGGCGAGTACTCATC 1830  
Db 576 LeuArgSerLeuAlaMetPheLeuGluLeuAsnHisAlaAlaProGlyAspLeuLeuTyr 595  
QY 1831 CACCAAGCGGATGCCCTGAGGCCCTCTACTTTGTCTGCTCTGCTCCATGGAGTGCTC 1890  
Db 596 HisThrGlyGluSerValAspAlaLeuTrpPheValValSerGlySerLeuGluValIle 615  
QY 1891 AAGGGTGGCACCCTGTCTCGCATCTAGGAAGGGCGACCTGATCGGCTGTGAGCTGCC 1950  
Db 616 GlnAspAspGluValValAlaIleLeuGlyLysGlyAspValPheGly----- 631  
QY 1951 CGGCGGGAGCAGGTGGTAAAGGCCAAT-----GCCACGTGAAG 1989  
Db 632 -----AspGluPheTrpLysAlaAsnGlySerThrGlyGlnSerAlaAlaAsnValArg 649  
QY 1990 GGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2049  
Db 650 AlaLeuThrTyrSerAspLeuHisMetIleLysLysAspLysLeuMetAspValLeuAsp 669  
QY 2050 CTGTACCCCGAGTTTGGCCCGCTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2109  
Db 670 PheTyrLysAlaPheAlaAsnSerPheAlaArgAsnMet-----ThrLeuThrTyrAsn 687

QY 2110 CTGGGTGTGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGGGCGACAATACC 2169  
Db 688 Leu-----ThrHisArgMetLysPheArgLys 696  
QY 2170 CTTATGTCCACGCTGGAGGAGAGAGAGACAGATGGGGAGCAG----- 2211  
Db 697 ValAlaAspValLysArgGluLysGluLeuAspAlaLysArgLysAsnGluLysLeuThr 716  
QY 2212 -----GGCCCC 2217  
Db 717 LeuProAsnAspHisProIleArgLysLeuLeuPheArgMetArgGluArgHisGlyPro 736  
QY 2218 ACGGTCTCCCGACGCCCA-----GCTGATGAGCCCTCCAGCCCCCTGTCTCCCTGGC 2271  
Db 737 ArgIlePheProSerProMetPheAlaAsp-----IleGluLysGly 750  
QY 2272 TGCACCTCCTCATCTCAGTGCACAGCTGCTATCCCCACGTGGAACAGCACCCCGCCT 2331  
Db 751 LeuLysLysSerThrGluIleSerArgIleSerSerLeuHisSerMetIleAspGluThr 770  
QY 2332 CGTCTAGTGGC-----AGAGGAGGCGCAGCAGGCGAGGGCT 2370  
Db 771 GlyGlyGlySerSerTyrValLysSerProArgSerLysProLysArgProProLeu 790  
QY 2371 TTGAAGGCTGAG--GCTGGCCCTCTGCTCCCCCACGGGCCCTAGAGGGCTACGGCTG 2427  
Db 791 MetLysArgGlnThrValAspGluAspAlaLeuSerArgThrSerTrpGlyMetAspLys 810  
QY 2428 CCCCCCATGCCATGG-----AATGTGCCCCCAT----- 2457  
Db 811 LysAspArgGluTrpSerSerLeuSerAsnIleLysThrGluMetLysSerLysPheAsp 830  
QY 2458 -----CTGAGCCCC 2466  
Db 831 IleIleGlyGluArgLeuThrIleIleGluGlnIleAsnSerArgLeuAlaLeuGlu 850  
QY 2467 AGGTAGTAGTGCATTTGAAGACGGCTGTGGC-----TCGGACCGCCCAAGTTCTCT 2520  
Db 851 ArgValLeuIleGlyAsnAsnGlyGlyAlaAsnThrProSerThrMetProValGlySer 870  
QY 2521 TTC---CGCTGGCGCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAG 2577  
Db 871 PheSerAlaLeuAsnGluSerGlyAsnArgLeuThrLeuAspAlaAlaProValAlaArg 890  
QY 2578 AGCGGCTGTCTACTGTTCCTCCATGGGCCCGCAGCGAGCAAGGAACACAGACACTGGAC 2637  
Db 891 SerValSerTrpSerGluGlnHisGlnProHisTrpGlnArg---ThrSerThrValPro 909  
QY 2638 AAGCTTCGGCAGCGGTGACAGAGCTGTTCAGAGCAGGTGTGCAGATCGCGGAAGACTG 2697  
Db 910 ProLeuArgGlu-----LeuGluAlaGlyGluTrpGluProIleArgGlu----- 925  
QY 2698 CAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTGGCGCCCCACAGGAGGGTCCGTGCCCT 2757  
Db 926 -----ProThrPro 928  
QY 2758 CGGGCATCGGAGAGGGCGCTGCCAGCCAGCCTCCGGGCTTCTGCAGCCTCTGTGT 2817  
Db 929 Asn-----ProSerThrSerSerArgValProHisIleGln 941  
QY 2818 GTGGACACTGGGGCATCCTCTCTACTGTGCCTGCAGCCCCCA 2856  
Db 942 IleAspGluAspGlyGluAla-----ArgProPro 951

RESULT 13

Q86U57  
ID Q86U57 PRELIMINARY; PRT; 772 AA.  
AC Q86U57;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Potassium voltage-gated channel, subfamily H (Eag-related), member



QY 1258 GGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGGACCGGACCGGG 1317  
Db 482 ---AsnSerSerGly----- 485  
QY 1318 CTGGAGCTGCTGGCGGCCGCTCGCTGCGCAGCGCCTACATACCTCCCTCTACTTCGCA 1377  
Db 486 -----LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThr 502  
QY 1378 CTCAGCAGCTCACCGCGTGGCTTCGGCAACGTTGCGCCACACCGGACACCGAGAAG 1437  
Db 503 PheSerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLys 522  
QY 1438 ATCTTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACGCGGTGGTGTGGGAAC 1497  
Db 523 IlePheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsn 542  
QY 1498 GTGACGGCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCCGACCGGC 1557  
Db 543 ValSerAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeu 562  
QY 1558 GACCTGCGGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTG 1617  
Db 563 ArgValArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlu 582  
QY 1618 GAGTACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCGAGCTGCTGCAG 1677  
Db 583 GluTyrPheGlnHisAlaTyrSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLys 602  
QY 1678 AGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCAAGGAGGTCTCTGCAG 1737  
Db 603 GlyPheProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuGln 622  
QY 1738 ---CTGCCACTGTTGAGCGCGCCAGCGGCTGCCTGCGGCACTGCTCTGGCCCTG 1794  
Db 623 HisCysLysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPhe 642  
QY 1795 CGGCCCGCTTCTGCACGCCGCGGAGTACCTCATCCACCAAGCGGATGCCCTGCAGGCC 1854  
Db 643 LysThrThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAla 662  
QY 1855 CTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTCTCGCCATC 1914  
Db 663 LeuTyrPheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIle 682  
QY 1915 CTAGGGAAG-----GGCGACCTGATCGGCTGTGAGCTGCCCGGCGGAGGTGGTA 1968  
Db 683 LeuGlyMetGlyTyrGlyAlaGlyThrGlyLeuGluMetPro----- 696  
QY 1969 AAGGCCAATGCCGACCTGAAGGGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTG 2027  
Db 697 -----SerAlaAlaSerArgGlyAlaSerLeuLeuAsnMetGlnSerLeuGlyLeuTyr 714  
QY 2028 ---TGGCCTGCACGACAGCTTGGCTGTACCCCGAGTTTGCCCGGCTTCACTGCTGG 2084  
Db 715 ThrTrpAspCysLeuGlnGlyHisTrpAlaProLeuIle-----HisLeuAsnSerGly 732  
QY 2085 CCTCCGAGGGAGCTCAGCTACACCTGGTGTGGGAGGCTCTGCAGA-----GGT 2138  
Db 733 ProProSerGlyAlaMetGluArgSerProThrTrpGlyGluAlaAlaGluLeuTrpGly 752  
QY 2139 GGACACACAGCTC 2150  
Db 753 SerHisIleLeu 756

RESULT 14  
Q18325

ID Q18325 PRELIMINARY; PRT; 791 AA.  
AC Q18325; Q9NG78;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C30D11.1 protein (HERG-like potassium channel).  
GN C30D11.1.

OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mortimore B.J.;  
RL Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Thomas J.H., Reiner D.J., Newton E.M.;  
RT "C. elegans unc-103 encodes a HERG-like potassium channel.";  
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Lloyd C.R.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; Z35596; CAA84644.2; -.  
DR EMBL; Z46787; CAA84644.2; JOINED.  
DR EMBL; AF257518; AAF68999.1; -.  
DR EMBL; Z46787; CAC42257.1; -.  
DR EMBL; Z35596; CAC42257.1; JOINED.  
DR PIR; T19579; T19579.  
DR HSSP; P03020; 2CGP.  
DR WormPep; C30D11.1; CE27805.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR InterPro; IPR000595; cNMP\_binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_nlg.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR Pfam; PF00027; cNMP\_binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; cNMP; 1.  
DR PROSITE; PS50042; cNMP\_BINDING\_3; 1.  
KW Ionic channel; Transmembrane.  
SQ SEQUENCE 791 AA; 88518 MW; 5BF65AF56C380BEA CRC64;

Alignment Scores:

pred. No.: 3,36e-53 Length: 791  
Score: 1084.00 Matches: 251  
Percent Similarity: 56.29% Conservative: 98  
Best Local Similarity: 40.48% Mismatches: 197  
Query Match: 17.80% Indels: 74  
DB: 5 Gaps: 17

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x Q18325 (1-791)

QY 604 TTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTGCTGCACTGTGGG 663  
Db 58 LeuProGluTyrLysLeuGlnProThrArgIleHisCysThrIleValHisTyrSer 77  
QY 664 GCACTGAGAGCCACCTGGGATGGTTCATCCTGCTGCCACACTCTATGTGGTGTCACT 723  
Db 78 ProPheLysAlaValTrpAspTrpIleIleLeuLeuValIleTyrThrAlaValPhe 97  
QY 724 GTGCCCTACAGCGTGTGTGTGAGCAGCAGCAGCGGAG-----CCAGT 765  
Db 98 ThrProTyr---ValAlaAlaPheLeuLeuArgGluLeuGlnAspThrAlaLysLysSer 116  
QY 766 GCCGCGCGCGCGCGCGCGCGTGTGTGACCTGGCGGTGAGGTCTCTTCTCATCCTTGAC 825



Db 117 ArgPheThrGluProLeuGluIleValAspLeuIleValAspIleMetPheIleValAsp 136  
QY 826 ATTGTGCTGAATTTCGGTACCACATTTCGTGTCCAAGTCGGGC-----CAGGTGGTG 876  
Db 137 IleIleIleAsnPheArgThrThrTyrValAsnGluAsnAspGluAlaCysGlnValVal 156  
QY 877 TTGTGCCCAAAGTCCATTGTCCCTCCACTACGTCACCACTGGTTCTCTGCTGGATGTCATC 936  
Db 157 SerAspProGlyLysIleAlaThrHisTyrPheLysGlyTrpPheIleIleAspMetVal 176  
QY 937 GCAGCGCTGCCCTTTGACCTGCTA-----CATGCCCTTCAAGTCAACGTGTAC 984  
Db 177 AlaAlaValProPheAspLeuLeuLeuValSerThrAsnSerAspGluThrThrLeu 196  
QY 985 TTCGGGGCCCATCTGCTGAAGACGGTGGCCCTGCTGCGCCTGCTGCGCCTGCTTCCGCGG 1044  
Db 197 IleGly-----LeuLeuLysThrAlaArgLeuLeuArgLeuValArgValAlaArgLys 214  
QY 1045 CTGGACCGGTACTCGAGTACAGCGCGTGGTGTGCTGACACTGCTCATGGCCGTGTTCCGCC 1104  
Db 215 LeuAspArgTyrSerGluTyrGlyAlaAlaValLeuLeuLeuMetAlaThrPheAla 234  
QY 1105 CTGCTCGCGCACTGGGTGCGCCTGCTGCTGTTTACATTGGCCAGCGGAGATCGAGAGC 1164  
Db 235 LeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIleGlySerAlaGluLeuSerHis 254  
QY 1165 AGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAGGAGCTGGCCCGCCGACTGGAGACT 1224  
Db 255 Lys-----GluTyrThrTrpLeuHisGlnLeuSerLysGlnLeuAlaGln 269  
QY 1225 CCCTACTACCTGGTGGCGCGGAGGCCAGCTGGAGGGAACAGCTCCGCCAGAGTGACAAC 1284  
Db 270 ProTyr----- 271  
QY 1285 TGCAGCAGCAGCAGCAGGCGCAACAGGGACGGGGCTGGAGCTGCTGGCGGCGCCGTGCTG 1344  
Db 272 -----ThrSerThrAsnGlyThr-----IleProThrGlyGlyProThrLeu 285  
QY 1345 CGCAGCGCTACACTCCCTCTACTTCGCACTCAGCAGCTCACCAGCGTGGGCTTC 1404  
Db 286 LysSerArgTyrValThrSerLeuTyrPheThrLeuSerThrIleThrSerIleGlyPhe 305  
QY 1405 GGCAACGTGTCCGCCAACACACGGACACCGAGAAGATCTTCTCCATCTGCACCATGTCATC 1464  
Db 306 GlyAsnValSerAlaThrThrAspSerGluLysIlePheThrIleIleMetMetIleLeu 325  
QY 1465 GCGGCCCTGATGCACGCGGTGGTGTGGGAACGTGACGGCCCATCATCCAGCGCATGTAC 1524  
Db 326 GlySerLeuMetTyrAlaSerValPheGlyAsnValSerAlaIleIleGlnArgLeuTyr 345  
QY 1525 GCGCGCGCTTTCTGTACCACAGCGCAGCGCGACCTGCGCGACTACATCCGCATCCAC 1584  
Db 346 SerGlyThrAlaArgTyrHisThrGluMetSerArgLeuArgGluPheIleArgPheHis 365  
QY 1585 CGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGGCGGTG 1644  
Db 366 GlnIleProAsnProLeuArgGlnArgLeuGluGluTyrPheGlnHisAlaTrpSerTyr 385  
QY 1645 AACAAATGGCATCGACACCACCGAGCTGCTGCAGAGCCTCCCTGACGAGCTGCGCGCAGAC 1704  
Db 386 ThrAsnGlyIleAspMetAsnLeuValLeuLysGlyPheProAspCysLeuGlnAlaAsp 405  
QY 1705 ATCGCCCATGCACCTGCACAAGGAGGTCTCTGCAG---CTGCCACTGTTGAGCGGCCAGC 1761  
Db 406 IleCysLeuHisLeuAsnArgAsnLeuLeuSerGlyCysAlaAlaPheAlaGlySerThr 425  
QY 1762 CGCGGCTGCTGCGGGCACTGTCTCTGGCCCTGCGGCCCGCCTTCTGCACGCCCGGGCAG 1821  
Db 426 ProGlyCysLeuArgAlaLeuSerMetArgPheArgThrThrHisSerProGlyAsp 445  
QY 1822 TACCTCATCCACCAAGCGGATGCCCTGCAGGCCCTCTACTTTGTCTGCTCTGGCTCCATG 1881  
Db 446 ThrLeuValHisArgGlyAspIleLeuThrGlyLeuTyrPheIleAlaArgGlySerVal 465

QY 1882 GAGTGCTCAAG---GGTGGCACCGTGCTCGCCATCCTAGGGAAGGGGACCTGATCGGC 1938  
Db 466 GluIleLeuAsnAspAspAsnThrValMetGlyIleLeuGlyLysAspAspIlePheGly 485  
QY 1939 TGTGAGCTGCCCCGCGGAGCAGTGCTGTAAGGCCAATGCCGACGTGAAGGGCTGACG 1998  
Db 486 GluAsnProLeuLeuTyrAspGluValGlyLysSerSerCysAsnValArgAlaLeuThr 505  
QY 1999 TACTGCTCCTGTCAGTGTCTGCAGCTGGCTGGCTGCACGACAGCCTGCGCTGATACCCC 2058  
Db 506 TyrCysAspLeuHisLysIleLeuArgAspAspLeuLeuAspValLeuAspMetTyrPro 525  
QY 2059 GAGTTTGGCCCCGCGCTTCAGTCTGTCGCTCCGAGGGGAGCTCAGCTACAACCTGGTGCT 2118  
Db 526 GluPheAlaGluThrPheCysLysAsnLeu-----ThrIleThrTyrAsnLeuArgAsp 543  
QY 2119 GGGGGAGGCTCT-----GCAGAGGTGGACACCAGCTCCCTGAGCGCGACAATACCCCTT 2172  
Db 544 AspAlaGlnSerLeuArgLysLysPheAspArgHisLysLeu-----LeuArg 559  
QY 2173 ATGTCACGCTGGAGGAGAGGAG-----ACAGATGGGGAGCAGGGCCCC 2217  
Db 560 MetSerSerSerMetAsnLysAspArgTyrThrThrProProAspGlyAspHisGlyAsn 579  
QY 2218 ACGGTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCTGGCTGCACC 2277  
Db 580 AlaAlaValArgArgSerAlaGluSerValSerArg-----CysAsp 593  
QY 2278 TCCTCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCTCGTCTA 2337  
Db 594 SerAsnPro-----IleAspArgArgGlnSerAlaGlySerArgSer 607  
QY 2338 GGTGGCAGAGGGAGGCCAGGCAGGGCAGGG-----GCTTTGAGGCTGAGGCTGGCCCC 2391  
Db 608 SerSerArgCysSerProProHisAlaAlaLeuThrAlaThrArgSerGluAlaThrPro 627

RESULT 15

Q8IV15  
ID Q8IV15 PRELIMINARY; PRT; 732 AA.  
AC Q8IV15;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to potassium voltage-gated channel, subfamily H (eag-related), member 7.  
DE  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC035815; AAH35815.1; --  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.  
DR GO; GO:0006812; P:cation transport; IEA.  
DR GO; GO:0006813; P:potassium ion transport; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR01622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR01610; PAC.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
SQ SEQUENCE 732 AA; 82904 MW; 42E86D3AA12E495D CRC64;

Alignment Scores:

Pred. No.:	9.98e-53	Length:	732
Score:	1075.50	Matches:	249
Percent Similarity:	47.30%	Conservative:	110
Best Local Similarity:	32.81%	Mismatches:	159
Query Match:	17.66%	Indels:	241
DB:	4	Gaps:	17
US-09-965-830-1_COPY_6_3257 (1-3252) x Q8IVL5 (1-732)			
QY	1	ATGCCGGCATGCGGGCCCTCCTGGCGCTCAGAACACCTTCCTGGACACCATCGCTACG	60
Db	1	MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuGlyThrIleIleArg	20
QY	61	CGTTTCGACGGCACGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC	120
Db	21	LysPheGluGlyGlnAsnLysLysPheIleIleAlaAsnAlaArgValGlnAsnCys---	39
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCGTGACCTCACGGGCTTCCTCCGGGCTGAGGTC	180
Db	40	AlaIleIleTyrCysAsnAspGlyPheCysGluMetThrGlyPheSerArgProAspVal	59
QY	181	ATGCAGCGGGGCTGTGCTCTCCTTCCTTCCTTATGGCCAGACACCATGAGCTCGTCCGC	240
Db	60	MetGlnLysProCysThrCysAspPheLeuHisGlyProGluThrLysArgHisAspIle	79
QY	241	CAACAGATCCGCAAGGCCCTGGACGACCAAGGAGTTCAAGGCTGACCTGATCCTGTAC	300
Db	80	AlaGlnIleAlaGlnAlaLeuLeuGlySerGluGluArgLysValGluValThrTyrTyr	99
QY	301	CGGAAGAGCGGGCTCCGTTCTGTGTCTCCTGGATGTGATACCATCAAGAAATGAGAAA	360
Db	100	HisLysAsnGlySerThrPheIleCysAsnThrHisIleIleProValLysAsnGlnGlu	119
QY	361	GGGAGGTGGCTCTCTCCTAGTCTCTCACAAAGGACATCAGCGAAACCAAGAACCGAGG	420
Db	120	GlyValAlaMetMetPheIleIleAsnPheGluTyrValThrAspAsnGluAsnAlaAla	139
QY	421	GGCCCCGACAGA-----	432
Db	140	ThrProGluArgValAsnProIleLeuProIleLysThrValAsnArgLysPheGly	159
QY	432	-----	432
Db	160	PheLysPheProGlyLeuArgValLeuThrTyrArgLysGlnSerLeuProGlnGluAsp	179
QY	432	-----	432
Db	180	ProAspValValIleAspSerSerLysHisSerAspSerValAlaMetLysHis	199
QY	433	-----TGAAGGAGACA-----	444
Db	200	PheLysSerProThrLysGluSerCysSerProSerGluAlaAspAspThrLysAlaLeu	219
QY	445	-----GGTGGT	450
Db	220	IleGlnProSerLysCysSerProLeuValAsnIleSerGlyProLeuAspHisSerSer	239
QY	451	GGCCGGCGCGCATATGCCCGG-----	471
Db	240	ProLysArgGlnTrpAspArgLeuTyrProAspMetLeuGlnSerSerSerGlnLeuSer	259
QY	472	---GCACGATCCAAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCTCTTACCAC	528
Db	260	HisSerArgSerArgGluSerLeuCysSerIleArgArgAlaSerSerVal---HisAsp	278
QY	529	CTGTCCGG-----	537
Db	279	IleGluGlyPheGlyValHisProLysAsnIlePheArgAspArgHisAlaSerGluGly	298
QY	538	-----CACCTGCAGAAGCAGCCCAAGGCAAG-----CACAAAGCTCAATAAG	579
Db	299	PropheAsnHisIleLysSerSerLeuLeuGlySerThrSerAspSerAsnLeuAsnLys	318

QY	580	-----GGGCTGTTTGGGGAG	594
Db	319	TyrSerThrIleAsnLysIleProGlnLeuThrLeuAsnPheSerGluValLysThrGlu	338
QY	595	AAACCAAAC-----	603
Db	339	LysLysAsnSerSerProProSerSerAspLysThrIleAlaProLysValLysAsp	358
QY	604	-----TTG	606
Db	359	ArgThrHisAsnValThrGluLysValThrGlnValLeuSerLeuGlyAlaAspValLeu	378
QY	607	CCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTGTGCACTGTGGGCA	666
Db	379	ProGluTyrLysLeuGlnThrProArgIleAsnLysPheThrIleLeuHisTyrSerPro	398
QY	667	CTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTCACTGTG	726
Db	399	PheLysAlaValTrpAspTrpLeuIleLeuLeuValIleTyrThrAlaIlePheThr	418
QY	727	CCCTACACCGTGTGTG-----AGCACAGACGGGAGCCCACT	765
Db	419	ProTyrSerAlaAlaPheLeuLeuAsnAspArgGluGlnLysArgArgGluCysGly	438
QY	766	GCCGCCCGCGGCCCGCCAGCGTCTGTGACCTGACCTGGCGGTGAGGTCTCTTTCATCCTTGAC	825
Db	439	TyrSerCysSerProLeuAsnValValAspLeuIleValAspIleMetPheIleIleAsp	458
QY	826	ATTGTGCTGAATTTCCGTACCAATTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTTGCCCA	885
Db	459	IleLeuIleAsnPheArgThrThrTyrValAsnGlnAsnGluGluValValSerAspPro	478
QY	886	AAGTCCATTGCTCCACTACGTCCACCTGTTCTCTGCTGGATGTCATCGCAGCGCTG	945
Db	479	AlaLysIleAlaIleHisTyrPheLysGlyTrpPheLeuIleAspMetValAlaAlaIle	498
QY	946	CCCTTTGACCTGTACATGCCCTTCAAGGTCAACGTGTACTTCGGGGCC-----	993
Db	499	PropheAspLeuLeu-----IlePheGlySerGlySerAspGlu	511
QY	994	-----CATCTGTGAAGACGGTGGCGCTGCTGCTGGCGCTGCTGCGCTGCTT	1038
Db	512	ThrThrThrLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArgLeuValArgValAla	531
QY	1039	CCGCGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTGCTGACACTGCTCATGGCCGTG	1098
Db	532	ArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuMetLeuMetCysIle	551
QY	1099	TTCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTGGTTTTACATTGGCCAGCGGAGATC	1158
Db	552	PheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIleGly-----	567
QY	1159	GAGAGCAGCGAATCCGAGCTGCCT-----GAGATTGGCTGCTGCAGGAGCTG	1206
Db	568	-----AsnValGluArgProTyrLeuThrAspLysIleGlyTrpLeuAspSerLeu	584
QY	1207	GCCCGCCGACTGGAGACTCCCTACTACTGGTGGCGGAGGCCAGCTGGAGGGAACAGC	1266
Db	585	GlyGlnGln-----IleGlyLysArg-----	591
QY	1267	TCCGGCCAGAGTGACAACTGCAGCAGCAGCAGGAGGCCAACGGGCGGCTGGAGCTG	1326
Db	592	-----TyrAsnAspSerAspSerSer-----	599
QY	1327	CTGGCGGCGCGTGGTGGCAGCGCTACATCACCTCCCTACTTCTGCTGCTGCTGCTGCTG	1386
Db	600	-----GlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSerSer	617
QY	1387	CTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGGACACCGAGAGATCTTCTCC	1446
Db	618	LeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePheSer	637
QY	1447	ATCTGCACCATGCTCATCGCGCCCTGTATGTCACGCGGTGGTGTGTTGGGAACGTGACGGCC	1506

Db	638	IleCysvalMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSerAla	657
QY	1507	ATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCACAGCCGCACGGCGACCTGCGC	1566
Db	658	IleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisMetGlnMetLeuArgValLys	677
QY	1567	GACTACATCCGATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTC	1626
Db	678	GlupheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyrPhe	697
QY	1627	CAGGCCACCTGGGCGGTGAACAATGGCATCGACACCCAGCGTGTGCAGAGCCCTC	1683
Db	698	GlnHisAlaTrrpThrTyrThrAsnGlyIleAspMetAsnMetValCysMetSerVal	716

Search completed: September 1, 2004, 15:52:08  
Job time : 462 secs





GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2004, 15:01:21 ; Search time 59 Seconds  
(without alignments)  
5740.073 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257  
Perfect score: 6089  
Sequence: 1 atgccggccatgcgggcct.....aagaaggcacaggggtctga 3252

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/uspto\_spool\_p/us09965830/runat\_01092004\_160109\_4795/app\_query.fasta\_1.3399  
-DB=SwissProt 42 -QFMT=fastan -SUFFIX=isp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09965830 @CGN 1 1 88 @runat\_01092004\_160109\_4795 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5704	93.7	1083	1 KCH3_HUMAN	Q9uld8 homo sapien
2	5428	89.1	1087	1 KCH3_RAT	O89047 rattus norv
3	5416	88.9	1087	1 KCH3_MOUSE	Q9wvj0 mus musculu
4	2529.5	41.5	1107	1 KCH8_HUMAN	Q96l42 homo sapien
5	2515	41.3	1102	1 KCH8_RAT	Q9qws8 rattus norv
6	2461.5	40.4	1017	1 KCH4_HUMAN	Q9uq05 homo sapien
7	2447.5	40.2	1017	1 KCH4_RAT	Q9rlt9 rattus norv
8	1778.5	29.2	876	1 KCH8_MOUSE	P59l11 mus musculu
9	1551	25.5	1158	1 KCH2_CANFA	Q9tsz3 canis fami
10	1551	25.5	1159	1 KCH2_HUMAN	Q12809 homo sapien
11	1547	25.4	1162	1 KCH2_MOUSE	O35219 mus musculu
12	1537.5	25.3	1163	1 KCH2_RAT	O08962 rattus norv
13	1536	25.2	1161	1 KCH2_RABIT	Q8wny2 oryctolagus
14	1509.5	24.8	994	1 KCH6_HUMAN	Q9h252 homo sapien
15	1475	24.2	950	1 KCH6_RAT	O54853 rattus norv
16	1400.5	23.0	1195	1 KCH7_MOUSE	Q9er47 mus musculu
17	1395.5	22.9	1195	1 KCH7_RAT	O54852 rattus norv
18	1390	22.8	1174	1 CIKE_DROME	Q02280 drosophila

19	1384.5	22.7	1196	1 KCH7_HUMAN	Q9ns40 homo sapien
20	1380.5	22.7	962	1 KCH1_RAT	Q63472 rattus norv
21	1371.5	22.5	989	1 KCH1_MOUSE	Q60603 mus musculu
22	1367.5	22.5	987	1 KCH1_BOVIN	O18965 bos taurus
23	1358.5	22.3	989	1 KCH1_HUMAN	O95259 homo sapien
24	1337.5	22.0	988	1 KCH5_RAT	Q9epi9 rattus norv
25	1332.5	21.9	988	1 KCH5_HUMAN	Q8ncm2 homo sapien
26	1035.5	17.0	526	1 KCH2_CHICK	Q9pt84 gallus gall
27	580	9.5	1186	1 HCN4_MOUSE	O70507 mus musculu
28	577	9.5	1198	1 HCN4_RAT	Q9jka7 rattus norv
29	566	9.3	1203	1 HCN4_HUMAN	Q9Y3q4 homo sapien
30	562.5	9.2	1175	1 HCN4_RABIT	Q9tv66 oryctolagus
31	527	8.7	889	1 HCN2_HUMAN	Q9ul51 homo sapien
32	513	8.4	863	1 HCN2_MOUSE	O88703 mus musculu
33	496	8.1	834	1 HCN2_RAT	Q9jka9 rattus norv
34	495	8.1	910	1 HCN1_MOUSE	O88704 mus musculu
35	487	8.0	779	1 HCN3_MOUSE	O88705 mus musculu
36	486	8.0	822	1 HCN1_RABIT	Q9mzsl oryctolagus
37	485	8.0	910	1 HCN1_RAT	Q9jkb0 rattus norv
38	484.5	8.0	780	1 HCN3_RAT	Q9jka8 rattus norv
39	480	7.9	890	1 HCN1_HUMAN	O60741 homo sapien
40	475.5	7.8	774	1 HCN3_HUMAN	Q9plz3 homo sapien
41	439	7.2	706	1 CNG3_BOVIN	Q29441 bos taurus
42	429.5	7.1	683	1 CNG1_RAT	Q62927 r cgm-p-gate
43	424.5	7.0	694	1 CNG3_HUMAN	Q16281 homo sapien
44	423.5	7.0	735	1 CNG1_CHICK	Q90805 gallus gall
45	422.5	6.9	631	1 CNG3_MOUSE	Q9jjz8 mus musculu

ALIGNMENTS

RESULT 1  
KCH3\_HUMAN  
ID KCH3\_HUMAN STANDARD; PRT: 1083 AA.  
AC Q9ULD8; Q9UQ06;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 3 (Ether-a-go-go-  
DE like potassium channel 2) (ELK channel 2) (ELK2) (Brain-specific eag-  
DE like channel 1) (BEC1).  
GN KCNH3 OR KIAA1282.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=99386988; PubMed=10455180;  
RA Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;  
RT "New ether-a-go-go K+ channel family members localized in human  
RT telencephalon.";  
RL J. Biol. Chem. 274:25018-25025(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20039619; PubMed=10574462;  
RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,  
RA Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XV.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 6:337-345(1999).  
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium  
CC channel. Elicits an outward current with fast inactivation.  
CC Channel properties may be modulated by cAMP and subunit assembly.  
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or  
CC heterotetrameric complex of pore-forming alpha subunits that can  
CC associate with modulating beta subunits.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Detected only in brain, in particular in the  
CC telencephalon. Detected in the cerebral cortex, occipital pole,

CC frontal and temporal lobe, putamen, amygdala, hippocampus and  
CC caudate nucleus.  
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is  
CC characterized by a series of positively charged amino acids at  
CC every third position.  
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag)  
CC subfamily.  
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC -!- SIMILARITY: Contains 1 PAS (PER-APNT-SIM) dimerization domain.  
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
CC  
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CC -----

DR EMBL; AB022696; BAA83590.1; --  
DR EMBL; AB033108; BAA86596.1; ALT\_INIT.  
DR Genew; HGNC:6252; KCN3.  
DR MIM; 604527; --  
DR GO; GO:0016021; C:integral to membrane; NAS.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; TAS.  
DR GO; GO:0006813; P:potassium ion transport; TAS.  
DR InterPro; IPR000595; cNMP\_binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc\_C.  
DR InterPro; IPR000014; PAS\_domain.  
DR Pfam; PF00027; cNMP\_binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SMO0100; cNMP; 1.  
DR SMART; SMO0086; PAC; 1.  
DR TIGRFAMS; TIGR00229; sensory\_box; 1.  
DR PROSITE; PS00888; CNMP\_BINDING\_1; FALSE\_NEG.  
DR PROSITE; PS00889; CNMP\_BINDING\_2; FALSE\_NEG.  
DR PROSITE; PS50042; CNMP\_BINDING\_3; 1.  
DR PROSITE; PS50112; PAS; 1.  
DR PROSITE; PS50113; PAC; 1.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
KW Glycoprotein; Multigene family.  
FT DOMAIN 1 228 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 229 249 SEGMENT S1 (POTENTIAL).  
FT TRANSMEM 260 280 SEGMENT S2 (POTENTIAL).  
FT DOMAIN 281 302 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 303 323 SEGMENT S3 (POTENTIAL).  
FT TRANSMEM 332 352 SEGMENT S4 (POTENTIAL).  
FT DOMAIN 353 361 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 362 382 SEGMENT S5 (POTENTIAL).  
FT DOMAIN 454 474 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
FT TRANSMEM 480 500 SEGMENT S6 (POTENTIAL).  
FT DOMAIN 501 1083 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 18 90 PAS.  
FT DOMAIN 93 145 PAC.  
FT DOMAIN 951 1057 PRO-RICH.  
FT NP BIND 582 697 CNMP.  
FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1083 AA; 117128 MW; EF35C8968D7418CC CRC64;

Alignment Scores: 1.13e-244 Length: 1083  
Pred. No.: 5704.00 Matches: 1083  
Score: 100.00% Conservative: 0  
Percent Similarity:

Best Local Similarity: 100.00%		Mismatches: 0
Query Match: 93.68%		Indels: 0
DB: 1		Gaps: 0
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QY	1	ATGCCGCGCATCGGGGCTCTCTGGCGCTCCTGAGACACACCTTCTCTGGACACCATCGCTACG 60
Db	1	MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
QY	61	CGCTTCGACGCGCACAGTAACTTCGTGCTGGCAACGCCAGCTGGCGGGCTCTTC 120
Db	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40
QY	121	CCCCTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTGAGGTC 180
Db	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60
QY	181	ATGCAGCGGGGCTGCTGCT 240
Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80
QY	241	CAACAGATCCGCAAGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCTCTGTAC 300
Db	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuTyr 100
QY	301	CGGAAGAGCGGGCTCCGTTCTGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db	101	ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120
QY	361	GGGGAGGTGGCT 420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140
QY	421	GGCCCCGACAGATGGAAGAGACAGGTGGTGGCGGCGCGCATATGGCCGGGACCATCC 480
Db	141	GlyProAspArgTrpLysGluThrGlyGlyGlyArgArgTyrGlyArgAlaArgSer 160
QY	481	AAAGGCTTCAATGCCAACCGCGCGGCGGAGCCGGCGCTCTCTCTCTCTCTCTCTCTCT 540
Db	161	LysGlyPheAsnAlaAsnArgArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180
QY	541	CTGCAGAAGCAGCCCCAAGGCAAGCACAAGCTCAATAAGGGGGTGTGTTGGGAGAAACA 600
Db	181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200
QY	601	AACCTGCTGAGTACAAAGTAGCCGCATCCGGAAGTCCGCTCTCTCTCTCTCTCTCTCT 660
Db	201	AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220
QY	661	GGGGACTGAGAGCCACCTGGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db	221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240
QY	721	ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGGAGGCCAGTCCCGCCCGCCCGCC 780
Db	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
QY	781	CCCAGCGTCTGTGACCTGGCGGTGGAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
QY	841	CGTACCACATTCGTGTCCAAGTCCGGGCGAGGTGGTGTGTTGCCCAAGTCCATTTGCCTC 900
Db	281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300
QY	901	CACCTACGTACACACCTGGTTCCTGCTGGATGTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db	301	HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320
QY	961	CATGCCCTTCAAGGTCAACGTGTACTTCCGGGGGCCCATCTCTGCTGAAGACGGTGGCGCTG 1020
Db	321	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340



QY	1021	CGCTGCTGCGCCTGCTTCCGGCGCTGGACCGGTACTCGCAGTACAGCGCCGTTGGTGTG	1080
Db	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
QY	1081	ACACTGCTCATGGCCGTTTCCGCCCTGCTCGCGCACTGGGTGCGCTGCGTCTGTTTAC	1140
Db	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
QY	1141	ATTGSCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG	1200
Db	381	IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln	400
QY	1201	GAGCTGGCCCCGCACTGGAGACTCCCTACTACCTGGTGGGCCGGAGCCAGCTGGAGGG	1260
Db	401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGACGGSGCTG	1320
Db	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440
QY	1321	GAGCTGCTGGCGGCCCGCTGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC	1380
Db	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
QY	1381	AGCAGCTCACCGCGTGGGCTTCGGCAACGTGTCGCGCAACACGGACACCGAGAAGATC	1440
Db	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluIysIle	480
QY	1441	TTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGACGCGGTGGTGTGGGAACGTG	1500
Db	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal	500
QY	1501	ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTATCCACAGCCGCAACGCGAC	1560
Db	501	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGCGCACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Db	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540
QY	1621	TACTTCCAGGCCACTGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGC	1680
Db	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560
QY	1681	CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGTCTGTCAGCTG	1740
Db	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGlnValLeuGlnLeu	580
QY	1741	CCACTGTTTGAGCGGCCAGCCGGCTGCTGCGGGCACTGTCTCTGGCCCTGCGGCC	1800
Db	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GCCTTCTGCTGCTCGGCGGAGTACCTCATCCACCAAGCGATGCCCTGCAGGCCCTCTAC	1860
Db	601	AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTGCCCATCCTAGG	1920
Db	621	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAGGCGCACTGATCGGCTGTGAGCTGCCCGCGGGAGCAGGTGGTAAAGGCCAATGCC	1980
Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla	660
QY	1981	GACGTGAGGGGCTGACGTACTGCTGCTGCAGTGTCTGCAGTGGCTGGCTGCACGAC	2040
Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
QY	2041	AGCCTTGCCTGTACCCCGAGTTTGCCCGCGCTTCAGTCGTGGCTCCGAGGGGAGCTC	2100
Db	681	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700

QY	2101	AGCTACAACCTTGGTGTCTGGGGAGGCTCTGCAGAGGTGGACACAGCTCCCTGAGCGGC	2160
Db	701	SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
QY	2161	GACAATACCTTTATGTCCACGCTGGAGGAGAGACAGATGGGGAGCAGGGCCCCCAG	2220
Db	721	AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr	740
QY	2221	GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCTCCCTGGCTGCACCTCC	2280
Db	741	ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer	760
QY	2281	TCATCTCAGCTGCCAAGCTGTCTATCCCCACGTGAAACAGACACCCCGCCCTCGTCTAGGT	2340
Db	761	SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
QY	2341	GGCAGAGGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCCCTCTGTCTCC	2400
Db	781	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	800
QY	2401	CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCCCATGCCATGGAATGTGCCCCCAGATCTG	2460
Db	801	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu	820
QY	2461	AGCCCCAGGCTAGTAGTGGCATTGAAGACGGCTGTGGCTCGGACCAAGCCCAAGTTCTCT	2520
Db	821	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	840
QY	2521	TTCCCGCTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCCTCCCTGGACCAAGAGC	2580
Db	841	PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer	860
QY	2581	GGCTGTCTCACTGTTCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG	2640
Db	861	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	880
QY	2641	CTTCGGCAGGCGGTGACAGAGCTGTGAGAGCAGGTGCTGCAGATGCGGGAGGAGTGCAG	2700
Db	881	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	900
QY	2701	TCACTTCGCCAGGCTGTGCAGCTTGTCTCTGGCGCCCCACAGGGAGGTCGTCGCCCTCGG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
QY	2761	GCATCGGGAGAGGGCCGTGCCACAGCCACACCTCCGGGCTTCTGCAGCCTCTGTGTGTG	2820
Db	921	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal	940
QY	2821	GACACTGGGCATCCTCCTACTGCTGCAGCCCCCAGCTGGCTCTGTCTTGAGTGGGACT	2880
Db	941	AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr	960
QY	2881	TGGCCCCACCTCGTCCGGGGCCCTCCTTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCA	2940
Db	961	TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro	980
QY	2941	CGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA	3000
Db	981	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	1000
QY	3001	GAGCCCCCTGCCTCAGGAGACCTCTGTCTGTAGCCCCAGCACCCCTGCCTCCCTCCCTCC	3060
Db	1001	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1020
QY	3061	TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC	3120
Db	1021	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1040
QY	3121	ACTGAGAGCCCCCACCAGGCTCAGGGGGCCCTGGCCCTTGGCCCTGGGACCCCCACAGCCTG	3180
Db	1041	ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu	1060
QY	3181	GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAAGC	3240

Db 1061 GluMetValIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly -080

Qy 3241 ACAGGGGTC 3249  
Db 1081 ThrGlyVal 1083

RESULT 2  
KCH3\_RAT  
ID KCH3 RAT STANDARD; PRT; 1087 AA.  
AC O89047;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 3 (Ether-a-go-go-like potassium channel 2) (ELK channel 2) (rElk2) (Brain-specific eag-like channel 1) (BEC1).  
DE like channel 1) (BEC1).  
GN KCH3 OR ELK2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
SEQUENCE FROM N.A.  
RC TISSUE=Brain cortex;  
RX MEDLINE=99043952; PubMed=9824707;  
RA Engelard B., Neu A., Ludwig J., Roeper J., Pongs O.;  
RT "Cloning and functional expression of rat ether-a-go-go-like K+ channel genes.";  
RL J. Physiol. (Lond) 513:647-654(1998).  
RN [2]  
SEQUENCE FROM N.A.  
RP TISSUE=Brain;  
RC TISSUE=Brain;  
RX MEDLINE=99386988; PubMed=10455180;  
RA Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;  
RT "New ether-a-go-go K+ channel family members localized in human telencephalon.";  
RL J. Biol. Chem. 274:25018-25025(1999).  
RN [3]  
SEQUENCE OF 120-273 FROM N.A.  
RP TISSUE=Brain;  
RC TISSUE=Brain;  
RX MEDLINE=98382545; PubMed=9714851;  
RA Shi W., Wang H.-S., Pan Z., Wymore R.S., Cohen I.S., McKinnon D.,  
RA Dixon J.E.;  
RT "Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in rat sympathetic ganglia.";  
RL J. Physiol. (Lond) 511:675-682(1998).  
RN [4]  
TISSUE SPECIFICITY.  
RX MEDLINE=20183472; PubMed=10718922;  
RA Wulfsen I., Hauber H.P., Schiemann D., Bauer C.K., Schwarz J.R.;  
RT "Expression of mRNA for voltage-dependent and inward-rectifying K channels in GH3/B6 cells and rat pituitary.";  
RL J. Neuroendocrinol. 12:263-272(2000).

CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits an outward current with fast inactivation.  
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Highly expressed in adult and embryonic brain, in particular in cerebellum, brain stem, hippocampus, cortex and striatum. Detected at slightly lower levels in heart, spinal cord, olfactory bulb, pituitary and medulla. In the hippocampus expression is strongest in the pyramidal cell body layers of the dentate gyrus. Also found in pituitary.  
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.  
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag) subfamily.  
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
CC  
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CC  
CC EMBL; AJ007627; CAA07586.1; -  
CC EMBL; AB022697; BAA83591.1; -  
CC EMBL; AF073892; AAC61522.1; -  
CC PIR; T31100; T31100.  
CC InterPro; IPR000595; cNMP\_binding.  
CC InterPro; IPR003967; Erg\_Channel.  
CC InterPro; IPR005821; Ion\_trans.  
CC InterPro; IPR001622; K+channel\_pore.  
CC InterPro; IPR005820; M+channel\_nlg.  
CC InterPro; IPR001610; PAC.  
CC InterPro; IPR000700; PAS-assoc\_C.  
CC InterPro; IPR000014; PAS\_domain.  
CC Pfam; PF00027; cNMP\_binding; 1.  
CC Pfam; PF00520; ion\_trans; 1.  
CC Pfam; PF00785; PAC; 1.  
CC PRINTS; PR01470; ERGCHANNEL.  
CC SMART; SM00100; cNMP; 1.  
CC SMART; SM00086; PAC; 1.  
CC SMART; SM00091; PAS; 1.  
CC TIGRfams; TIGR00229; sensory\_box; 1.  
CC PROSITE; PS00888; cNMP\_BINDING\_1; FALSE\_NEG.  
CC PROSITE; PS00889; cNMP\_BINDING\_2; FALSE\_NEG.  
CC PROSITE; PS00442; cNMP\_BINDING\_3; 1.  
CC PROSITE; PS0112; PAS; 1.  
CC PROSITE; PS0113; PAC; 1.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
KW Glycoprotein; Multigene family.  
FT DOMAIN 1 228 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 229 249 SEGMENT S1 (POTENTIAL).  
FT TRANSMEM 260 280 SEGMENT S2 (POTENTIAL).  
FT DOMAIN 281 302 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 303 323 SEGMENT S3 (POTENTIAL).  
FT TRANSMEM 332 352 SEGMENT S4 (POTENTIAL).  
FT DOMAIN 353 361 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 362 382 SEGMENT S5 (POTENTIAL).  
FT DOMAIN 457 477 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
FT TRANSMEM 483 503 SEGMENT S6 (POTENTIAL).  
FT DOMAIN 504 1087 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 18 90 PAS.  
FT DOMAIN 93 145 PAC.  
FT DOMAIN 954 1061 PRO-RICH.  
FT NP\_BIND 585 700 cNMP.  
FT CARBOHYD 421 421 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1087 AA; 117579 MW; 16B5AFFC3B0A405B CRC64;

Alignment Scores:  
Pred. No.: 1.66e-232 Length: 1087  
Score: 5428.00 Matches: 1039  
Percent Similarity: 96.60% Conservative: 11  
Best Local Similarity: 95.58% Mismatches: 33  
Query Match: 89.14% Indels: 4  
DB: 1 Gaps: 2

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x KCH3\_RAT (1-1087)

Qy 1 ATGCCGGCCATCGGGCCCTCTCTGGCGCTCAGAACACCTTCCTGGACACCATCGCTACG 60  
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGCTTCGACGGCACAGTAACCTTCGTGCTGGGCAACGCCACAGTGGCGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGACGGGGCTGTGCCTGCTCCTTCCTTTATGGCCAGACACACAGTGAGCTCGTCCGC 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGAAGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTCACAAGGACATCAGCGAACCATAAAGAATGAGAAA 360  
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAACCATAAAGAATGAGAAA 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGCCCCGACAGATGGAAGAGACAGGTGGTGGCGGCGCGGATATGGCCGGCAGCATCC 480  
Db 141 GlyProAspAsnTrpLysGluArgGlyGlyGlyArgArgArgTyrGlyArgAlaGlySer 160  
QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCCCGGCGCGTCTTACCACCTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAAGCAGCCCAAGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGCTGAGTACAAAGTAGCCGCCATCCCGGAAGTCGCCCTTCACTCTGTGCACTGT 660  
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuHisCys 220  
QY 661 GGGGCACTGAGAGCCACTGGGATGGCTTCACTGCTGCCACACTCTATGTGGCTGTC 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCAGTGCCGCCGCGGCCG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCACTCTTGACATTGTGCTGAATTTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTGCTGCCAAGTCGGGCCAGGTGGTGTGTTGCCCCCAAGTCCATTGCTC 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
QY 901 CACTACGTCAACACCTGGTTCCCTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGCTA 960  
Db 301 HisTyrValThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320  
QY 961 CATGCCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGTGTAAGACGGTGGCCTGCTG 1020  
Db 321 HisAlaPheLysValAsnValTyrValGlyAlaHisLeuLeuLysThrValArgLeuLeu 340  
QY 1021 CGCCTGTGGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTCTG 1080  
Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360  
QY 1081 ACACCTGCTCATGGCGGTGTTCCGCCCTGCTCGCGCACCTGGGTGCGCTGCTGTTTTAC 1140  
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG 1200

Db 381 IleGlyGlnGlnGlnIleGluAsnSerGluSerGluLeuProGluIleGlyTrpLeuGln 400  
QY 1201 GAGCTGGCCCGCGACTGGAGACTCCCTACTACTCTGGTGGCCGCGAGGCCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValSerArgSerProAspGlyGly 420  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGC-----AGCGAGGCCAACGGG 1311  
Db 421 AsnSerSerGlyGlnSerGluAsnCysSerSerGlyGlyGlySerGluAlaAsnGly 440  
QY 1312 ACGGGGCTGGAGCTGCTGGGGCGGCCCTCGCTGCGCAGCGCCTACATCACCTCCCTCTAC 1371  
Db 441 ThrGlyLeuGluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyr 460  
QY 1372 TTCGCACCTCAGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGACACC 1431  
Db 461 PheAlaLeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThr 480  
QY 1432 GAGAAAGATCTTCTCCATCTGCACCATGCTCATCGCGCGCCTGATGCACGCGTGTGTT 1491  
Db 481 GluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPhe 500  
QY 1492 GGGAAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCGCGCTTTCTGTACCACAGCCG 1551  
Db 501 GlyAsnValThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArg 520  
QY 1552 ACGCGCGACCTGCGCGACTACATCCGCATCCACCTCCACCTATCCCCAAGCCCCCTCAAGACGCG 1611  
Db 521 ThrArgAspLeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArg 540  
QY 1612 ATGCTGGAGTACTTCCAGGCCACCTGGGCGGTGAACATGGCATCGACACCACCGAGCTG 1671  
Db 541 MetLeuGluTyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeu 560  
QY 1672 CTGCAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTC 1731  
Db 561 LeuGlnSerLeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluVal 580  
QY 1732 CTGCAGCTGCCACTGTTGAGGCGGCCAGCGCGGTGCTCGTGGGCACTGTCTCTGGCC 1791  
Db 581 LeuGlnLeuProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAla 600  
QY 1792 CTGCGGCCCGCCTTTCACGCCCGCGCGAGTACCTCATCCACCAGGCGGATGCCCTGCAG 1851  
Db 601 LeuArgProAlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGln 620  
QY 1852 GCCCTCTACTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTGCTGCC 1911  
Db 621 AlaLeuTyrPheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAla 640  
QY 1912 ATCCTAGGGAAGGGGACCTGTATCGGCTGTGAGCTGCCCGGGGAGGAGGTGGTAAAG 1971  
Db 641 IleLeuGlyLysGlyAspLeuIleGlyCysGluLeuProGlnArgGluGlnValLys 660  
QY 1972 GCCAATGCCGACGTGAAGGGGTGACGTACTGCGTCCCTGCAAGTGTCTGCAAGTGGCTGSC 2031  
Db 661 AlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGly 680  
QY 2032 CTGCACGACAGCCTTTCGCTGTATCCCGAGTTTTCGCCCGCGCTTCAGTGTGGCTCCGA 2091  
Db 681 LeuHisGluSerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArg 700  
QY 2092 GGGGAGCTCAGCTACAACCTGGGTGCTGGGGGAGGCTCTGCAGAGGTGGACACCAGTCC 2151  
Db 701 GlyGluLeuSerTyrAsnLeuLeuGlyAlaGlyGlyValSerAlaGluValAspThrSerSer 720  
QY 2152 CTGACGGCGGACAAATACCTTATGTCCACGCTGGAGGAGAGAGACAGATGGGAGCAG 2211  
Db 721 LeuSerGlyAspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGln 740  
QY 2212 GGCCCCACGGTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTGTCCCTGGC 2271



Db 741 GlyHisThrIleSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGly 760  
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Db 761 CysThrSerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgPro 780  
QY 2332 CGTCTAGTGGCAGAGGAGGCCAGGCGAGGGCTTTGAAGGCTGAGGCTGGCC 2391  
Db 781 ArgLeuGlyGlyArgGlyArgProSerArgAlaGlyValLeuLysProGluAlaGlyPro 800  
QY 2392 TCTGCTCCCAAGCGGCCCTAGAGGGCTACGGCTGCCCACTGCGGCTGGAATGTGCC 2451  
Db 801 SerAlaHisProArgThrLeuAspGlyLeuGlnLeuProMetProTrpAsnValPro 820  
QY 2452 CCAGATCTGAGCCCAAGGCTAGTAGTGAAGACGGCTGTGGCTCGGACCAAGCC 2511  
Db 821 ProAspLeuSerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnHis 840  
QY 2512 AAGTTCTCTTCCGGTGGGCCAGTCTGGCCCGAATGTAGCAGCAGCCCTCCCTCGA 2571  
Db 841 LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerProSerProGly 860  
QY 2572 CCAGAGAGCGGCTCTCACTGTTCCTCCATGGGCCAGGCGAGGCAAGAACACAGACA 2631  
Db 861 ThrGluSerGlyLeuLeuThrValProLeuValProSerGluAlaArgAsnThrAspThr 880  
QY 2632 CTGGACAAGCTTCGGCAGCGGTGACAGAGCTGTGACAGCAGGTGTGACAGTGGGAA 2691  
Db 881 LeuAspLysLeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGlu 900  
QY 2692 GGAAGTGCAGTCACTTCGCGAGGCTGTGACGCTTGTCTGGCGCCCAAGGAGGCTCG 2751  
Db 901 GlyLeuGlnSerLeuArgGlnAlaValGlnLeuLeuValProGlnGlyGluGln 920  
QY 2752 TGCCCTCGGCATCGGAGAGGGCGGTGCCAGCCAGCACCTCCGGCTCTGCGACCT 2811  
Db 921 CysProArgValSerGlyGluGlyProCysProAlaThrAlaSerGlyLeuLeuGlnPro 940  
QY 2812 CTGTGTGTGACACTGGGCAATCTCTACTGCTGAGCCCGCCAGCTGGCTCTGCTTG 2871  
Db 941 LeuArgValAspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeu 960  
QY 2872 AGTGGGACTTGGCCCAACCTCGTCCGGGG---CCTCTCCCTCATGGCACCCCTGGCC 2928  
Db 961 SerGlyThrTrpProHisProArgProGlyHisProProProLeuMetAlaProTrpPro 980  
QY 2929 TGGGTCCCCCAGCGTCTCAGAGTCCCGCTGGCTCGAGCCAGCAGCTTTCTGGACCTCC 2988  
Db 981 TrpGlyProProAlaSerGlnSerSerProTrpProArgAlaThrAlaLeuTrpThrSer 1000  
QY 2989 ACCTCAGACTCAGAGCCCGCTGCTCAGGAGACCTCTGCTGTGAGCCAGCACCCCTGCC 3048  
Db 1001 ThrSerAspSerGluProProGlySerGlyAspLeuCysSerGluProSerThrProAla 1020  
QY 3049 TCCCTCTCTCTTCTGAGGAAGGGGCTAGGACTGGGGCCCGCAGAGCCTGTGAGCCAGGCT 3108  
Db 1021 SerProProProProGluGluGlyAlaArgThrGlyThrProAlaProValSerGlnAla 1040  
QY 3109 GAGGTACAGCACTGGAGAGCCCAAGAGGTGAGGGGCTGGGCTTGCCTGGGAC 3168  
Db 1041 GluAlaThrSerThrGlyGluProProProGlySerGlyArgAlaLeuProTrpAsp 1060  
QY 3169 CCCCACAGCTGGAGATGGTCTATTGGTCCCATGGCTGTGACAGTCCAGTGGAC 3228  
Db 1061 ProHisSerLeuGluMetValLeuIleGlyCysHisGlyProGlySerValGlnTrpThr 1080  
QY 3229 CAGGAAGAGGCACAGGGGTC 3249  
Db 1081 GlnGluGluGlyThrGlyVal 1087

RESULT 3  
KCH3\_MOUSE  
ID\_KCH3\_MOUSE STANDARD; PRT; 1087 AA.

AC Q9WVJ0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 3 (Ether-a-go-go-like potassium channel 2) (ELK channel 2) (mElk2).  
DE like potassium channel 2) (ELK channel 2) (mElk2).  
GN KCNH3 OR ELK2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=99208772; PubMed=10191308;  
RA Trudeau M.C., Titus S.A., Branchaw J.L., Ganetzky B., Robertson G.A.;  
RT "Functional analysis of a mouse brain Elk-type K+ channel.";  
RL J. Neurosci. 19:2906-2918(1999).  
CC -|- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits an outward current with fast inactivation.  
CC Channel properties may be modulated by cAMP and subunit assembly.  
CC -|- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -|- TISSUE SPECIFICITY: Detected in brain, but not in other tissues.  
CC -|- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.  
CC -|- SIMILARITY: Belongs to the potassium channel family. H (Eag) subfamily.  
CC -|- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC -|- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
CC -|- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
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CC EMBL; AF109143; AAD40578.1; -.  
DR MGD; MGI:1341723; Kcnh3.  
DR InterPro; IPR000595; cNMP binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc\_C.  
DR InterPro; IPR000014; PAS\_domain.  
DR Pfam; PF00027; cNMP\_binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; cNMP; 1.  
DR SMART; SM00086; PAC; 1.  
DR SMART; SM00091; PAS; 1.  
DR TIGRFAMs; TIGR00229; sensory\_box; 1.  
DR PROSITE; PS00888; CNMP\_BINDING\_1; FALSE\_NEG.  
DR PROSITE; PS00889; CNMP\_BINDING\_2; FALSE\_NEG.  
DR PROSITE; PS50042; CNMP\_BINDING\_3; 1.  
DR PROSITE; PS50112; PAS; 1.  
DR PROSITE; PS50113; PAC; 1.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
KW Glycoprotein; Multigene family.  
FT DOMAIN 1 228 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 229 249 SEGMENT S1 (POTENTIAL).  
FT TRANSMEM 260 280 SEGMENT S2 (POTENTIAL).  
FT DOMAIN 281 302 CYTOPLASMIC (POTENTIAL).



1792 CTGGCGCGCGCTTCTGCACGCCGGGCGAGTACCTCATCCACCAAGCGATGCCCTGCAG 1851  
601 LeuArgProAlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGln 620  
1852 GCCCTCTACTTGTCTGTCTGTGGCTCCATGGAGGTGCTCAAGGGTGGACCGTGTCTGCC 1911  
621 AlaLeuTyrPheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAla 640  
1912 ATCCTAGGGAAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGGAGCGAGTGGTAAAG 1971  
641 IleLeuGlyLysGlyAspLeuIleGlyCysGluLeuProGlnArgGluGlnValValLys 660  
1972 GCCAATGCCGACGTGAAGGGCTGACGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2031  
661 AlaAsnAlaValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGly 680  
2032 CTGCACGACAGCTTGCCTGTATACCCGAGTTTGGCGGCTTCACTGCTGCTGCTGCTGCT 2091  
681 LeuHisGluSerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArg 700  
2092 GGGAGCTCAGTACAACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACAGCTCC 2151  
701 GlyGluLeuSerTyrAsnLeuGlyAlaGlyGlyValSerAlaGluValAspThrSerSer 720  
2152 CTGAGCGGCGACATACCTTATGTCCACGCTGGAGGAGAAGAGACAGATGGGAGCAG 2211  
721 LeuSerGlyAspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGln 740  
2212 GGCCCCACGGTCTCCCGACGCCAGCTGATGAGCCCTCCAGCCCTGCTGTCCCTGCTGCC 2271  
741 GlyHisThrIleSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGly 760  
2272 TGCACCTCTCATCTCAGCTGCCAAGCTGCTATCCCGACGTCGAACAGCACCCCGGCT 2331  
761 CysThrSerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgPro 780  
2332 CGTCTAGTGGCAGAGGAGCGCCAGGCGAGGCGCTTGAAGCTGAGGCTGGCGCTGCC 2391  
781 ArgLeuGlyGlyArgGlyArgProSerArgAlaGlyValLeuLysProGluAlaGlyPro 800  
2392 TCTGCTCCCCACGGGCTTACAGAGGGCTACGGCTGCCCGCCCTATGCCATGGATGTGCC 2451  
801 SerAlaHisProArgThrLeuAspGlyLeuGlnLeuProProMetProTrpAsnValPro 820  
2452 CCAGATCTGAGCCCCAGGCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2511  
821 ProAspLeuSerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnHis 840  
2512 AAGTTCTCTTCCCGCTGGCGAGTCTGGCCCGGATGTAGCAGCAGCAGCAGCAGCAGCAG 2571  
841 LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGly 860  
2572 CCAGAGAGCGGCTGCTCACTGTCTCCCTATGGCCCGGATGTAGCAGCAGCAGCAGCAGCAG 2631  
861 ThrGluSerGlyLeuLeuThrValProLeuValProSerGluAlaArgAsnThrAspThr 880  
2632 CTGGACAAGCTTCGGCAGCGGTGACAGAGCTGTACAGCAGGCTGTGACAGATGCGGAA 2691  
881 LeuAspLysLeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGlu 900  
2692 GGACTGCAGTCACTTCGCCAGGCTGTGACAGTGTGCTGCGGCGCCACAGGGAGGCTCG 2751  
901 GlyLeuGlnSerLeuArgGlnAlaValGlnLeuIleLeuValProGlnGlyGluGln 920  
2752 TGCCCTCGGGCATCGGAGAGGGCGGTGCCAGCCAGCACCTCGGGCTTCTGCAGCCT 2811  
921 CysProArgValSerGlyGluGlyProCysProAlaThrAlaCysGlyLeuLeuGlnPro 940  
2812 CTGTGTGTGACACTGGGGCATCTCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2871  
941 LeuArgValAspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeu 960  
2872 AGTGGGACTTGGCCCCACCCCTCGTCCGGGG--CCTCCTCCCTCATGGCACCCCTGGCCC 2928

961 SerGlyThrTrpProHisProArgProGlyHisProProLeuMetAlaProTrpPro 980  
2929 TGGGTCCCCAGCGTCTCAGAGCTCCCTCCCTGGCCTCGAGCCACAGCTTCTGGACCTCC 2988  
981 TrpGlyProProAlaSerGlnSerSerProTrpProArgAlaThrAlaLeuTrpThrSer 1000  
2989 ACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGTCTGAGCCAGCACCCCTGCC 3048  
1001 ThrSerAspSerGluProProGlySerGlyAspLeuCysSerGluProSerThrProAla 1020  
3049 TCCCTCTCTCTTCTGAGGAAGGGCTAGGACTGGCCCGCAGAGCCTGTGAGCCAGGCT 3108  
1021 SerProProProGluGluGlyAlaArgThrGlyThrProAlaProValSerGlnAla 1040  
3109 GAGGCTACCACTGGAGAGCCCCCAGGAGGCTCAGGGGGCTGGCCCTGCTGCTGGGAC 3168  
1041 GluAlaThrSerThrGlyGluProProProGlySerGlyGlyArgAlaLeuProTrpAsp 1060  
3169 CCCACAGCTGGAGATGGTGTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3228  
1061 ProHisSerLeuGluMetValLeuIleGlyCysHisGlyProGlySerValGlnTrpThr 1080  
3229 CAGGAAGAAGCACAGGGGTC 3249  
1081 GlnGluGluGlyThrGlyVal 1087

RESULT 4  
KCH8\_HUMAN STANDARD; PRT; 1107 AA.  
AC Q96L42;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 8 (Ether-a-go-go-like potassium channel 3) (ELK channel 3) (ELK3) (ELK1) (hElk1).  
GN KCNH8.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=21895915; PubMed=11897058;  
RA Baxter D.F., Kirk M., Garcia A.F., Raimondi A., Holmqvist M.H., Flint K.K., Bojanic D., DiStefano P.S., Curtis R., Xie Y.;  
RT "A novel membrane potential-sensitive fluorescent dye improves cell-based assays for ion channels.";  
RL J. Biomol. Screen. 7:79-85(2002).  
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits a slowly activated, outward rectifying current.  
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.  
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag) subfamily.  
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).



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CC EMBL; AY053503; AAL15429.1; -.
DR Genew; HGNC:18864; KCNH8.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR003967; Erg_channel.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000700; PAS-assoc_C.
DR InterPro; IPR000014; PAS_domain.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF00785; PAC; 1.
DR PRINTS; PR01470; ERGCHANNEL.
DR SMART; SM00100; cNMP; 1.
DR SMART; SM00086; PAC; 1.
DR TIGRFAMs; TIGR00229; sensory_box; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; FALSE_NEG.
DR PROSITE; PS00889; cNMP_BINDING_2; FALSE_NEG.
DR PROSITE; PS00042; cNMP_BINDING_3; 1.
DR PROSITE; PS01113; PAC; 1.
DR PROSITE; PS01112; PAS; FALSE_NEG.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Potassium transport; Transmembrane;
KW Glycoprotein; Multigene family.
FT DOMAIN 1 225 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 226 246 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 256 276 SEGMENT S2 (POTENTIAL).
FT DOMAIN 277 298 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 299 319 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 328 348 SEGMENT S4 (POTENTIAL).
FT DOMAIN 349 357 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 358 378 SEGMENT S5 (POTENTIAL).
FT DOMAIN 420 440 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT TRANSMEM 449 469 SEGMENT S6 (POTENTIAL).
FT DOMAIN 470 1107 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 18 90 PAS.
FT DOMAIN 93 145 PAC.
FT DOMAIN 951 1064 SER-RICH.
FT DOMAIN 711 723 POLY-GLU.
FT NP BIND 551 668 cNMP.
FT CARBOHYD 320 320 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1107 AA; 123832 MW; 4DC93BF85B674905 CRC64;

Alignment Scores:
Pred. No.: 9.87e-105 Length: 1107
Score: 2529.50 Matches: 559
Percent Similarity: 60.24% Conservative: 150
Best Local Similarity: 47.49% Mismatches: 267
Query Match: 41.54% Indels: 201
DB: 1 Gaps: 27

US-09-965-830-1_COPY_6_3257 (1-3252) x KCH8_HUMAN (1-1107)

QY 1 ATGCCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGTTTCAGCGGCACGACAGTAACCTTCGTGTCGGCAACGCCAGGTGGCGGCTCTTC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40

QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
41 ProfileValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60

QY 181 ATGACGCGGGCTGTGCCCTGCTCTCTTCCTTTATGGCCAGACACCATGAGCTCGTCCGC 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80

QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
81 LeuGlnIleGluLysSerLeuGluGluLysThrGluPheLysGlyGluIleMetPheTyr 100

QY CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTCGATGTGATACCCATAAAGAAATGAGAAA 360
Db ::|||::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 LysLysAsnGlySerProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120

QY GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140

QY GGGCCCGACAGATGGAAGGAGACAGGTGGTGGCCCGCCGATATGGCCGGGACGATCC 480
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
141 ThrProGluAspLysLysGluAsp-----LysValLysGlyArgSerArgAla 156

QY 481 ---AAAGGCTTCAATGCCAACCGCGCGGAGCCGGGCGCTCTCTACCACTGTCGGG 537
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 GlyThrHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176

QY CACCTGCAGAAAGCAGCCCAAGGCAAGCACCAAGTCAATAAGGGGTGTTGGGAGAAA 597
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
177 HisLeuGlnArgArgGluLysAsnLysLysLeuLysIleAsnAsnValPheValAspLys 196

QY CCAAACTTGCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTTCATCCTGTGCAC 657
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuHis 216

QY TGTGGGGCACTGAGAGCCACCTGGGATGGTTCATCCTGCTCGCCACACTCTATGTGGCT 717
Db ::|||::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
217 PheSerThrPheLysAlaGlyTrpAspTrpLeuLeuAlaThrPheTyrValAla 236

QY GTCACCTGTGCCCTACAGCGTGTGTGAGCACAGCAGCGGAGCCAGTCCGCGCCCGCGGC 777
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
237 ValThrValProTyrAsnValCysPheIleGlyAsnAspAspLeuSerThrThrArgSer 256

QY CCGCCCAAGCTGTGTGACCTGGCCGTGGAGTCTCTTTCATCCTTGACATTTGTGAAT 837
Db ::|||::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
257 ---ThrThrValSerAspIleAlaValGluIleLeuPheIleIleAspIleIleLeuAsn 275

QY TTCCGTACCACATTCGTGTCCAAGTCGGGCGCAGGTGGTGTTCGCCCAAAGTCCATTGC 897
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
276 PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295

QY CTCCACTAGCTCACCACTGCTGTTCTCTGCTGGATGTATCGCAGCGCTGCTTGCACCTG 957
Db ::|||::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
296 IleHisTyrValThrThrTrpPheIleIleAspLeuIleAlaIleLeuPropheAspLeu 315

QY CTACATGCTTCAAGTCAACGTCTACTTCGGGGCCCATCTGCTGAAGACGGTCCGCTG 1017
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLysThrValArgLeu 335

QY CTGCGCTGTGCGCCTGCTTCGCGGCTGGACCGGTACTCGAGTACAGCGCGCTGGTG 1077
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355

QY CTGACACTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGGTGCGCTCGCTT 1137
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
356 LeuThrLeuLeuMetSerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleTrpTyr 375

QY TACATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTG 1197
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
376 ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu 395

QY CAGGAGCTGGCCCGCCTGAGACTCCCTACTACCTGGTGGCGCGGAGGCCAGCTGGA 1257
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
396 HisGluLeuGlyLysArgLeuGluSerProTyrTyr----- 407

QY GGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGGAGGCCAACGGACGGGG 1317
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
408 GlyAsnAsnThr----- 411

QY CTGAGAGTGTGGGCGCGCTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCA 1377
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 412 -----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr 428  
QY 1378 CTCAGAGCCTCACCAGCGTGGCTTCGGCAACGTGTCGCCAACACACGACACCGAGAAG 1437  
Db 429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys 448  
QY 1438 ATCTTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACGCGTGGTGTGTTGGGAAC 1497  
Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468  
QY 1498 GTGACGGGCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACACGCGCACGCGC 1557  
Db 469 ValThrAlaIleIleGlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys 488  
QY 1558 GACCTGGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTG 1617  
Db 489 AspLeuLysAspPheIleArgValHisLeuProGlnGlnLeuLysGlnArgMetLeu 508  
QY 1618 GAGTACTTCCAGGCGACCTGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAG 1677  
Db 509 GluTyrPheGlnThrThrTrpSerValAsnAsnGlyIleAspSerAsnGluLeuLys 528  
QY 1678 AGCCTCCCTGACGAGCTGCGGCAGACATCGCCATGCACCTGCACAAAGAGGTCTGTCAG 1737  
Db 529 AspPheProAspGluLeuArgSerAspIleThrMetHisLeuAsnLysGluIleLeuGln 548  
QY 1738 CTGCCACTGTGAGCGCGCCAGCGCGCTGCTGCGGCACCTGTCTCTGGCCCTGCGG 1797  
Db 549 LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuSerLeuHisIleLys 568  
QY 1798 CCGCCTTCTGCACGCGCGGAGTACCTCATCCACCAAGCGATGCCCTGCAGGCCCTC 1857  
Db 569 ThrSerPheCysAlaProGlyGluTyrLeuLeuArgGlnGlyAspAlaLeuGlnAlaIle 588  
QY 1858 TACTTTGTCTGCTCGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTGCCATCCTA 1917  
Db 589 TyrPheValCysSerGlySerMetGluValLeuLysAspSerMetValLeuAlaIleLeu 608  
QY 1918 GGAAGGGCGACCTGATCGGCTGTGAGCTGCCCGGGGAGCAGGTGGTAAAGGCCAAT 1977  
Db 609 GlyLysGlyAspLeuIleGlyAlaAsnLeuSerIleLysAspGlnValIleLysThrAsn 628  
QY 1978 GCGCAGCTGAAGGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2037  
Db 629 AlaAspValLysAlaLeuThrTyrCysAspLeuGlnCysIleIleLeuLysGlyLeuPhe 648  
QY 2038 GACAGCCTTGCGCTGTACCCCGAGTTTGCCCGCGCTTCAGTCTGCTGCTGCTGCTGCTG 2097  
Db 649 GluValLeuAspLeuTyrProGluTyrAlaHisLysPheValGluAspIleGlnHisAsp 668  
QY 2098 CTCAGCTACAACCTGGGTGCTGGG-----GGAGGCTCT 2130  
Db 669 LeuThrTyrAsnLeuArgGluGlyHisGluSerAspValIleSerArgLeuSerAsnLys 688  
QY 2131 GCAGAGGTGGACACACAGCTCCCTGACGGCGGACAAATACCTTATGTCCACGCTG----- 2184  
Db 689 SerMetValSerGlnSerGluProLysGlyAsnGlyAsnIleAsnLysArgLeuProSer 708  
QY 2185 -----GAGGAGAGGAGACAGATGGGAGCAGGGCCCGACCGTCTCCCCAGCC 2232  
Db 709 IleValGluAspGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 726  
QY 2233 CCAGCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2292  
Db 727 -----LeuSerProIleCysThrArgGlySerSer 737  
QY 2293 GCCAAGCTGCTATCCCCACGTCGAACAGACACCCCGGCTCGTCTAGTGGCAGAGGAGG 2352  
Db 738 -----Arg 738  
QY 2353 CCAGGACGGGCGGCTTTGAAGGCTGAGGCTGGCCCTCTGCT----- 2397  
Db 739 AsnLysLysValGlySerAsnLysAlaTyrLeuGlyLeuSerLeuLysGlnLeuAlaSer 758

QY 2397 ----- 2397  
Db 759 GlyThrValProPheHisSerProIleArgValSerArgSerAsnSerProLysThrLys 778  
QY 2398 -----CCCCCA-----CGGGCCCTAGAGGGGCTACGGCTGCCCCCC 2433  
Db 779 GlnGluIleAspProProAsnHisAsnLysArgLysGluLysAsnLeuLysLeuGlnLeu 798  
QY 2434 ATGCCATGGAAT-----GTGCCCCCAGATCTGAGCCCCCAGGGVAGTAGATGGCATTTGAA 2487  
Db 799 SerThrLeuAsnAsnAlaGlyProProAspLeuSerProArgIleValAspGlyIleGlu 818  
QY 2488 GACGGCTGTGGCTCGGACCAGCCCAAG-----TTCTCTTTCCGCGTGGGCCAGTCTGGCCCG 2544  
Db 819 AspGlyAsnSerSerGluGluSerGlnThrPheAspPheGlySerGluArgIleArgSer 838  
QY 2545 GAATGTAGCAGCAGCCCTCCCTCGGA-----CCAGAGAGCGGCTGCTCAGTGTCCCAT 2601  
Db 839 GluProArgIleSerProProLeuGlyAspProGluIleGlyAlaAlaValLeuPheIle 858  
QY 2602 GGGCCCCAGCAGGCAAGGAACACAGACACACTGGACAAGCTTCGGCAGCGGCTGACAGAG 2661  
Db 859 LysAlaGluGluThrLys-----GlnGlnIleAsnLysLeuAsnSerGluValThrThr 876  
QY 2662 CTGTCTGAGCAGCGTCTGCAGATGCGGGAAGACTGCAGTCACTTCGCCAGGCTGTGCAG 2721  
Db 877 LeuThrGlnGluValSerGlnLeuGlyLysAspMetArgAsnValIleArgLeuLeuGlu 896  
QY 2722 CTTGTCTGCGGCC-----CACAGGAGGGTCCGTGC 2754  
Db 897 AsnValIleSerProGlnGlnProSerArgPheCysSerLeuHisSerThrSerValCys 916  
QY 2755 CCTCGGGCA-----TCGGGAGAGGGCGCTGCCAGCC 2787  
Db 917 ProSerArgGluSerLeuGlnThrArgThrSerTrpSerAlaHisGlnProCys----- 934  
QY 2788 AGCACCTCGGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGGCATCTCTCTACTGCTC- 2844  
Db 935 -----LeuHisLeuGlnThrGlyAlaAlaTyrThrGln 946  
QY 2845 CTGCAGCCCCAGTGGCTCTGTCTGTAGTGGGACTTGGCCCCCACCCTCGTCCGGGGCCT 2904  
Db 947 AlaGlnLeuCysSerSerAsnIleThrSerAspIleTrpSer----- 960  
QY 2905 CCTCCCTCATGGCACCTCGGCTGGGTCCCGGTCCCGGTCTCAGAGCTCCCGCTGGCCT 2964  
Db 961 -----ValAspProSerSerValGlySerSer---Pro 970  
QY 2965 CGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCTCAGGAGACCTC 3024  
Db 971 GlnArgThrGly-----AlaHisGluGlnAsnProAlaAspSerGluLeu 985  
QY 3025 TGTCTGAGCCCCAGCACCCCTGCTCCCT----- 3054  
Db 986 TyrHisSerProSerLeuAspTyrSerProSerHisTyrGlnValGlnGluGlyHis 1005  
QY 3055 -----CCTCCTTCTGAGGAAGGGGTAGGACTGGGCCCGCAGAG 3093  
Db 1006 LeuGlnPheLeuArgCysIleSerProHisSerAspSerThrLeuThr---ProLeuGln 1024  
QY 3094 CCTGTGAGCCAGGCTGAGGTACAGCACTGGAGAGCCCCCAGGTCAGGGGGCCTG 3153  
Db 1025 SerIleSerAlaThrLeuSerSerSerValCysSerSerSerGluThrSerLeuHisLeu 1044  
QY 3154 GCCTTGCCTGGGACCCCCACAGCTGGAGATGGTGTATTGGCTGCCATGGCTCTGGC 3213  
Db 1045 ValLeuPro-----SerArgSerGluGlu-----GlySerPheSerGlnGly 1058  
QY 3214 ACAGTC-----CAGTGGACCCAGGAA 3234  
Db 1059 ThrValSerSerPheSerLeuGluAsnLeuProGlySerTrpAsnGlnGlu 1075





Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80  
Qy 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 81 LeuGlnIleGluLysSerLeuGluGluLysValGluPheLysGlyGluIleMetPheTyr 400  
Qy 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAAATGAGAAA 360  
Db 101 LysLysAsnGlyAlaProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 420  
Qy 361 GGGAGGTGGCTCTCTTCTAGTCTCTCACAAGGACATCAGCGGAACCAAGAACCGA --- 417  
Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 440  
Qy 418 GGGGGCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCGATATGGCCGGGCACGA 477  
Db 141 ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly----- 457  
Qy 478 TCCAAAGGCTTCAATGCCAACCGCGGGGAGCCGGCCGCTGTCTTACACCTGTCCGGG 537  
Db 158 ---SerHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 476  
Qy 538 CACCTGCAGAGCAGCCCAAGGCAAGCACAACTCAATAAGGGGTGTTGGGAGAAA 597  
Db 177 HisLeuGlnArgGluLysAsnLysLeuLysIleAsnAsnValPheValAspLys 196  
Qy 598 CCAAACTTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTGCAC 657  
Db 197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216  
Qy 658 TGTGGGCACTGAGAGCCACCTGGGATGGCTTCCTCTGCTCGCCACACTCTATGTGGCT 717  
Db 217 PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAla 236  
Qy 718 GTCACGTGTCCTACAGCTGTGTGTGAGCACAGACGGGAGCCAGTCGCCGCCCGCGGC 777  
Db 237 ValThrValProTyrAsnValCysPheIleGlyAsnGluAspLeuSerThrThrArgSer 256  
Qy 778 CGGCCAGCGTCTGTGACCTGGCCGTGGAGTCTCTTCTATCCTTGACATGTGCTGAAT 837  
Db 257 ---ThrThrValSerAspIleAlaValGluIleLeuPheIleIleAspIleIleLeuAsn 275  
Qy 838 TTCCGTACACATTCGTGTCAAAGTCGGGCCAGGTGGTGTTCGCCCAAAGTCCATTGTC 897  
Db 276 PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295  
Qy 898 CTCCACTACGTACACCACTGTTCTGCTGGATGTATCGCAGCGCTGCCCTTTGACCTG 957  
Db 296 IleHisTyrValThrTrpPheIleIleAspLeuIleAlaAlaLeuProPheAspLeu 315  
Qy 958 CTACATGCCCTTCAAGTCAAGTCACTTCGGGGCCCATCTGCTGAAGACGGTGGCCCTG 1017  
Db 316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu 335  
Qy 1018 CTGCGCTGCTGCGCTGCTTCCGCGCTGACCGGTACTCGCAGTACAGCGCCGTGGTG 1077  
Db 336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355  
Qy 1078 CTGACACTGCTCATGGCCGTGTTGCGCTGCTCGCGCACTGGGTGCGCTGCGTCTGTTT 1137  
Db 356 LeuThrLeuLeuMetSerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleTrpTyr 375  
Qy 1138 TACATTGGCCGCGGAGATCGAGAGCAGCGAAATCCGAGCTGCTGAGATTGGCTGGCTG 1197  
Db 376 ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu 395  
Qy 1198 CAGGAGCTGGCCCGCAGTGGAGACTCCCTACTACCTGGTGGCCGGAGGCCAGCTGGA 1257  
Db 396 HisGluLeuGlyLysArgLeuGluSerProTyrTyr----- 407  
Qy 1258 GGGAAACAGCTCCGCCAGAGTGACAACTGCAGCAGCAGCGAGCGGCCAACGGGACGGG 1317  
Db 408 GlyAsnAsnThr----- 411

Qy 1318 CTGAGCTGCTGGGGCGGCGCTCGCTGCGGAGCGGCTACATCACCTCCCTCTACTTCGCA 1377  
Db 412 -----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr 428  
Qy 1378 CTCAGCAGCCTCACGAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGACACCGAGAAG 1437  
Db 429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys 448  
Qy 1438 ATCTTCTCCATCTGCACCATGTCTATCGCGCCCTGTATGCACGCGGTGGTGTGGGAAC 1497  
Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468  
Qy 1498 GTGACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCCGACGCGC 1557  
Db 469 ValThrAlaIleIleGlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys 488  
Qy 1558 GACCTGGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTG 1617  
Db 489 AspLeuLysAspPheIleArgValHisHisLeuProGlnLeuLysGlnArgMetLeu 508  
Qy 1618 GAGTACTTCCAGCCACCTGGCGGTGAACAATGGCATCGACACCACCGAGTGTGCAG 1677  
Db 509 GluTyrPheGlnThrThrTrpSerValAsnAsnGlyIleAspSerAsnGluLeuLys 528  
Qy 1678 AGCTCCCTGACGAGTGCAGCGCATCCGCATCGCATCCCAAGCCCTCAAGCAGCGCATG 1737  
Db 529 AspPheProAspGluLeuArgSerAspIleThrMetHisLeuAsnLysGluIleLeuGln 548  
Qy 1738 CTGCCACTGTTTGAAGCGCGCAGCGCGGTGCTGCGGGCAGTGTCTCTGCCCTGCGG 1797  
Db 549 LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuSerLeuHisIleLys 568  
Qy 1798 CCCGCCTTCTGCACGCGCGGCGAGTACCTCATCCACCAAGCGCATGCCCTGAGGCCCTC 1857  
Db 569 ThrSerPheCysAlaProGlyGluTyrLeuLeuArgGlnGlyAspAlaLeuGlnAlaIle 588  
Qy 1858 TACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTGCGCATCCTA 1917  
Db 589 TyrPheValCysSerGlySerMetGluValLeuLysAspSerMetValLeuAlaIleLeu 608  
Qy 1918 GGGAAAGGCGACCTGATCGGCTGTGAGTGCCTCCCGCGGGAGCAGGTGGTAAAGGCCAAT 1977  
Db 609 GlyLysGlyAspLeuIleGlyAlaAsnLeuSerIleLysAspGlnValIleLysThrAsn 628  
Qy 1978 GCGCAGCTGAAGGGCTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2037  
Db 629 AlaAspValLysAlaLeuThrTyrCysAspLeuGlnCysIleIleLeuLysGlyLeuPhe 648  
Qy 2038 GACAGCCTTGGCGTGTACCCCGAGTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2097  
Db 649 GluValLeuGlyLeuTyrProGluTyrAlaHisLysPheValGluAspIleGlnHisAsp 668  
Qy 2098 CTCAGCTACAACCTGGGTGCTGGG-----GGAGGCTCT 2130  
Db 669 LeuThrTyrAsnLeuArgGluGlyHisGluSerAspValIleSerArgLeuSerAsnLys 688  
Qy 2131 GCAGAGTGGACACACAGCTCCCTGAGCGGCGACAAATACCTTATGTCCACGCTG----- 2184  
Db 689 SerThrValProGlnAlaGluProLysGlyAsnGlySerIleLysLysArgLeuProSer 708  
Qy 2185 -----GAGGAGAGGAGACAGATGGGAGCAGGGGCCCGCCAGGTCTCCCGACGCCCA 2235  
Db 709 IleValGluAspGluGluGluValGluGluGluGluGluGluGluGluGluGluGluGlu 728  
Qy 2236 GCTGATGAGCCCTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2295  
Db 729 IleTyrThrArgGlySerSerValSerHisSerLysLysThrGlySerSerLysSerTyr 748  
Qy 2296 AAGCTGCTATCCCGACGTCGA-----ACAGCACCC-----CGGCT---CGT 2334  
Db 749 LeuGlyLeuSerLeuLysGlnLeuThrSerGlyThrValProPheHisSerProIleArg 768

QY 2335 CTAGGTGGCAGAGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCTCT 2394  
Db : : : : :  
769 ValSerSerAlaAsnSerPro-----LysThrLysGlnGluAlaAspProPro 784  
QY 2395 GCTCCCCCAGGGCCCTAGAG-----GGGCTACGGCTGCCGCCCATGCCATGGAAT 2445  
Db : : : : :  
785 AsnHisGlyThrArgLysGluLysAsnLeuLysValGlnLeuCysSerLeuGlyThrAla 804  
QY 2446 GTGCCCCCAGATCTGAGCCCCAGGGTAGATGATGATGAGACGGCTGTGGCTCGGAC 2505  
Db : : : : :  
805 GlyThrProGluLeuSerProArgIleValAspGlyIleGluAspGlyAsnSerSerGlu 824  
QY 2506 CAGCCCCAAG---TTCTCTTTCCGGTGGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCC 2562  
Db : : : : :  
825 GluThrGlnThrPheAspPheGlySerGluGlnIleArgProGluProArgIleSerPro 844  
QY 2563 TCCCTGTGACCAGAG-----AGCGGCTGTCTCCTCTTCCCATGGGCCAGCGAG 2613  
Db : : : : :  
845 SerLeuGlyGluSerGluIleGlyAlaAlaPheLeuPheIle-----Lys 859  
QY 2614 GCAAGGAACACA---GACACACTGGACAAGCTTCGGGAGCGGTGACAGAGCTGTCTAG 2670  
Db : : : : :  
860 AlaGluGluThrLysGlnGlnIleAsnLysLeuAsnSerGluValThrThrLeuThrGln 879  
QY 2671 CAGGTGCTGCAGATCGGGAGGAGTGCAGTCACTTCGCAGGCTGTGCAGCTTCTCTG 2730  
Db : : : : :  
880 GluValSerGlnLeuGlyLysAspMetArgSerIleMetGlnLeuLeuGluAsnIleLeu 899  
QY 2731 GCGCCCCACAGGAGGTCCGTGCCCTCGGGCATCGGAGAGGGCGGTGCCAGCCAGC 2790  
Db : : : : :  
900 SerProGlnGlnProSerGlnPheCysSerLeuHisProThrSerIleCysProSerArg 919  
QY 2791 ACCTCCGGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGGCATCTCTCTACTGCTGCAG 2850  
Db : : : : :  
920 GluSerPheGlnThrArg-----ValSerTrpSerAlaHisGlnProCysLeuHis 936  
QY 2851 CCCCCAGCT-----GGCTGTGTCTTGTAGTGGGACTGGCCCTCC 2889  
Db : : : : :  
937 LeuGlnAlaAsnGlyAlaHisLeuTyrHisGlyAsnValThrSerAspIleTrp----- 954  
QY 2890 CCTCGTCCGGGGCTCTCTCCCTCATATGGCACCTCGGCTGGGTCCCGCAGCGTCTCAG 2949  
Db : : : : :  
955 -----SerValAspProSerLeuValGlySerAsnProGlnArgThrGluAlaHisGlu 972  
QY 2950 AGCTCCCC----- 2958  
Db : : : : :  
973 GlnSerProValAspSerGluLeuHisHisSerProAsnLeuAlaTyrSerProSerHis 992  
QY 2959 -----TGGCCTCGAGCCACA 2973  
Db : : : : :  
993 CysGlnValIleGlnGluGlyHisLeuGlnPheLeuArgCysIleSerProHisSerAsp 1012  
QY 2974 GCTTCTGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAG 3033  
Db : : : : :  
1013 ThrThrLeuThrProLeuGlnSerIleSerAlaThrLeuSerSerSerValCysSerSer 1032  
QY 3034 CCCAGCACCCCT-----GCCTCCCTCCTCTCTGAGGAGGGGCTAGGACT--- 3081  
Db : : : : :  
1033 SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGluGlySerIleThrHis 1052  
QY 3082 GGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACAGCACTGGAGAGCCCCCAGGAGG 3141  
Db : : : : :  
1053 GlyProValSerSerPheSerLeu-----GluAsnLeuProGly 1065  
QY 3142 TCAGGGGCGCTGGCCTTGGCCCTGGGAC 3168  
Db : : : : :  
1066 Ser-----TrpAsp 1068  
RESULT 6  
KCH4\_HUMAN  
ID KCH4\_HUMAN  
AC Q9UQ05;  
DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 4 (Ether-a-go-go-  
DE like potassium channel 1) (ELK channel 1) (ELK1) (Brain-specific eag-  
DE like channel 2) (BEC2).  
GN KCNH4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=99386988; PubMed=10455180;  
RA Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;  
RT "New ether-a-go-go K+ channel family members localized in human  
RT telencephalon.";  
RL J. Biol. Chem. 274:25018-25025(1999).  
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium  
CC channel. Elicits an outward current, but shows no inactivation.  
CC Channel properties may be modulated by cAMP and subunit assembly.  
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- Or  
CC heterotetrameric complex of pore-forming alpha subunits that can  
CC associate with modulating beta subunits.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Detected only in brain, in particular in the  
CC telencephalon. Detected in putamen and caudate nucleus, and at  
CC lower levels in cerebral cortex, occipital and hippocampus.  
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is  
CC characterized by a series of positively charged amino acids at  
CC every third position.  
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Bag)  
CC subfamily.  
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; AB022698; BAA83592.1; --  
DR Genew; HGNC:6253; KCNH4.  
DR MIM; 604528; --  
DR GO; GO:0008076; C:voltage-gated potassium channel complex; TAS.  
DR GO; GO:0005249; F:voltage-gated potassium channel activity; TAS.  
DR GO; GO:0006813; P:potassium ion transport; TAS.  
DR InterPro; IPR000595; cNMP\_binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc\_C.  
DR InterPro; IPR000014; PAS\_domain.  
DR Pfam; PF00027; cNMP\_binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; cNMP; 1.  
DR SMART; SM00086; PAC; 1.  
DR SMART; SM00091; PAS; 1.  
DR TIGRFAMs; TIGR00229; sensory\_box; 1.  
DR PROSITE; PS00888; cNMP\_BINDING\_1; FALSE\_NEG.  
DR PROSITE; PS00889; cNMP\_BINDING\_2; FALSE\_NEG.  
DR PROSITE; PS50042; cNMP\_BINDING\_3; 1.  
DR PROSITE; PS50112; PAS; 1.  
DR PROSITE; PS50113; PAC; 1.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;

KW Potassium channel; Potassium transport; Transmembrane;  
KW Glycoprotein; Multigene family.  
FT DOMAIN 1 228 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 229 249 SEGMENT S1 (POTENTIAL).  
FT TRANSMEM 260 280 SEGMENT S2 (POTENTIAL).  
FT DOMAIN 281 302 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 303 323 SEGMENT S3 (POTENTIAL).  
FT TRANSMEM 333 353 SEGMENT S4 (POTENTIAL).  
FT DOMAIN 354 361 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 362 382 SEGMENT S5 (POTENTIAL).  
FT DOMAIN 428 448 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
FT TRANSMEM 483 503 SEGMENT S6 (POTENTIAL).  
FT DOMAIN 504 1017 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 14 90 PAS.  
FT DOMAIN 93 145 PAC.  
FT NP BIND 556 671 CNMP.  
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1017 AA; 111692 MW; 4B480DFC75816A38 CRC64;

Alignment Scores:  
Pred. No.: 9.77e-102 Length: 1017  
Score: 2461.50 Matches: 538  
Percent Similarity: 59.19% Conservative: 119  
Best Local Similarity: 48.47% Mismatches: 245  
Query Match: 40.43% Indels: 208  
DB: 1 Gaps: 23

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x KCH4\_HUMAN (1-1017)

QY 1 ATGCCGGCCATCGGGGCTCTCTGGCCCTCAGAACACCTTCCTGGACACCAATCGCTACG 60  
Db MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCACGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyThrArgGlyPhe 40  
QY 121 CCCGTGGTCTACTGCTGATGCTTCTGTGACCTCAGCGGCTTCTCCCGGGCTGAGTTC 180  
Db ProIleValTyrCysSerAspGlyPheCysGluLeuThrGlyTyrArgThrGluVal 60  
QY 181 ATGCAGCGGGCTGTGCTGCTCTCTCTCTTTATGGGCGACACACAGTGTGCTCCGC 240  
Db MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGluThrSerGluProAlaLeu 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db GlnArgLeuHisLysAlaLeuGluGlyHisGlnGluHisArgAlaGluIleCysPheTyr 100  
QY 301 CGGAAGAGCGGCTCCCGTTCGTGCTCTCTGATGTATGATACCCATAAAGAATGAGAA 360  
Db ArgLysAspGlySerAlaPheTyrCysLeuLeuAspMetMetProIleLysAsnGluMet 120  
QY 361 GGGAGGTGGCTCTCTCTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db GlyGluValValLeuPheLeuPheSerPheLysAspIleThrGlnSerGlySerProGly 140  
QY 421 ---GGCCCGCAGATGGAAGGACAGGTGGTGGCCCGCCGATATGGCCGGCCACGA 477  
Db LeuGlyProGln-----GlyGlyArgGlyAspSerAsnHisGluAsn 154  
QY 478 TCCAAAGGC-----TTCAATGCCAACCGCGCGGCGGAGCCGGGCC 516  
Db SerLeuGlyArgArgGlyAlaThrTrpLysPheArgSerAlaArgArgSerArgThr 174  
QY 517 GTGCTCTACCACTGTCCGGGCACCTGCAGAACGACCCCAAGGGCAAGCAAGCTCAAT 576  
Db ValLeuHisArgLeuThrGlyHisPheGlyArgGlyGlnGlyMetLysAlaAsn 194  
QY 577 AAGGGGTGTTGGGAGAAACCAAACTTGCCTCAGTACAAAGTAGCCGCATCCGGAAG 636

Db 195 AsnAsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGly 214  
QY 637 TCGCCCTTCATCTCTGTCACACTGTGGGCACTGAGAGCCACCTGGATGGCTTCATCTC 696  
Db 215 SerArgCysLeuLeuLeuHisTyrSerValSerLysAlaIleTrpAspGlyLeuIleLeu 234  
QY 697 CTCGCCACACTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAG 756  
Db 235 LeuAlaThrPheTyrValAlaValThrValProTyrAsnValCysPheSerGlyAspAsp 254  
QY 757 GAGCCAGTGCCTCCCGCGGCCAGCGTCTGTGACCTGGCGGTGGAGTCTCTCTTC 816  
Db 255 AspThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPhe 274  
QY 817 ATCCTTGACATTTGCTGAATTTCCGTACCACTTCTGTGTCCAGTTCGAGTGGCCAGGTG 876  
Db 275 IleLeuAspIleIleLeuAsnPheArgThrThrTyrValSerGlnSerGlyGlnValIle 294  
QY 877 TTTGCCCAAGTCCATTGCTCCCTCCACTACGTACCACTTCTGTGTCTGTGATGTATC 936  
Db 295 SerAlaProArgSerIleGlyLeuHisTyrLeuAlaThrTrpPhePheIleAspLeuIle 314  
QY 937 GCAGCGCTGCCCTTGACCTGTCTGACACTGCTATGCTTCAAGTCAACGTGTACTTCGGG 996  
Db 315 AlaAlaLeuProPheAspLeuLeuTyrIlePheAsnIleThrValThrSerLeuValHis 334  
QY 997 CTGCTGAAGACGGTGCCTGCTGCGCTGCTGCGCTGCTTCCGCGGTGGACCGGTAC 1056  
Db 335 LeuLeuLysThrValArgLeuLeuArgLeuLeuGlnLysLeuGluArgTyr 354  
QY 1057 TCGCAGTACAGCGCGTGTGTGCTGACACTGCTATGCGCGCTGTTCGCGCTGCTCGCCAC 1116  
Db 355 SerGlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHis 374  
QY 1117 TGGTTCGCTGCTGCTGCTTTTACATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAG 1176  
Db 375 TrpMetAlaCysIleTrpTyrValIleGlyArgArgGluMetGluAlaAsnAspProLeu 394  
QY 1177 CTGCTGAGATTGGTGTGCTGAGGAGTGGCGCGGCTGCGGCTGAGACTCCCTACTACCTG 1236  
Db 395 LeuTrpAspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluValProTyr 412  
QY 1237 GTGGCGGAGGCCAGCTGGAGGGAACAGCTCCGCGCCAGAGTGACAACTGCAGCAGCAGC 1296  
Db 412 ----- 412  
QY 1297 AGCAGGCCAACGGGACGGGCTGGAGCTGTGGCGGCGCGCTGCTGCGCAGCGCTAC 1356  
Db 413 -----ValAsnGlySer-----ValGlyGlyProSerArgSerAlaTyr 426  
QY 1357 ATCACTCCCTCTACTTTCGCACTCAGCAGCTCACCAGCGTGGCTTCGGCAACGTGTCC 1416  
Db 427 IleAlaAlaLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCys 446  
QY 1417 GCCAACACGACACCGAGAGATCTTCTCCATCTGCACCATGCTCATCGCGCCCTGATG 1476  
Db 447 AlaAsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet 466  
QY 1477 CACGCGGTGTGTTGGGAACGTGACGGCCATCATCCAGCGATGTACGCCCGCGCTTT 1536  
Db 467 HisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgSer 486  
QY 1537 CTGTACCAACAGCCGACCGCGGACCTGCGCGACTACATCCGATCCACCGTATCCCCAAG 1596  
Db 487 LeuTyrHisSerArgMetLysAspLeuLysAspPheIleArgValHisArgLeuProArg 506  
QY 1597 CCCCTCAACGACGCGCATGTGGAGTACTTCCAGGCCACCTGGCGGTGAACAATGGCATC 1656  
Db 507 ProLeuLysGlnArgMetLeuGluTyrPheGlnThrThrTrpAlaValAsnSerGlyIle 526  
QY 1657 GACACCCAGCTGCTGCAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCAC 1716  
Db 527 AspAlaAsnGluLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHis 546





J. Neurosci. 21:4609-4624 (2001).

-!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium channel. Elicits an outward current, but shows no inactivation. Channel properties may be modulated by cAMP and subunit assembly.

-!- SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: Highly expressed in adult testis, and in adult and embryonic brain. In adult brain found in piriform cortex, olfactory tubercle, cerebral cortex, hippocampus pyramidal cells and dentate gyrus and basal ganglia of caudate/putamen and accumbens nucleus. Detected at intermediate levels in lung, spinal cord, and pituitary.

-!- DEVELOPMENTAL STAGE: Expressed at day E18 in embryonic brain.

-!- DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.

-!- SIMILARITY: Belongs to the potassium channel family. H (Bag) subfamily.

-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.

-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; AJ007628; CAA07587.1; -.

EMBL; AB022699; BAA83593.1; -.

PIR; T31354; T31354.

InterPro; IPR000595; cNMP\_binding.

InterPro; IPR003967; Erg\_channel.

InterPro; IPR005821; Ion\_trans.

InterPro; IPR001622; K+channel\_pore.

InterPro; IPR005820; M+channel\_nlg.

InterPro; IPR001610; PAC.

InterPro; IPR000700; PAS-assoc\_C.

InterPro; IPR000014; PAS\_domain.

Pfam; PF00027; cNMP\_binding; 1.

Pfam; PF00520; ion\_trans; 1.

Pfam; PF00785; PAC; 1.

PRINTS; PR01470; ERGCHANNEL.

SMART; SM00100; cNMP; 1.

SMART; SM00086; PAC; 1.

SMART; SM00091; PAS; 1.

SMART; SM00091; PAS; 1.

TIGRFAMS; TIGR00229; sensory\_box; 1.

PROSITE; PS00888; cNMP\_BINDING\_1; FALSE\_NEG.

PROSITE; PS00889; cNMP\_BINDING\_2; FALSE\_NEG.

PROSITE; PS50042; cNMP\_BINDING\_3; 1.

PROSITE; PS50112; PAS; 1.

PROSITE; PS50113; PAC; 1.

Transport; Ion transport; Ionic channel; Voltage-gated channel; Potassium channel; Potassium; Potassium transport; Transmembrane; Glycoprotein; Multigene family.

DOMAIN 1 232 CYTOPLASMIC (POTENTIAL).

TRANSMEM 233 SEGMENT S1 (POTENTIAL).

TRANSMEM 263 SEGMENT S2 (POTENTIAL).

DOMAIN 284 305 CYTOPLASMIC (POTENTIAL).

TRANSMEM 306 326 SEGMENT S3 (POTENTIAL).

TRANSMEM 335 355 SEGMENT S4 (POTENTIAL).

DOMAIN 356 364 CYTOPLASMIC (POTENTIAL).

TRANSMEM 365 385 SEGMENT S5 (POTENTIAL).

DOMAIN 428 448 SEGMENT H5 (PORE-FORMING) (POTENTIAL).

TRANSMEM 455 475 SEGMENT S6 (POTENTIAL).

DOMAIN 476 1017 CYTOPLASMIC (POTENTIAL).

DOMAIN 14 90 PAS.

DOMAIN 93 145 PAC.

NP\_BIND 557 cNMP.

FT CARBOHYD 415 415 N-LINKED (GLCNAC... ) (POTENTIAL).

FT CONFLICT 825 825 R -> W (IN REF. 1).

SQ SEQUENCE 1017 AA; 111403 MW; BFDB0F1B35437C9F CRC64;

Alignment Scores: Length: 1017

Pred. No.: 2447.50 Matches: 533

Score: 60.09% Conservative: 131

Percent Similarity: 48.24% Mismatches: 243

Best Local Similarity: 40.20% Indels: 198

Query Match: 1 Gaps: 23

DB: 1

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x KCH4\_RAT (1-1017)

QY 1 ATGCCGGCCATGCGGGGCTCTCTGCGGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60

Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGCTTCGACGGCAGCACAGTAATCTCTGCTGGGCAACGCCAGGTGGGGGCTCTTC 120

Db 21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyProArgGlyPhe 40

QY 121 CCCGTGGTCTACTGCTCTGATGGTCTCTGTGACCTCAGGGCTTCTCCCGGCTGAGGTC 180

Db 41 ProileValTyrCysSerAspGlyPheCysGluLeuThrGlyTyrGlyArgThrGluVal 60

QY 181 ATGCAGCGGGCTGCGCTGCTCTCTCTTATGGGCCAGACACCATGAGCTGCTCCGC 240

Db 61 MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGluThrSerGluProAlaLeu 80

QY 241 CAACAGATCCGCAAGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCTGTAC 300

Db 81 GlnArgLeuGlnLysAlaLeuGluGlyHisGlnGluHisArgAlaGluIleCysPheTyr 100

QY 301 CGGAAGAGCGGGCTCCGTTCTGCTGCTCTCTCTGATGTATACCCATATAAGATGAGAAA 360

Db 101 ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetMetProIleLysAsnGluLeu 120

QY 361 GGGGAGGTGGTCTCTCTCTAGTCTCTCACAAAGGACATCAGCGAAACCAAGAACCGAGG 420

Db 121 GlyGluValValLeuPheLeuPheSerPheLysAspIleSerGlnSerGlyGlyProGly 140

QY 421 -----GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGC 459

Db 141 LeuGlySerProGlyIleHisGlyAspAsnAsnAsnHisGluAsnSerLeuGlyArg--- 159

QY 460 CGATATGCGCGGCACGATCCAAAGGCTTCAATGCCAACCGGGCGGAGCGCGGCGGTG 519

Db 160 -----ArgGlyAlaSerSerArgLeuArgSerThrArgArgGlnAsnArgThrVal 176

QY 520 CTCTACACCTGTCCGGGCACCTGCAGAACGACAGCCCAAGGCAAGCACAAGCTCAATAAG 579

Db 177 LeuHisArgLeuThrGlyHisPheGlyArgArgAspGlnGlySerValLysAlaAsnSer 196

QY 580 GGGGTGTTGGGGAGAAACCAAACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCG 639

Db 197 AsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGlySer 216

QY 640 CCCTTCATCCTGTGCACTGTGGGGCACTGAGAGCCACCTGGGATGGTCTCATCTGCTC 699

Db 217 ArgCysLeuLeuLeuHisTyrSerIleProLysAlaValTrpAspGlyLeuIleLeu 236

QY 700 GCCACACTCTATGTGGCTGTCACTGTGCTGCTACAGCGTGTGTGTGACGACGCGGAG 759

Db 237 AlaThrPheTyrValAlaValThrValProTyrAsnValCysPheAlaGlyAspAsp 256

QY 760 CCCAGTCCCGCCCGCGCCCGCCAGCGTCTGTGACCTGGCGGTGGAGTCTCTTCATC 819

Db 257 ThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPheIle 276

QY 820 CTTGACATTGTGCTGAATTTCCGTACCAATTCGTGTCCAAAGTCCGGCCAGGTGGTGT 879

Db 277 LeuAspIleIleLeuAsnPheArgThrThrTyrValSerGlnSerGlnValValSer 296







Db 101 ValHisLeuLeuLysThrValArgLeuLeuArgLeuLeuGlnLysLeuAsp 120  
QY 1051 CGGTACTCGAGTACAGCGCGTGGTGTGACTGACACTGTCTCATGGCGGTGTTCGCCCTGCTC 1110  
Db 121 ArgTyrSerGlnHisSerThrIleValLeuThrLeuLeuMetSerMetPheAlaLeuLeu 140  
QY 1111 GCGCACTGGTGCCTGCGTCTGCTGTTTACATTGGCCAGCGGGAGATCGAGACGCGAA 1170  
Db 141 AlaHisTrpMetAlaCysIleTrpTyrValIleGlyLysMetGluArgGluAspAsnSer 160  
QY 1171 TCCGAGTGCCTGAGATTGGTGGTGTGAGGAGTGGCCCGCGACTGGAGACTCCCTTAC 1230  
Db 161 LeuLeuLysTrpGluValGlyTrpLeuHisGluLeuGlyLysArgLeuGluSerProTyr 180  
QY 1231 TACCTGGTGGCCGGAGGCCAGCTGGAGGGAACAGCTCCGGGCCAGAGTGACAACTGCAGC 1290  
Db 181 Tyr-----GlyAsnAsnThr 185  
QY 1291 AGCAGCAGCGAGGCCAACGGGACGGGGCTGGAGCTGCTGGGCGGCCCGTGCCTGCGCAGC 1350  
Db 186 -----LeuGlyGlyProSerIleArgSer 193  
QY 1351 GCCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTCACCAGCGTGGGCTTCGGCAAC 1410  
Db 194 AlaTyrIleAlaAlaLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsn 213  
QY 1411 GTGTCCGCCAACACGGACACGGAGACCGAGAAGATCTTCTCCATCTGCACCATGCTCATCGCGCC 1470  
Db 214 ValSerAlaAsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAla 233  
QY 1471 CTGATGCACGCGGTGGTGTGGAAACGTGACGGCCATCATCCAGCGCATGTACGCCCGC 1530  
Db 234 LeuMetHisAlaLeuValPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArg 253  
QY 1531 CGCTTTCTGTATCCACAGCGCACGCGCACCTGCGCGACTACATCCGCGATCCACCGTATC 1590  
Db 254 TrpSerLeuTyrHisThrArgThrLysAspLeuLysAspPheIleArgValHisLeu 273  
QY 1591 CCCAAGCCCCCTCAGCAGCGCATGTGGAGTACTTCCAGGCCACCTGGGCGGTGAACAAT 1650  
Db 274 ProGlnGlnLeuLysGlnArgMetLeuGluTyrPheGlnThrThrTrpSerValAsnAsn 293  
QY 1651 GGCATCGACACCCAGAGCTGCTGCAGAGCCTCCCTGACGAGCTGCGCGCACACATCGCC 1710  
Db 294 GlyIleAspSerAsnGluLeuLeuLysAspPheProAspGluLeuArgSerAspIleThr 313  
QY 1711 ATGCACCTGCACAAGGAGGTCTTGACGTGCGCACTGTTTGGCGCGGCCAGCCGGCTGC 1770  
Db 314 MetHisLeuAsnLysGluIleLeuGlnLeuSerLeuPheGluCysAlaSerArgGlyCys 333  
QY 1771 CTGCGGCACTGTCTCTGGCCCTGCGGCCCGCTTCTGCACGCCCGGGGAGTACCTCATC 1830  
Db 334 LeuArgSerLeuSerLeuHisIleLysThrSerPheCysAlaProGlyGluTyrLeuLeu 353  
QY 1831 CACCAAGGCGATGCCCTGCAGGCCCTCTACTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1890  
Db 354 ArgGlnGlyAspAlaLeuGlnAlaIleTyrPheValCysSerGlySerMetGluValLeu 373  
QY 1891 AAGGTTGGCACCGTGTCTGCCCATCTTAGGGAAGGCGACCTGATCGGCTGTGAGCTGCC 1950  
Db 374 LysAspSerMetValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAsnLeuSer 393  
QY 1951 CGGCGGAGCAGGTGGTAAAGGCCAATGCCGACGTGAAGGGGTGACGTACTGCGTCTCTG 2010  
Db 394 IleLysAspGlnValIleLysThrAsnAlaAspValLysAlaLeuThrTyrCysAspLeu 413  
QY 2011 CAGTGTCTGAGCTGGCTGGCTGCACGACAGCCTTGGCGTGTACCCCGAGTTTGGCCCG 2070  
Db 414 GlnCysIleIleLeuLysGlyLeuPheGluValLeuGlyLeuTyrProGluTyrAlaHis 433  
QY 2071 CGCTTCAGTCGTGGCTCCGAGGGGAGCTCAGCTACAACTGGGTGCTGG----- 2121  
Db 434 LysPheValGluAspIleGlnHisAspLeuThrTyrAsnLeuArgGluGlyHisGluSer 453

QY 2122 -----GGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGCGGGCAG 2163  
Db 454 AspValIleSerArgLeuSerAsnLysSerThrValSerGlnAlaGluProLysGlyAsn 473  
QY 2164 AATACCTTATGTCCACGCTG-----GAGGAGAGGAGACAGATGGGGAG 2208  
Db 474 GlySerIleAsnLysArgLeuProSerIleValGluAspGluGluGluValGlu 493  
QY 2209 CAGGGCCCCACGGTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTCCCT 2268  
Db 494 GluGluGluThrThrSerLeuSerProIleTyrThrArgGlySerSerValSerHisSer 513  
QY 2269 GGCTGCACCTCTCATCTCAGCTGCCAAGCTGTATCCACAGCTCGAACACAGCACCCCGG 2328  
Db 514 LysLysThrGlySerAsnLysThrTyrLeuGlyLeuSerLeuLysGlnLeuAlaSerGly 533  
QY 2329 CCT-----CGTCTAGGTGGCAGAGGAGGCCAGGCAGGGCAGGG 2367  
Db 534 ThrValProPheHisSerProIleArgValSerSerAlaAsnSerPro----- 549  
QY 2368 GCTTTGAAGGCTGAGGTGGCCCTCTCTGCTCCCCCAGCGGCCCTAGAG-----GGG 2418  
Db 550 LysThrLysGlnGluAlaAspProProAsnHisGlyArgLysLysGluLysAsnLeuLys 569  
QY 2419 CTACGGCTGCCCCCCATGCCATGGAATGTGCCCCCAAGATCTGAGCCCCAGGGTAGTAGAT 2478  
Db 570 ValGlnLeuSerSerLeuGlySerAlaGlyThrProGluLeuSerProArgIleValAsp 589  
QY 2479 GGCATTGAAGACGGCTGTGGCTCGGACCCAGCCCAAG---TTCTCTTTCCGCGTGGGCAG 2535  
Db 590 GlyIleGluAspGlyAsnSerAsnGluGluThrGlnThrPheAspPheGlySerGluGln 609  
QY 2536 TCTGGCCCGGAATGTAGCAGCAGCCCTCCCTCGACAGAGCGGCTGCTCACTGTT 2595  
Db 610 IleArgProGluProArgIleSerPro---ProLeuAlaGluSerGluIle----- 625  
QY 2596 CCCCATGGGCCCAGC-----GAGGCAAGGAACACA---GACACACTGGACAAG 2640  
Db 626 -----GlyAlaAlaPheLeuPheIleLysAlaGluThrLysGlnGlnIleAsnLys 643  
QY 2641 CTTCGGCAGGCGGTGACAGAGCTGTACAGCAGAGGTGCTGCAGATCGGGAAGGACTGCAG 2700  
Db 644 LeuAsnSerGluValThrThrLeuThrGlnGluValSerGlnLeuGlyArgAspMetArg 663  
QY 2701 TCACCTTCGCCAGGCTGTGCAGCTTGTCTCTGGCGCCCCACAGGGAGGGT----- 2748  
Db 664 SerIleMetGlnLeuLeuGluAsnIleLeuSerProGlnGlnProSerGlnPheCysSer 683  
QY 2749 -----CCGTGCCCTCGGGCATCGGGAGAGGGCGCGTGGCCAGCCAGCACCTCCGGGCTT 2802  
Db 684 LeuHisProThrProMet-----CysProSerArgGluSer----- 695  
QY 2803 CTGCAGCCTCTGTGTGGACACTGGGCGCATCTCCTACTGCTGAGCCCCCAGCT--- 2859  
Db 696 LeuGlnThrArg---ValSerTrpSerAlaHisGlnProCysLeuHisLeuGlnAlaGly 714  
QY 2860 -----GGCTCTGTCTTTGAGTGGGACITTTGGCCCCCACCCTCGTCCGGGG 2901  
Db 715 GlyAlaHisLeuTyrHisGlyAsnValAlaSerGlyIleTrp-----SerVal 730  
QY 2902 CCTCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCAGCGTCTCAGAGCTCCCCC 2958  
Db 731 AspProSerLeuValGlySerSerProGlnArgThrGluAlaHisGluGlnAsnProAla 750  
QY 2958 ----- 2958  
Db 751 AspSerGluLeuHisHisSerProAsnLeuAspTyrSerProSerHisCysGlnValIle 770  
QY 2959 -----TGGCCTCGAGCCACAGCTTTCTGGACC 2985  
Db 771 GlnGluGlyHisLeuGlnPheLeuArgCysIleSerProHisSerAspThrThrLeuThr 790

QY 2986 TCCACCTCAGACTCAGAGCCCCCTGCTCAGGAGACCTCTGCTCTGAGCCAGCACCCCT 3045  
Db 791 ProLeuGlnSerIleSerAlaThrLeuSerSerSerValCysSerSerSerGluThrSer 810  
QY 3046 -----GCCTCCCTCCTCTCTGAGGAAGGGCTAGGACT---GGGCCCGCAGAG 3093  
Db 811 LeuHisLeuValLeuProSerArgSerGluGluGlySerIleThrHisGlyProValSer 830  
QY 3094 CCTGTGAGCAGGCTGAGGCTACGAGCTGAGAGCCCCCAGGCTCAGGGTCCAGGGCCCTG 3153  
Db 831 SerPheSerLeu-----GluAsnLeuProGlySer----- 840  
QY 3154 GCCTTGCCCTGGGAC 3168  
Db 841 -----TTPASP 842

RESULT 9  
KCH2\_CANFA STANDARD; PRT; 1158 AA.  
AC Q9TSZ3; 002719; 018820;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go  
DE related gene potassium channel 1) (ERG1) (c-erg) (DERG) (Ether-a-go-  
DE go related protein 1) (Eag related protein 1).  
GN KCNH2 OR ERG OR CERG.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=21310885; PubMed=11417212;  
RA Zehelein J., Zhang W., Koenen M., Graf M., Heinemann S.H., Katus H.A.;  
RT "Molecular cloning and expression of CERG, the ether a go-go-related  
RL gene from canine myocardium."  
RN Pflugers Arch. 442:188-191(2001).  
RN [2]  
RP SEQUENCE OF 407-566 FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=97164986; PubMed=9012748;  
RA Wymore R.S., Gintant G.A., Wymore R.T., Dixon J.E., McKinnon D.,  
RA Cohen I.S.;  
RT "Tissue and species distribution of mRNA for the IKr-like K+ channel,  
RL erg."  
RN Circ. Res. 80:261-268(1997).  
RN [3]  
RP SEQUENCE OF 616-714 FROM N.A.  
RC TISSUE=Heart atrium;  
RX MEDLINE=99221626; PubMed=10205145;  
RA Yue L., Melnyk P., Gaspo R., Wang Z., Nattel S.;  
RT "Molecular mechanisms underlying ionic remodeling in a dog model of  
RL atrial fibrillation."  
RN Circ. Res. 84:776-784(1999).  
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated inwardly  
CC rectifying potassium channel. Channel properties are modulated by  
CC CAMP and subunit assembly. Mediates the rapidly activating  
CC component of the delayed rectifying potassium current in heart  
CC (IKr) (By similarity).  
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or  
CC heterotetrameric complex of pore-forming alpha subunits that can  
CC associate with modulating beta subunits. Heteromultimer with  
CC KCNH6/ERG2, KCNH7/ERG3, KCNE1 and KCNE2 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Highly expressed in left and right atria of  
CC the heart, in cortex and hippocampus; detected at intermediate  
CC levels in left and right ventricle, Purkinje fibers, cerebellum,  
CC thalamus and basal ganglia; detected at low levels in liver,  
CC spleen and kidney.  
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is  
CC characterized by a series of positively charged amino acids at

CC every third position.  
CC -!- PTM: Phosphorylated on serine and threonine residues (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag)  
CC subfamily.  
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AJ243344; CAB64868.1; --  
CC EMBL; U75213; AAC48722.1; --  
CC EMBL; AF017429; AAB70524.1; --  
CC InterPro; IPR000595; CNMP\_binding.  
CC InterPro; IPR003967; Erg\_Channel.  
CC InterPro; IPR005821; Ion\_trans.  
CC InterPro; IPR001622; K+channel\_pore.  
CC InterPro; IPR005820; M+channel\_nlg.  
CC InterPro; IPR001610; PAC.  
CC InterPro; IPR000700; PAS-assoc\_C.  
CC InterPro; IPR000014; PAS\_domain.  
CC Pfam; PF00027; CNMP\_binding; 1.  
CC Pfam; PF00520; ion\_trans; 1.  
CC Pfam; PF00785; PAC; 1.  
CC PRINTS; PR01470; ERGCHANNEL.  
CC SMART; SM00100; CNMP; 1.  
CC SMART; SM00086; PAC; 1.  
CC SMART; SM00091; PAS; 1.  
CC PROSITE; PS00888; CNMP\_BINDING\_1; FALSE\_NEG.  
CC PROSITE; PS00889; CNMP\_BINDING\_2; FALSE\_NEG.  
CC PROSITE; PS50042; CNMP\_BINDING\_3; 1.  
CC PROSITE; PS50112; PAS; 1.  
CC PROSITE; PS50113; PAC; 1.  
CC Transport; Ion transport; Ionic channel; Voltage-gated channel;  
CC Potassium channel; Potassium; Potassium transport; Transmembrane;  
CC Phosphorylation; Glycoprotein; Multigene family.  
CC DOMAIN 1 402 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 403 423 SEGMENT S1 (POTENTIAL).  
CC TRANSMEM 450 470 SEGMENT S2 (POTENTIAL).  
CC DOMAIN 471 494 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 495 515 SEGMENT S3 (POTENTIAL).  
CC TRANSMEM 520 540 SEGMENT S4 (POTENTIAL).  
CC DOMAIN 541 546 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 547 567 SEGMENT S5 (POTENTIAL).  
CC DOMAIN 611 631 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
CC TRANSMEM 638 658 SEGMENT S6 (POTENTIAL).  
CC DOMAIN 659 1158 CYTOPLASMIC (POTENTIAL).  
CC DOMAIN 17 88 PAS.  
CC DOMAIN 92 144 PAC.  
CC DOMAIN 296 299 POLY-PRO.  
CC NP\_BIND 741 858 CNMP.  
CC CARBOHYD 597 597 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CONFLICT 442 442 P -> T (IN REF. 2).  
CC SEQUENCE 1158 AA; 126644 MW; 53CB49032B4AA3D0 CRC64;  
SQ

Alignment Scores:  
Pred. No.: 1,35e-61 Length: 1158  
Score: 1551.00 Matches: 411  
Percent Similarity: 44.40% Conservative: 136  
Best Local Similarity: 33.36% Mismatches: 351  
Query Match: 25.47% Indels: 334  
DB: 1 Gaps: 33

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x KCH2\_CANFA (1-1158)

QY 1 ATGCCGGCCATGGGGGCGCTCTGCTGAGCCCTCAGACACCTTCCTGGACACCATCGCTACG 60



Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg 20  
QY 61 CGCTTCGACGGCAGCACAGTAACTTCGTGCTGGCAACGCCAGGTCGGGGCTCTTC 120  
Db 21 LysPheGluGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys--- 39  
QY 121 CCCGTGGTCTACTGCTCTGTAGGCTTCTGTGACCTCAGGGCTTCTCCCGGCTGAGGTC 180  
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59  
QY 181 ATGCAGCGGGCTGTGCCTGCTCCTTCTTATGGGCCAGACACAGTCAGCTCGTCCGC 240  
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79  
QY 241 CAACAGATCCGCAAGGCCCTGGACGACCAAGAGTTCAAGCGTGAAGCTGATCCTGTAC 300  
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTCTGGATGTGATFACCCATAAAGAATGAGAAA 360  
Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp 119  
QY 361 GGGGAGGTGGCTCTCTTCCTA-----GTCTCTCACAAAGGACATC----- 399  
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139  
QY 400 -----AGCGAAACCAAGAACCGAGGGGGCCCGACAGATGGAAGGAGACAGGT--- 447  
Db 140 SerProThrHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159  
QY 447 ----- 447  
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrThrArgGluSerSer 179  
QY 447 ----- 447  
Db 180 AlaArgProGlyGlyValGlySerAlaGlyAlaProGlyAlaValValValAspValAsp 199  
QY 447 ----- 447  
Db 200 LeuSerProAlaValProSerArgGluSerLeuAlaLeuAspGluValThrAlaMetAsp 219  
QY 447 ----- 447  
Db 220 AsnHisValAlaGlyLeuGlyProMetGluGlnArgAlaLeuValGlySerSerSer 239  
QY 447 ----- 447  
Db 240 ProProAlaGlyAlaProGluProLeuProSerProArgAlaHisSerLeuAsnProAsp 259  
QY 448 -----GGTGGCCGGCGCGATATGGCCGGCACGATCCAAAGGCTTCAATGCCAACCGG 501  
Db 260 AlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSerVal 279  
QY 502 CGGCGG----- 507  
Db 280 ArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyLeuProProPro 299  
QY 508 -----AGCCGGGCGGTGCTTACACCTGTCCGGGCACCTGCAGAGCAG----- 552  
Db 300 ArgHisAlaSerThrGlyAlaMetHisProLeuArgGlyGlyLeuLeuAsnSerThrSer 319  
QY 552 ----- 552  
Db 320 AspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeuAsnPhe 339  
QY 552 ----- 552  
Db 340 ValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIleIleAla 359  
QY 553 CCCAAGGGCAAGCACAGCTCAATAAGGGGTGTTTGGGGAGAAAACCAAC----- 603

Db 360 ProLysIleLysGluArgThrHisAsn-----ValThrGluLysValThrGlnValLeu 377  
QY 604 -----TTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTC 645  
Db 378 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp 397  
QY 646 ATCCTGTTCACACTGTGGGGCACTGAGAGCCACCTGGGATGGCTTCATCTCTGCTGCCACA 705  
Db 398 ThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuVal 417  
QY 706 CTCTATGTGGCTGTACATGTGCCCTACAGCGTGTGTGTG-----AGCACAGCACGG 756  
Db 418 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu 437  
QY 757 GAGCCAGTGCC-----GCCCGCGGCGCCCGCCAGCGTCTGTGACCTGGCC 801  
Db 438 GlyProProAlaProAspCysGlyTyrAlaCysGlnProLeuAlaValValAspPheIle 457  
QY 802 GTGAGGTCCTCTTCATCCTTGACATTGTGCTGAATTTCGTTACCATTCGTGTCCAAAG 861  
Db 458 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsnAla 477  
QY 862 TCGGGCCAGGTGGTGTTCGCCCCAAAGTCCATTTGCTCCACTACGTCAACCACCTGGTTC 921  
Db 478 AsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrpPhe 497  
QY 922 CTGCTGGATGTATCGACGGCTGCCCTTTGACCTGTACATGCCCTTCAAGGTCAACGTG 981  
Db 498 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 510  
QY 982 TACTTCGGGGCC-----CATCTGCTGAAGACGGTGGCGCTGCTGCGC 1023  
Db 511 IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 530  
QY 1024 CTGCTGCGCTGCTTCGCGGGCTGGACCGGTACTCGCAGTACAGCGCGTGGTGTGACACA 1083  
Db 531 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 550  
QY 1084 CTGCTCATGGCCGCTGTTGCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTGTTTACATT 1143  
Db 551 LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIle 570  
QY 1144 GGCCAGCGGGAGATCGAGAGCAGCAATCCGAGCTGCTGAGATTGGTGGCTGCAGGAG 1203  
Db 571 GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTrpLeuHisAsn 587  
QY 1204 CTGGCCCGCGCACTGGAGACTCCCTACTACTGCTGGTGGCGGAGGCCAGCTGGAGGAAC 1263  
Db 588 LeuGlyAspGlnIleGlyLysProTyr----- 597  
QY 1264 AGTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCACCGGACGGGCTGGAG 1323  
Db 598 SerSerGly----- 600  
QY 1324 CTGCTGGCGGGCCCGTTCGCTGCGCAGCGCCTACATCACTCCCTCTACTTCGCACTCAGC 1383  
Db 601 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 619  
QY 1384 AGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGACACCGAGAAGATCTTC 1443  
Db 620 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 639  
QY 1444 TCATCTGCACCATGTCTATCGGCGCCTGTATGCACGGGTGGTGTGTTGGGAACGTGACG 1503  
Db 640 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 659  
QY 1504 GCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCCGACCGCGGACCTG 1563  
Db 660 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 679  
QY 1564 CGCGACTACATCCGCGATCCACCGTATCCCCCAAGCCCTCAAGCAGCGCATGTGGAGTAC 1623  
Db 680 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr 699

2596 -----CCCCATGGGGCCAGCGAGGCAAGGAACACAGACACTGGACAGCTTCGGCAG 2649  
1031 ArgArgProArgGlyAspValGluGlyArg-----LeuAspAlaLeuGlnArg 1046  
2650 GCGGTGACAGAGCTGTTCAGAGCAGGTG---CTGCAGATGCGGGAAGGACTGCAGTCACTT 2706  
1047 GlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThrValLeuGlnLeuLeu 1066  
2707 CGCCAGGCTGTGACAGCTTGTCTCTGGCGCCCCACAGGAGGGTCCGTGCTCGGCATCG 2766  
1067 GlnArgGlnMetThrLeuLeuProAlaTyrSerAlaValThrPro----- 1083  
2767 GGAGAGGGCGCTGCCAGCCAGCAGCAGCCTCGGGCTTCTGCAGCCTCTGTGTGGACACT 2826  
1084 -----GlyProGlyProThrSerThrSerLeuLeuProValSerProIleProThr 1101  
2827 GGGGCATCCTCTACTGCTGCAG-----CCCCCA 2856  
1102 LeuThrLeuAspSerLeuSerGlnValSerGlnPheMetAlaPheGluLeuProPro 1121  
2857 GCTGGCTCTGTCTTGTGAGTGGGACTTGGCCCGCCAGCCTCGTCCGGGGCTCCT---CCCCCTC 2913  
1122 GlyAlaProGluLeu-----ProGlnAspGlyProProArgArgLeu 1135  
2914 ATGGCACCTGGCTGGGTCCCCCAGCGTCTCAG 2949  
1136 SerLeuProGlyGlnLeuGlyAlaLeuThrSerGln 1147  
RESULT 10  
KCH2\_HUMAN STANDARD; PRT; 1159 AA.  
ID KCH2\_HUMAN Q12809; O75418; O75680; Q9BT72; Q9H3P0;  
AC Q12809; O75418; O75680; Q9BT72; Q9H3P0;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-MAY-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go  
DE related gene potassium channel 1) (H-ERG) (Ergl) (Ether-a-go-go  
DE related protein 1) (Eag related protein 1) (eag homolog).  
GN KCNH2 OR HERG OR ERG1 OR ERG OR ERG1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Hippocampus;  
RX MEDLINE=94211879; PubMed=8159766;  
RA Warmke J.W., Ganetzky B.;  
RT "A family of potassium channel genes related to eag in Drosophila and  
mammals.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT LQT2 CYS-534.  
RX MEDLINE=98260867; PubMed=9600240;  
RA Itoh T., Tanaka T., Nagai R., Kamiya T., Sawayama T., Nakayama T.,  
RA Tomoike H., Sakurada H., Yazaki Y., Nakamura Y.;  
RT "Genomic organization and mutational analysis of HERG, a gene  
responsible for familial long QT syndrome.";  
RL Hum. Genet. 102:435-439(1998).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Downie D., Chapman C.G., Punia P., Rice S., Bahmani F., Murdock P.,  
RA Pearson N., Randall A.D., Meadows H.J.;  
RT "Potent inhibition of HERG K+ channels by the neuroprotective agent  
Sipatrigine.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Heart;  
RX MEDLINE=21269186; PubMed=11374908;  
RA Soejima H., Kawamoto S., Akai J., Miyoshi O., Arai Y., Morohka T.,  
RA Matsuo S., Niikawa N., Kimura A., Okubo K., Mukai T.;  
RT "Isolation of novel heart-specific genes using BodyMap database.";

1624 TTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACACCGAGCTGTGCAGAGCCTC 1683  
700 PheGlnHisAlaTyrSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 719  
1684 CCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAGGAGTCTCTGCAG---CTG 1740  
720 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys 739  
1741 CCACTGTTGAGCGGCCAGCGCGCTGCTGCGGCACCTGTCTCTGGCCCTGCGGCC 1800  
740 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 759  
1801 GCCTTCTGACGCGCGGAGTACCTCATCCACCAAGCGATGCCCTGCAGGCCCTCTAC 1860  
760 ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr 779  
1861 TTTGTCTGTCTGCTCCATGAGGTGCTCAAGGTGGCACCGTGTCTGCCATCTAGGG 1920  
780 PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly 799  
1921 AAGGGCAGCTGATCGGCTGTGAGTGCCTCCCGCGGAGCAGGTGTTAAGGCCAATGCC 1980  
800 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 819  
1981 GACGTGAAGGGCTGACCTACTGCTGCTCCCGCGCTTCAAGGTGGCACCGTGTCTGCCATCTAGGG 2040  
820 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu 839  
2041 AGCCTTGGCTGTACCCCGAGTTTGCCTCCCGCGCTTCAAGGTGGCACCGTGTCTGCCATCTAGGG 2100  
840 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle 857  
2101 AGCTACAACCTG-----GGTGTGGGGAGGCTCTGCAGAGGTGGAC 2142  
858 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerAlaGluLeuGlu 877  
2143 ACCAGTCTCCTGAGCGCGGACAAATACCTTATGTCCACGCTGGAGGAGGAGGACAGAT 2202  
878 GlyGlyPheAsnArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspArgAsp 897  
2203 GGGGAGCAGGGCCCGCAGCGTCTCCCGCAGCCAGCTGATGAGCCCTCCAGCCCTGCTG 2262  
898 ProGluGln----- 900  
2263 TCCCTGCTGTCACCTCTCATCTCAGCTGCCAAGCTGTATCCCGCAGCTCGAAGCA 2322  
901 ---ProGlyGluValSerAla-----LeuGlyProGlyArgAlaGly 913  
2323 CCGCGCTCTAGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2382  
914 AlaGlyPro-----SerGlyArgGlyArgProGlyProGlyProGlyProSer 931  
2383 GCTGGCCCTCTGCTCCCGCA-----CGCGCCCTAGAGGGG 2418  
932 SerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerSerPro 951  
2419 CTACGGCTG-----CCCCCATGCGCATGGAATGTGCCCCCAGATCTGAGCCCC 2466  
952 LeuArgLeuValProPheSerSerProArgProProGlyGluProProGlyGluPro 971  
2467 AGGGTAGTAGGCGCATTAAGACGGCTGTGGCTCGGACCGCCCAAG----- 2514  
972 LeuThrGluAspGly---GluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 990  
2515 -----TTCTCTTTCGCGTGGGCGCAGTGTGGCCGGAATGTAGCAGC 2556  
991 SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyHisGlnTyrGlnGlu 1010  
2557 AGCCCC---TCCCTGGACGAGAGCGGCTGCTCACTGTT----- 2595  
1011 LeuProArgCysProAlaProThrProSerLeuLeuAsnIleProLeuSerSerProCys 1030

RL Genomics 74:115-120(2001).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RA Crociani O., Guasti L., Balzi M., Becchetti A., Wanke E., Olivotto M.,  
RA Wymore R.S., Arcangeli A.;  
RT "Cell cycle-dependent expression of HERG1 and HERG1b isoforms in tumor  
RT cells.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 1-376 FROM N.A. (ISOFORM 2).  
RC TISSUE=Heart;  
RX MEDLINE=98012815; PubMed=9351462;  
RA London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,  
RA Gilbert D.J., Jenkins N.A., Satler C.A., Robertson G.A.;  
RT "Two isoforms of the mouse ether-a-go-go-related gene coassemble to  
RT form channels with properties similar to the rapidly activating  
RT component of the cardiac delayed rectifier K<sup>+</sup> current.";  
RL Circ. Res. 81:870-878(1997).  
RN [7]  
RP SEQUENCE OF 1-376 FROM N.A. (ISOFORM 2).  
RC TISSUE=Heart atrium;  
RX MEDLINE=98012799; PubMed=9351446;  
RA Lees-Miller J.P., Kondo C., Wang L., Duff H.J.;  
RT "Electrophysiological characterization of an alternatively processed  
RT ERG K<sup>+</sup> channel in mouse and human hearts.";  
RL Circ. Res. 81:719-726(1997).  
RN [8]  
RP SEQUENCE OF 27-1159 FROM N.A. (ISOFORM 1).  
RA Yang P., Paulussen A., Verhasselt P., Crabbe R., Luyten W.,  
RA Armstrong M.;  
RT "Analysis of the human HERG gene: intron localisation and  
RT identification of a novel inherited mutation associated with long  
RT QT.";  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE OF 795-1159 FROM N.A. (ISOFORM 3).  
RC TISSUE=Heart ventricle;  
RX MEDLINE=98438490; PubMed=9765245;  
RA Kupersmidt S., Snyder D.J., Raes A., Roden D.M.;  
RT "A K<sup>+</sup> channel splice variant common in human heart lacks a C-terminal  
RT domain required for expression of rapidly activating delayed  
RT rectifier current.";  
RL J. Biol. Chem. 273:27231-27235(1998).  
RN [10]  
RP SEQUENCE OF 59-1159 FROM N.A. (ISOFORM 4), AND SEQUENCE OF 711-1159  
RP FROM N.A. (ISOFORM 1/2).  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [11]  
RP MUTAGENESIS OF ASN-598; ASN-629 AND SER-631, AND N-GLYCOSYLATION.  
RX MEDLINE=22057172; PubMed=12063277;  
RA Gong Q., Anderson C.L., January C.T., Zhou Z.;  
RT "Role of glycosylation in cell surface expression and stability of  
HERG potassium channels.";  
RL Am. J. Physiol. 283:H77-H84(2002).  
RN [12]  
RP MUTAGENESIS OF SER-283; SER-890; THR-895 AND SER-1137, AND  
RP PHOSPHORYLATION.  
RX MEDLINE=20299343; PubMed=10837251;  
RA Cui J., Melman Y., Palma E., Fishman G.I., McDonald T.V.;  
RT "Cyclic AMP regulates the HERG K(+) channel by dual pathways.";  
RL Curr. Biol. 10:671-674(2000).  
RN [13]  
RP INTERACTION WITH KCNE1.  
RX MEDLINE=97373956; PubMed=9230439;  
RA McDonald T.V., Yu Z., Ming Z., Palma E., Meyers M.B., Wang K.-W.,  
RA Goldstein S.A., Fishman G.I.;  
RT "A minK-HERG complex regulates the cardiac potassium current I(Kr).";  
RL Nature 388:289-292(1997).  
RN [14]  
RP INTERACTION WITH KCNE2.  
RX MEDLINE=99235979; PubMed=10219239;  
RA Abbott G.W., Sesti F., Splawski I., Buck M.E., Lehmann M.H.,  
RA Timothy K.W., Keating M.T., Goldstein S.A.;  
RT "MiRP1 forms IKr potassium channels with HERG and is associated with  
RT cardiac arrhythmia.";  
RL Cell 97:175-187(1999).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-135, AND MUTAGENESIS OF  
RP PHE-29 AND TYR-43.  
RX MEDLINE=99059500; PubMed=9845367;  
RA Morais Cabral J.H., Lee A., Cohen S.L., Chait B.T., Li M.,  
RA Mackinnon R.;  
RT "Crystal structure and functional analysis of the HERG potassium  
RT channel N terminus: a eukaryotic PAS domain.";  
RL Cell 95:649-655(1998).  
RN [16]  
RP VARIANTS LOT2 ASP-470; VAL-561 AND SER-628.  
RX MEDLINE=95196272; PubMed=7889573;  
RA Curran M.E., Splawski I., Timothy K.W., Vincent G.M., Green E.D.,  
RA Keating M.T.;  
RT "A molecular basis for cardiac arrhythmia: HERG mutations cause long  
RT QT syndrome.";  
RL Cell 80:795-803(1995).  
RN [17]  
RP VARIANT LOT2 MET-822.  
RX MEDLINE=97071892; PubMed=8914737;  
RA Satler C.A., Walsh E.P., Vesely M.R., Plummer M.H., Ginsburg G.S.,  
RA Jacob H.J.;  
RT "Novel missense mutation in the cyclic nucleotide-binding domain of  
RT HERG causes long QT syndrome.";  
RL Am. J. Med. Genet. 65:27-35(1996).  
RN [18]  
RP VARIANT LOT2 ARG-593.  
RX MEDLINE=96259954; PubMed=8635257;  
RA Benson D.W., MacRae C.A., Vesely M.R., Walsh E.P., Seidman J.G.,  
RA Seidman C.E., Satler C.A.;  
RT "Missense mutation in the pore region of HERG causes familial long QT  
RT syndrome.";  
RL Circulation 93:1791-1795(1996).  
RN [19]  
RP VARIANT LOT2 THR-561.  
RX MEDLINE=97031865; PubMed=8877771;  
RA Dausse E., Berthet M., Denjoy I., Andre-Fouet X., Cruaud C.,  
RA Bennaceur M., Faure S., Coumel P., Schwartz K., Guicheney P.;  
RT "A mutation in HERG associated with notched T waves in long QT  
RT syndrome.";  
RL J. Mol. Cell. Cardiol. 28:1609-1615(1996).  
RN [20]  
RP VARIANTS LOT2 ILE-474; HIS-611; VAL-614 AND LEU-630.  
RX MEDLINE=97176600; PubMed=9024139;  
RA Tanaka T., Nagai R., Tomoike H., Takata S., Yano K., Yabuta K.,  
RA Haneda N., Nakano O., Shibata A., Sawayama T., Kasai H., Yazaki Y.,  
RA Nakamura Y.;  
RT "Four novel KVLQT1 and four novel HERG mutations in familial long-QT  
RT syndrome.";





QY	1264	AGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGGAGGCCAAACGGACGGGGCTGGAG	1323
Db	599	SerSerGly-	601
QY	1324	CTGCTGGGGCGGCCGTCGTCGGCAGCGCCTACATCACTCCCTCTACTTCGCACCTCAGC	1383
Db	602	---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer	620
QY	1384	AGCCTCACAGCGTGGGTTCCGCAACAGTGTCCGCCAACACACGACACCGAGAAAGATCTTC	1443
Db	621	SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe	640
QY	1444	TCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGTGGTGTGTTGGGAACGTGACG	1503
Db	641	SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer	660
QY	1504	GCCATCATCCAGCGCATGTACGCCCGCGCTTTCTGTACCACAGCCGCACCGCGACCTG	1563
Db	661	AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal	680
QY	1564	CGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTAC	1623
Db	681	ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluTyr	700
QY	1624	TTCCAGGCCACCTGGCGGTGAACAATGGCAATGCACACACCGAGCTGTCGACAGCCTC	1683
Db	701	PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe	720
QY	1684	CCTGACGAGTGGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCTCTGCAG---	1740
Db	721	ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys	740
QY	1741	CCACTGTTGAGCGGCCAGCGCGGCTGCCTGCGGGCACTGTCTCTGCGCCCTGCGGCC	1800
Db	741	LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr	760
QY	1801	GCCTTCTGCAGCGCGGCGAGTACCTCATCCACCAAGCGATGCCCTGCGAGGCCCTCTAC	1860
Db	761	ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr	780
QY	1861	TTTGTCGTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTGCGCCATCCTAGGG	1920
Db	781	PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly	800
QY	1921	AAGGGCACTGATCGGTGTGAGTGCCTCCCGCGGAGCAGGTGTAAAGGCCAATGCC	1980
Db	801	LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly	820
QY	1981	GACGTGAAGGGCTGACGTACTCGTCTGTCAGTGTCTGTCAGCTGGCTGGCCTGCACGAC	2040
Db	821	AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu	840
QY	2041	AGCCTTGGCTGTACCCCGAGTTTGCCCGCGCTTCAGTGTGGCTCCGAGGGGAGCTC	2100
Db	841	ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle	858
QY	2101	AGCTACAACCTG-----GGTGTGGGGAGGCTCTGCAGAGGTGGAC	2142
Db	859	ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu	878
QY	2143	ACCAGCTCCCTGAGCGCGACAATAACCTTATGTCCACGCTGGAGGAGAAGGACAGAT	2202
Db	879	GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp	898
QY	2203	GGGAGCAGGGCCCCACGGTCTCCACGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTG	2262
Db	899	ThrGluGln-----	901
QY	2263	TCCCTGGCTGCACCTCCTCATCTCAGCTGCCAAGCTGTATCCCCACGTCCGAACGCA	2322
Db	902	---ProGlyGluValSerAla-----LeuGlyProGlyArgAlaGly	914
QY	2323	CCCCGGCCTCGTCTAGGTGGCAGAGGGAGGCCAGGCAGGGCGGGCTTTGAAGGCTGAG	2382
Db	915	AlaGlyPro-----SerSerArgGlyArgProGlyGlyProTrpGlyGluSerProSer	932
QY	2383	GCTGGCCCCCTCTGTCTCCCCA-----CGGGCCCCTAGAGGGG	2418
Db	933	SerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerSerPro	952
QY	2419	CTACGGCTG-----CCCCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCC	2466
Db	953	LeuArgLeuValProPheSerSerProArgProProGlyGluProProGlyGlyGluPro	972
QY	2467	AGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCCAGCCCAAG-----	2514
Db	973	---LeuMetGluAspCysGluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe	991
QY	2515	-----TTCTCTTTC-----CGCGTGGGOCAGTCT	2538
Db	992	SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyrGlnGlu	1011
QY	2539	GGCCCGAATGTAGCAGCAGCCCTCCCTCGACACGAGCGCGCTGCTCACTGTT---	2595
Db	1012	LeuProArgCys-----ProAlaProThrProSerLeuLeuAsnIlePro	1026
QY	2596	-----CCCCATGGSCCCAGCGAGGCAAGGAACACAGACACACTG	2634
Db	1027	LeuSerSerProGlyArgArgProArgGlyAspValGluSerArg-----Leu	1042
QY	2635	GACAAGCTTCGCGAGCGGTGACAGAGCTGTTCAGAGCAGGTG---CTGCAGATGCGGAA	2691
Db	1043	AspAlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThr	1062
QY	2692	GGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTGGCGCCCCACAGGGAGGTCCG	2751
Db	1063	ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu-----	1073
QY	2752	TGCCCTCGGGCATCGGAGAGGGGCGCTGCCCAGCAGCACCTCCGGGCTTCTGCAGCCT	2811
Db	1074	-----ValProProAlaTyrSerAla--	1080
QY	2812	CTGTGTGTGACACTGGGGCATCCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTTG	2871
Db	1081	----ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr	1099
QY	2872	AGTGGGACTTGGCCCCCACCTCGTCGGGGCCCTCTCCCTCATGGCACCTGGCCCTGG	2931
Db	1099	oLeu-----ProThrLeuThrLeuAspSerLeuSerGln-----	1110
QY	2932	GGTCCCCCAGCGTCTC-----AGAGCTCCCCCTGGCCTCAGCCACAGCTTTCTTG	2982
Db	1111	-ValSerGlnPheMetAlaCysGluGluLeuProProGly---AlaProGluLeuProGl	1129
QY	2983	ACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGTCTGTAGCCCCAGCAC	3042
Db	1129	nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr	1149
QY	3043	CCTG 3046	
Db	1149	oLeu 1150	
RESULT 11			
KCH2_MOUSE			
ID	KCH2_MOUSE	STANDARD;	PRT; 1162 AA.
AC	O35219; O35220; O35221; O35989;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go		
DE	related gene potassium channel 1) (ERGL) (MERG) (Mergl) (Ether-a-go-		
GN	KNH2 OR ERG OR MERGL.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		

OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), AND VARIANTS ARG-186;  
RC STRAIN=129/Sv. and BALB/c; TISSUE=Heart;  
RX MEDLINE=98012815; PubMed=9351462;  
RA London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,  
RA Gilbert D.J., Jenkins N.A., Satler C.A., Robertson G.A.;  
RT "Two isoforms of the mouse ether-a-go-go-related gene coassemble to  
RT form channels with properties similar to the rapidly activating  
RT component of the cardiac delayed rectifier K<sup>+</sup> current.";  
RL Circ. Res. 81:870-878(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).  
RC TISSUE=Atrial tumor;  
RX MEDLINE=98012799; PubMed=9351446;  
RA Lees-Miller J.P., Kondo C., Wang L., Duff H.J.;  
RT "Electrophysiological characterization of an alternatively processed  
RT ERG K<sup>+</sup> channel in mouse and human hearts.";  
RL Circ. Res. 81:719-726(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-186.  
RC TISSUE=Colon smooth muscle;  
RA Shoen F., Malykhina A., Akbarali H.I.;  
RT "Smooth muscle KCNH2 erg potassium channel.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
CC -|- FUNCTION: Pore-forming (alpha) subunit of voltage-gated inwardly  
CC rectifying potassium channel. Channel properties are modulated by  
CC CAMP and subunit assembly. Mediates the rapidly activating  
CC component of the delayed rectifying potassium current in heart  
CC (IKr) (By similarity).  
CC -|- SUBUNIT: The potassium channel is probably composed of a homo- or  
CC heterotetrameric complex of pore-forming alpha subunits that can  
CC associate with modulating beta subunits. Heteromultimer with  
CC KCNH6/ERG2, KCNH7/ERG3, KCNE1 and KCNE2 (By similarity).  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Experimental confirmation may be lacking for some  
CC isoforms;  
CC Name=1; Synonyms=1A, A;  
CC IsoId=O35219-1; Sequence=Displayed;  
CC Name=2; Synonyms=1A';  
CC IsoId=O35219-2; Sequence=VSP\_000969;  
CC Name=3; Synonyms=1B, B;  
CC IsoId=O35219-3; Sequence=VSP\_000970;  
CC -|- TISSUE SPECIFICITY: Isoform 1 is expressed in heart, brain and  
CC testis and at low levels in lung. Isoform 3 is expressed  
CC predominantly in heart. The expression of isoform 2 is low in all  
CC tissues tested.  
CC -|- DOMAIN: The segment S4 is probably the voltage-sensor and is  
CC characterized by a series of positively charged amino acids at  
CC every third position.  
CC -|- PTM: Phosphorylated on serine and threonine residues (By  
CC similarity).  
CC -|- SIMILARITY: Belongs to the potassium channel family. H (Eag)  
CC subfamily.  
CC -|- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
CC -|- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
CC -|- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
CC -|- CAUTION: Ref.3 sequence was originally reported as deriving from  
CC rabbit.  
CC -|- CAUTION: Ref.3 sequence differs from that shown due to a  
CC frameshift in position 1057.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC

DR EMBL; AF012868; AAC53418.1; --  
DR EMBL; AF012869; AAC53419.1; --  
DR EMBL; AF012871; AAC53420.1; --  
DR EMBL; AF012870; AAC53420.1; JOINED.  
DR EMBL; AF012871; AAC53421.1; --  
DR EMBL; AF012871; AAC53422.1; --  
DR EMBL; AF012870; AAC53422.1; JOINED.  
DR EMBL; AF034762; AAB87571.1; --  
DR EMBL; AF439342; AAL35327.2; ALT\_FRAME.  
DR MGI:1341722; Kcnh2.  
DR InterPro; IPR000595; cNMP binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc\_C.  
DR InterPro; IPR000014; PAS\_domain.  
DR Pfam; PF00027; cNMP\_binding; 1.  
DR Pfam; PF00520; Ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; cNMP; 1.  
DR SMART; SM00086; PAC; 1.  
DR PROSITE; PS00888; cNMP\_BINDING\_1; FALSE\_NEG.  
DR PROSITE; PS00889; cNMP\_BINDING\_2; FALSE\_NEG.  
DR PROSITE; PS50042; cNMP\_BINDING\_3; 1.  
DR PROSITE; PS50112; PAS; 1.  
DR PROSITE; PS50113; PAC; 1.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
KW Phosphorylation; Glycoprotein; Multigene family; Polymorphism;  
KW Alternative splicing.  
FT DOMAIN 1 405 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 406 426 SEGMENT S1 (POTENTIAL).  
FT TRANSMEM 453 473 SEGMENT S2 (POTENTIAL).  
FT DOMAIN 474 497 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 498 518 SEGMENT S3 (POTENTIAL).  
FT TRANSMEM 523 543 SEGMENT S4 (POTENTIAL).  
FT DOMAIN 544 549 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 550 570 SEGMENT S5 (POTENTIAL).  
FT DOMAIN 614 634 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
FT TRANSMEM 641 661 SEGMENT S6 (POTENTIAL).  
FT DOMAIN 662 1162 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 17 88 PAS.  
FT DOMAIN 92 144 PAC.  
FT DOMAIN 299 302 POLY-PRO.  
FT NP\_BIND 744 861 cNMP.  
FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPPLIC 1 59 Missing (in isoform 2).  
FT VARSPPLIC 1 378 /FTId=VSP\_000969.  
FT FT 1 378 MPVRRGHVAPQNTFLDTIIRKFEQSRKFIANRVENCAY  
FT FT IYNDGFCCELCGYRAEVWQPCCTCDFLHGPRTORAAQI  
FT FT AQALLGAEERKVEIAFYRKDGSCFLCLVDVVPVKNEDGAVI  
FT FT MFLNFVMEKDMVGSVPAHDTNHRGPSTSLASGRKTFR  
FT FT LKLPALLALTARESSVTRTSMHSGAGAPGAVVDVLTTPAAP  
FT FT SSESALDEVSAVDNHVAGLPAERARRALVPGSGASPVASI  
FT FT RGPSPRAQSLNPDASGSSCLARTSRRESASPVASSA  
FT FT DDIEAMRAGALPPPPRHASTGAMHPLRSLGLNSTSDSLVR  
FT FT YRTISKIPQITLNFVLDKDPFLASPTSDREIIAPTKERT  
FT FT HNVTEKVTQ -> MAIPTKESRTGALQPRQAQKGRVRAVR  
FT FT ISSLVAQE (in isoform 3).  
FT FT /FTId=VSP\_000970.  
FT FT H -> R (IN STRAIN BALB/C).  
FT FT A -> T (IN STRAIN BALB/C).  
FT FT C -> Y (IN STRAIN BALB/C).  
FT FT D -> N (IN STRAIN BALB/C).  
FT FT D -> G (IN REF. 3).  
FT FT I -> V (IN REF. 3).  
FT FT V -> A (IN REF. 3).  
FT FT E -> G (IN REF. 3).  
FT FT V -> A (IN REF. 3).  
FT FT S -> P (IN REF. 3).  
FT FT  
FT VARIANT 186 186  
FT VARIANT 455 455  
FT VARIANT 752 752  
FT VARIANT 1006 1006  
FT CONFLICT 111 111  
FT CONFLICT 126 126  
FT CONFLICT 198 198  
FT CONFLICT 214 214  
FT CONFLICT 537 537  
FT CONFLICT 908 908  
FT



FT CONFLICT 929 929 G -> R (IN REF. 3).  
SQ SEQUENCE 1162 AA; 126885 MW; A9455F7F10B61E46 CRC64;

Alignment Scores:

Pred. No.: 2.03e-61 Length: 1162  
Score: 1547.00 Matches: 413  
Percent Similarity: 44.21% Conservative: 144  
Best Local Similarity: 32.78% Mismatches: 352  
Query Match: 25.41% Indels: 351  
DB: 1 Gaps: 31

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x KCH2\_MOUSE (1-1162)

```
QY 1 ATGCCGGCCATCGCGGGCTCTCTGCGCCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
Db      |||||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleileArg 20
Db      |||||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 CGCTTCGACGGCACGCACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120
Db      ::|||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 21 LysPheGluGlyGlnSerArgLysPheIleileAlaAsnAlaArgValGluAsnCys--- 39
Db      ::|||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 121 CCCGTGGTCTACTGCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGTGAGGTC 180
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 181 ATGCAGCGGGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 241 CAACAGATCCGCAAGCCCTGGACGAGCAAGAGAGTTCAAGGTGAGCTGATCTGTAC 300
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 301 CGGAAGAGCGGGTCCCGTTCTGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp 119
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 361 GGGAGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 400 -----ACGGAACCAAGAACCGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 447
Db      ::|||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerTrpLeuAlaSerGlyArg 159
Db      ::|||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 447 ----- 447
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 447 ----- 447
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 180 ValArgThrGlySerMetHisSerAlaGlyAlaProGlyAlaValValValAspValAsp 199
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 447 ----- 447
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 200 LeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValSerAlaMetAsp 219
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 447 ----- 447
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 220 AsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProGlySer 239
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 447 ----- 447
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnSerLeuAsn 259
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 448 -----GGTGGCGGCGCGGATATGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 495
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 260 ProAspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAla 279
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 496 AACCGGCGGCGGAGCCGGGCC-----GTGCTCTACCACTGTCCGGGCGCACCTGCAG 546
Db      ::|||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 280 SerValArgArgAlaSerSerAlaAspIleGluAlaMetArgAlaGlyAlaLeuPro 299
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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QY 547 AAGCAGCCCAAG-----GGCAAGCACAAAGCTCAATAAGGGGTGTTGGG 591
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 300 ProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn 319
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 592 GAGAAACCAAC----- 603
Db      ::|||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 320 SerThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThr 339
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 603 ----- 603
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 340 LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu 359
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 603 ----- 603
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 360 IleIleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnVal 379
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 604 -----TTGCCTGAGTACAAAGTAGCCGCCATCCGGAAAGTCGCC 642
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 380 LeuSerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArg 399
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 643 TTCATCCTGTTGCACCTGTGGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCC 702
Db      ::|||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 400 TrpThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeu 419
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 703 AACTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTG----- 744
Db      ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 420 ValIleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGlu 439
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 745 -----AGCACAGCACGGGAGCCAGTGCOCGCCCGCGCGCGCGCGCGCGCGCGCGCTG 798
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 440 AspGlySerGlnAlaProAspCysGlyTyrAlaCysGlnProLeuAlaValValAspLeu 459
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 799 GCCGTGGAGTCTCTTCATCCTTGACATTGTGTAATTTCCGTACACATTCGTGTCC 858
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 460 IleValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsn 479
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 859 AAGTCGGGGCCAGGTGGTGTTCGCCCCCAAGTCCATTTGCCCTCCACTACGTACACCTGG 918
Db      ::|||  ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 480 AlaAsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrp 499
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 919 TTCCTGTGGATGTATCGCAGCGCTGCCCTTTGACCTGTCTACATGCCTCAAGGTCAAC 978
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 500 PheLeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 513
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 979 GTGTACTTCGGGGCC-----CATCTGTGAAGACGGTGCCTGCTGCTG 1020
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 514 ---IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeu 532
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1021 CGCTGTGCGCCTGCTTCCCGCGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTGCTG 1080
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 533 ArgLeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeu 552
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1081 ACACCTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGGCTGCTGTTTTC 1140
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 553 PheLeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAla 572
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1141 ATTGGCCAGCGGAGATCGAGACAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG 1200
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 573 IleGlyAsnMetGluGlnProHisMetAspSer-----HisIleGlyTrpLeuHis 589
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1201 GAGTGGCCCGCGACTGGAGACTCCCTACTACTCTGGTGGCGCGGAGCCAGCTGGAGGG 1260
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 590 AsnLeuGlyAspGlnIleGlyLysProTyr----- 599
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1261 AACAGCTCCGGCCAGAGTCAACAACCTGCAGCAGCAGCAGCGGCAACGGGCGGCTG 1320
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 600 AsnSerSerGly----- 603
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 1321 GAGCTGTGGCGGCGCGCTCGCTGCGCAGCGCGCTACATCACCTCCCTCTACTTCGCACTC 1380
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 604 -----LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPhe 621
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 1381 AGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCGCCCAACACGGACACCGAGAAGATC 1440
Db      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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Db 622 SerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIle 641  
QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACGGGTGGTGTGGGAACGTG 1500  
Db 642 PheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnVal 661  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTATCACAGCCGACCGCGGAC 1560  
Db 662 SerAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArg 681  
QY 1561 CTGCGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGTGGAG 1620  
Db 682 ValArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlu 701  
QY 1621 TACTTCCAGCCACCTGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGC 1680  
Db 702 TyrPheGlnHisAlaTyrSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGly 721  
QY 1681 CTCCCTGACGAGCTGGCGCAGACATCGGCATGCACCTGCACAGGAGTCTCTGCAG--- 1737  
Db 722 PheProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuHis 741  
QY 1738 CTGCCACTGTTGAGCGCGCCAGCGCGGCTGCCTGCGGCACCTGTCTCTGCGCCCTGCGG 1797  
Db 742 CysLysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLys 761  
QY 1798 CCGGCCTTCTGCACCGCGCGGAGTACCTATCCACCAAGCGATGCCCTGCAGGCCCTC 1857  
Db 762 ThrThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeu 781  
QY 1858 TACTTTGTCTGCTCGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTCGCCATCCTA 1917  
Db 782 TyrPheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeu 801  
QY 1918 GGAAGGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGTTAAAGGCCAAT 1977  
Db 802 GlyLysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsn 821  
QY 1978 GCCGACGTGAAGGGGTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2037  
Db 822 GlyAspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeu 841  
QY 2038 GACAGCTTGGCTGTACCCCGAGTTTGGCCCGCTTACGTGCTGGCTCCGAGGGGAG 2097  
Db 842 GluValLeuAspMetTyrProGluPheSerAspHisPheTyrSerSerLeu-----Glu 859  
QY 2098 CTCAGCTACAACCTG-----GGTGTGGGGGAGGCTCTGCAGAGGTG 2139  
Db 860 IleThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerAlaGluLeu 879  
QY 2140 GACACAGCTCCCTGAGCGCGGACAAATACCTTATGTCCAGCTGGAGGAGAGAGACA 2199  
Db 880 GluSerGlyPheAsnArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLys 899  
QY 2200 GATGGGAGCAGGGCCCGCTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGCCCGCTG 2259  
Db 900 AspThrGluGln----- 903  
QY 2260 CTGTCCCTGGCTGCACCTCTCATCTCTCAGCTGCCAAGCTGCTATCCCGCTCGAACA 2319  
Db 904 -----ProGlyGluValSerAlaLeuGlyGln-----GlyProAlaArgVal 917  
QY 2320 GCACCCCGCCTCGTCTAGTGGCAGAGGAGGCGCAGGCGGAGGCGGCTTTGAAGGCT 2379  
Db 918 GlyProGlyProSerCys-----ArgGlyGlnProGlyGlyProTrpGlyGluSerPro 935  
QY 2380 GAGGCTGGCCCTCTGTCTCCCGCA-----CGGCGCCCTAGAG 2415  
Db 936 SerSerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerSer 955  
QY 2416 GGGCTACGGCTGCCCGCCCATGCGCATGGAATGTCCCGCCAGATCTGAGCCCGCAGGTAGTA 2475

Db 956 ProLeuArgLeuValProPheSerSerProArgProProGlyAspProProGlyGlyGlu 975  
QY 2476 GATGGCATTTGAAGACGGCTGTGGCTCGGACCGCCCAAG----- 2514  
Db 976 ProLeuThrGluAspGlyGluLysSerAspThrCysAsnProLeuSerGlyAlaPheSer 995  
QY 2515 -----TTCTCTTTC-----CGCGTGGGCCAGTCTGGC 2541  
Db 996 GlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyrGlnGluLeu 1015  
QY 2542 CCGGAATGTAGCAGACGCCCTCCCTGGACGAGAGCGGCGCTGCTCACTGTTCCC--- 2598  
Db 1016 ProArgCys-----ProAlaProAlaProSerLeuLeuAsnIleProLeu 1030  
QY 2599 -----CATGGGCCCGCAGCGAGGCAAGGAACACAGACACTGGAC 2637  
Db 1031 SerSerProGlyArgArgSerArgGlyAspValGluSerArg-----LeuAsp 1046  
QY 2638 AAGCTTCGGCAGCGGTGACAGAGCTGTCCAGAGCAGGTG---CTGCAGATGCGGAAGGA 2694  
Db 1047 AlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThrVal 1066  
QY 2695 CTGCAGTCACTTCCCGCAGGCTGTGCAGCTGTCTCTGGCGCCCGCAGGAGGGTCCGTGC 2754  
Db 1067 LeuGlnLeuGln-ArgGlnMetThrLeu----- 1076  
QY 2755 CCTCGGCGATCGGAGAGGGGCGCTGCCCGCAGCAGCCTCCGGGCTTCTGCAGCCTCTG 2814  
Db 1077 -----ValProAlaTyrSerAla--- 1083  
QY 2815 TGTGTGGACACTGGGGCATCTCTCTACTGCTGCTGAGCCCCAGCTGGCTCTGTCTTGAGT 2874  
Db 1084 -ValThrThrProGlyProGlyProThrSerAlaSerProLeuLeuPro-----Va 1100  
QY 2875 GGGACTTGGCCCGCCACCTCGTCCGGGCGCTCTCTCCCTCATGGCACCTGGCCCTGGGT 2934  
Db 1100 lGlyProValProThrLeuThrLeuAspSerLeuSerGln-----Va 1114  
QY 2935 CCCCCAG-----CGTCTCAGAGCTCCCGCTGGGCTCGAGCCACAGCTTCTGGACCTCC 2988  
Db 1114 lSerGlnPheValAlaPheGluGluLeuProAlaGlyAlaProGluLeuProGlnAspGln 1134  
QY 2989 ACCTCAGACTCAGAGCCCGCTGCCTCAGGAGACCTCTGCTCTGAGCCCGCAGCCCGCTG 3046  
Db 1134 yProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnProLeu 1153

RESULT 12

KCH2\_RAT  
ID KCH2 RAT STANDARD; PRT; 1163 AA.  
AC O08962; O08720;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go  
DE related gene potassium channel 1) (ERGI) (r-ERG) (RERG) (Ether-a-go-  
DE go related protein 1) (Eag related protein 1).  
GN KCNH2 OR ERG.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain cortex;  
RX MEDLINE=98329322; PubMed=9664620;  
RA Bauer C.K., Engeland B., Wulfsen I., Ludwig J., Pongs O.,  
RA Schwarz J.R.;  
RT "RERG is a molecular correlate of the inward-rectifying K current in  
RT clonal net pituitary cells."  
RL Recept. Channels 6:19-29(1998).  
RN [2]  
RP SEQUENCE OF 409-568 FROM N.A.  
RX MEDLINE=97164986; PubMed=9012748;

Wymore R.S., Gintant G.A., Wymore R.T., Dixon J.E., McKinnon D., Cohen I.S.;  
"Tissue and species distribution of mRNA for the IKr-like K+ channel, erg.";  
Circ. Res. 80:261-268(1997).

TISSUE SPECIFICITY.  
MEDLINE=20183472; PubMed=10718922;  
Wulfsen I., Hauber H.P., Schiemann D., Bauer C.K., Schwarz J.R.;  
"Expression of mRNA for voltage-dependent and inward-rectifying K channels in GH3/B6 cells and rat pituitary.";  
J. Neuroendocrinol. 12:263-272(2000).

INTERACTION WITH KCNH6 AND KCNH7, AND MUTAGENESIS OF GLY-630.  
MEDLINE=21079731; PubMed=11212207;  
Wimmers S., Wulfsen I., Bauer C.K., Schwarz J.R.;  
"Erg1, erg2 and erg3 K channel subunits are able to form heteromultimers.";  
Pflugers Arch. 441:450-455(2001).

FUNCTION: Pore-forming (alpha) subunit of voltage-gated inwardly rectifying potassium channel. Channel properties are modulated by cAMP and subunit assembly. Mediates the rapidly activating component of the delayed rectifying potassium current in heart (IKr) (By similarity).

SUBUNIT: The potassium channel is probably composed of a homo- or heterotetrameric complex of pore-forming alpha subunits that can associate with modulating beta subunits. Heteromultimer with KCNH6/ERG2 and KCNH7/ERG3. Heteromultimer with KCNE1 and KCNE2 (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.  
TISSUE SPECIFICITY: Highly expressed in brain and testis, slightly less so in heart, adrenal, retina and thymus. Detected at lower levels in lung, soleus, tibialis, and at very low levels in cornea and lens. A shorter transcript is detected in skeletal muscle. Found in pituitary.

DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.

PTM: Phosphorylated on serine and threonine residues (By similarity).

SIMILARITY: Belongs to the potassium channel family. H (Eag) subfamily.

SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.

SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.

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EMBL; Z96106; CAB09536.1; -;  
EMBL; U75210; AAC53160.1; -;  
InterPro; IPR000595; CNMP binding.  
InterPro; IPR003967; Erg\_channel.  
InterPro; IPR005821; Ion\_trans.  
InterPro; IPR001622; K+channel\_pore.  
InterPro; IPR005820; M+channel\_nlg.  
InterPro; IPR001610; PAC.  
InterPro; IPR000700; PAS-assoc\_C.  
InterPro; IPR000014; PAS domain.  
Pfam; PF00027; CNMP binding; 1.  
Pfam; PF00520; ion\_trans; 1.  
Pfam; PF00785; PAC; 1.  
PRINTS; PR01470; ERGCHANNEL.  
SMART; SM00100; CNMP; 1.  
SMART; SM00086; PAC; 1.  
SMART; SM00091; PAS; 1.  
PROSITE; PS00888; CNMP BINDING 1; FALSE NEG.  
PROSITE; PS00889; CNMP\_BINDING\_2; FALSE\_NEG.

DR PROSITE; PS50042; CNMP\_BINDING\_3; 1.  
DR PROSITE; PS50112; PAS; 1.  
DR PROSITE; PS50113; PAC; 1.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
KW Phosphorylation; Glycoprotein; Multigene family.  
FT DOMAIN 1 405 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 406 426 SEGMENT S1 (POTENTIAL).  
FT TRANSMEM 453 473 SEGMENT S2 (POTENTIAL).  
FT DOMAIN 474 497 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 498 518 SEGMENT S3 (POTENTIAL).  
FT TRANSMEM 523 543 SEGMENT S4 (POTENTIAL).  
FT DOMAIN 544 549 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 550 570 SEGMENT S5 (POTENTIAL).  
FT DOMAIN 614 634 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
FT TRANSMEM 641 661 SEGMENT S6 (POTENTIAL).  
FT DOMAIN 662 1163 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 17 88 PAS.  
FT DOMAIN 92 144 PAC.  
FT NP\_BIND 744 861 CNMP.  
FT CARBOHYD 600 600 N-LINKED (GLCNAC...) (POTENTIAL).  
FT MUTAGEN 630 630 G->S: DOMINANT NEGATIVE MUTANT; ABOLISHES ERG CURRENT.  
FT CONFLICT 411 411 V -> A (IN REF. 2).  
SQ SEQUENCE 1163 AA; 126951 MW; F0D75B0B532D9EA2 CRC64;  
  
Alignment Scores:  
Pred. No.: 5.32e-61 Length: 1163  
Score: 1537.50 Matches: 412  
Percent Similarity: 44.09% Conservative: 144  
Best Local Similarity: 32.67% Mismatches: 353  
Query Match: 25.25% Indels: 352  
DB: 1 Gaps: 31  
  
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QY 1 ATGCCGGCCATGCGGGCCCTCTCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60  
Db 1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleArg 20  
QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 21 LysPheGluGlyGlnSerArgLysPheIleAlaAsnAlaArgValGluAsnCys--- 39  
QY 121 CCCGTGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCGGCTGAGGTC 180  
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59  
QY 181 ATGACGCGGGCTGTGCTGCTCTCTCTCTCTCTCTATGGCCAGACACCATGAGTCTCGTCCG 240  
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgArgAlaAla 79  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCAGACAGGAGTTCAAGGCTGAGCTGATCTGTAC 300  
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGTGTTCTCTCTCTCTCTCTGATGTATACCATAAAGATGAGAAA 360  
Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValValProValLysAsnGluAsp 119  
QY 361 GGGGAGGTGGCTCTCTCTCTA-----GTCTCTCAAGGACATC----- 399  
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139  
QY 400 -----AGCGAAACCAAGACCGAGGGGGCCCGACAGATGAAGGAGACAGGT--- 447  
Db 140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerThrLeuAlaSerGlyArg 159  
QY 447 ----- 447  
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerPro 179  
QY 447 ----- 447



Db	533	ArgLeuValArgValAlaAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeu	552
QY	1081	ACACTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTCCCTCGCTCTGGTTTAC	1140
Db	553	PheLeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAla	572
QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG	1200
Db	573	IleGlyAsnMetGluGlnProHisMetAspSer-----HisIleGlyTrpLeuHis	589
QY	1201	GAGCTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGGCCGAGGCCAGCTGGAGGG	1260
Db	590	AsnLeuGlyAspGlnIleGlyLysProTyr-----	599
QY	1261	AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGCGTG	1320
Db	600	AsnSerSerGly-----	603
QY	1321	GAGCTGCTGGGCGCCGCTCGCTGGCGAGCGCCTACATCACCTCCCTCTACTTCGCACTC	1380
Db	604	-----LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPhe	621
QY	1381	ACGAGCCTCACAGCGTGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATC	1440
Db	622	SerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIle	641
QY	1441	TTCTCCATCTGCACCATGCTCATCGGCGCCTGATGCACGCGGTGGTGTTTGGGAACGTG	1500
Db	642	PheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnVal	661
QY	1501	ACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTCTGTACCAACAGCCGACCGCGGAC	1560
Db	662	SerAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArg	681
QY	1561	CTGCGCGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Db	682	ValArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGlu	701
QY	1621	TACTTCCAGGCCACCTGGCGGTGAACAATGSCATCGACACCACCGAGCTGTCGAGAGC	1680
Db	702	TyrPheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGly	721
QY	1681	CTCCTGACGAGTGGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCTCGCAG---	1737
Db	722	PheProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHis	741
QY	1738	CTGCCACTGTTGAGGCGCCAGCCGCGGTGCTGCGGGCACTGTCTCTGGCCCTGCGG	1797
Db	742	CysLysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLys	761
QY	1798	CCCGCCTTCTGCACGCCGGGAGTAGCTCATCCACCAAGCGATGCCCTGCAGGCCCTC	1857
Db	762	ThrThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeu	781
QY	1858	TACTTTGTCTGCTCTGGCTCCATGAGGTGCTCAAGGCTGGCACCGTGTCTGCCATCCTA	1917
Db	782	TyrPheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeu	801
QY	1918	GGGAAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGGCCAAT	1977
Db	802	GlyLysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsn	821
QY	1978	GCCGACGTGAAGGGGTGACGTACTGCTCGTCTGTGTCTGTGAGCTGGCTGGCCTGCAC	2037
Db	822	GlyAspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeu	841
QY	2038	GACAGCCTTGGCTGTACCCCGAGTTTGCCCGCGCTTCAGTCTGTGGCCTCCGAGGGAG	2097
Db	842	GluValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----Glu	859
QY	2098	CTCAGCTACACCTG-----GGTGTGGGGAGGCTCTGTGAGAGGTG	2139
Db	860	IleThrPheAsnLeuArgAspThrAsnMetIleProGlySerProSerAlaGluLeu	879

D	b	180	MetArgThrGlySerThrGlySerProGlyAlaProGlyAlaValValValAspValAsp	199
Q	y	447	-----	447
D	b	200	LeuThrProAlaAProSerSerGluSerLeuAlalaueaspGluValSerAlaMetAsp	219
Q	y	447	-----	447
D	b	220	AsnHisValAlaGlyLeuGlyProAlaGluArgArgAlalaLeuValGlyProAlaSer	239
Q	y	447	-----	447
D	b	240	AlaSerProValAlaSerIleProGlyProHisProSerProArgAlaGlnSerLeuAsn	259
Q	y	448	-----GGTGGCGCGCCGATATGCCGGCAGCATCCAAGCTTCATATGCC	495
D	b	260	ProAspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAla	279
Q	y	496	AACCGCGCGGAGCCGGCC-----GTGCTCTACCACCTGTCCGGGCACCTGCAG	546
D	b	280	SerValArgArgAlaSerSerAlaAspAspileGluAlaMetArgAlaGlyAlaLeuPro	299
Q	y	547	AAGCAGCCCCAAG-----GGCAAGCACAAAGCTCAATAAGGGGTGTTGGG	591
D	b	300	LeuProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn	319
Q	y	592	GAGAACCAAC-----	603
D	b	320	SerThrSerAspSerAspLeuValArgTyrArgThrIleSerLysileProGlnIleThr	339
Q	y	603	-----	603
D	b	340	LeuAsnPheValAspleuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu	359
Q	y	603	-----	603
D	b	360	IleIleAlaProLysileLysGluArgThrHisAsnValThrGluLysValThrGlnVal	379
Q	y	604	-----TTGCCTGAGTACAAGTAGCCGCCATCCGGAAGTCGCC	642
D	b	380	LeuSerLeuGlyAlaAspValLeuProGluTyrllysLeuGlnAlaProArgIleHisArg	399
Q	y	643	TTCATCCTGTGCACTGTGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCC	702
D	b	400	TrpThrIleLeuHistyrsrPropheLysAlaValTrpAspTipLeuilleLeuLeuLeu	419
Q	y	703	ACACTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTTGTG-----	744
D	b	420	ValIleTyThrAlaValPheThrProTyrsrAlaAlaPheLeuLeuLysGluThrGlu	439
Q	y	745	-----AGCACAGCAGGAGCCCAGTGCCGCCGCCGCCGCCGCGTCTGTGACCTG	798
D	b	440	AspGlySerGlnAlaProAspCysGlyTyralaCysGlnProLeuAlaValValAspLeu	459
Q	y	799	GCCGTGGAGGTCTCTTCATCTTGACATTGTGCTGAATTCCTGACCATCATTCGTGTCC	858
D	b	460	LeuValAspileMetPheIleValAspileLeuilleAsnPheArgThrThrtyrValAsn	479
Q	y	859	AAGTCGGGCCAGGTGTGTTTTGCCCCAAAAGTCCATTTGCTCCCACTACGTACCACCTGG	918
D	b	480	AlaAsnGluGluValValSerHisProGlyArgIleAlaValHistyrsrPheLysGlyTrp	499
Q	y	919	TTCCCTGCTGATGTTCATCGCAGCGCTGCCCTTTGACCTGTACATGCCCTTCAAGGTCAAC	978
D	b	500	PheLuilleaspMetValAlaAlaIleProPheAspLeuLeu-----	513
Q	y	979	GTGTACTTCGGGCC-----CATCTGCTGAAGACGGTGCGCCCTGCTG	1020
D	b	514	---IlePheGlySerGlySerGluGluLeuilleGlyLeuLeuLysThrAlaArgLeuLeu	532
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QY 2200 GATGGGAGCAGGCGCCACCGGTCTCCCGACGCGCCAGCTGATGAGCCCTCCAGCCCTG 2259
Db      ||| |||||
900  AspThrGluGln----- 903
QY 2260 CTGTCCCTCGCTGCACCTCTCATCTCAGCTGCCAAGCTGTCATCCACAGTCGAACA 2319
Db      ||||| ||||| |||||
904  -----ProGlyGluValSerAlaLeuGlyGln-----GlyProAlaArgVal 917
QY 2320 GCACCCCGCCTCGTCTAGGTGGCAGAGGAGCCAGGAGGCGGAGGCGCTTTGAAGGCT 2379
Db      ||| ||| ||||| :::::
918  GlyProGlyProSerCys-----ArgGlyGlnProGlyGlyProTrpGlyGluSerPro 935
QY 2380 GAGGCTGGCCCTCTGCTCCCTCCCA-----CGGCGCCCTAGAG 2415
Db      ::||| ||||| ::|||
936  SerSerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerSer 955
QY 2416 GGGGTACGCTGCCCGCCCATGCGCATGATGTGCCCCCAGATCTGAGCCCCAGGGTAGTA 2475
Db      ||||| ||| ||||| |||||
956  ProLeuArgLeuValProPheSerSerProArgProProGlyAspSerProGlyGlyGlu 975
QY 2476 GATGGCATTAAGACGGCTGTGGCTCGGACCGCC----- 2511
Db      ||||| ||| ||||| |||
976  ProLeuThrGluAspGlyGluValSerSerSerAspThrCysAsnProLeuSerGlyAlaPhe 995
QY 2512 -----AAGTCTCTTTC-----CGGTGGGCGCAGTCT 2538
Db      ||||| ||||| |||||
996  SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyrGlnGlu 1015
QY 2539 GGCCCGGAATGTAGCAGAGCCCTCCCTGGACCGAGAGCGCCTGCTCACTGTTCCC 2598
Db      ||| ||| ||||| ||||| |||||
1016  LeuProArgCys-----ProAlaProAlaProSerLeuLeuAsnIlePro 1030
QY 2599 -----CATGGGCCCGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2634
Db      ||||| ||||| ||||| |||||
1031  LeuSerSerProGlyArgArgSerArgGlyAspValGluSerArg-----Leu 1046
QY 2635 GACAAGCTTCGGCAGCGGTGACAGAGCTGTACAGCAGGTG---CTGCAGATGCGGGAA 2691
Db      ||| ||||| ::||| ||||| ::|||
1047  AspAlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThr 1066
QY 2692 GGAAGTCACTTCGCCAGGCTGTGCAGCTGTCTCTGGCGCCCGCCAGGAGGCTCG 2751
Db      ||||| ||||| ||||| |||||
1067  ValLeuGlnLeuGln-ArgGlnMetThrLeu----- 1077
QY 2752 TGCCCTCGGGCATCGGAGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2811
Db      ||||| ||||| ||||| |||||
1078  -----ValProAlaTyrSerAla-- 1084
QY 2812 CTGTGTGTGACACTGGGCGATCTCTACTGCTGCAGCGCCCGCAGCTGCTGTCTTG 2871
Db      ||| ||| ||||| ||||| |||||
1085  ----ValThrProGlyProGlyProGlyProThrSerThrSerProLeuLeuPro----- 1100
QY 2872 AGTGGACTTGGCCCGCCACCTCTGTCGGGCGCTCTCTCCCTCATGGCACCTGGCCCTGG 2931
Db      ||||| ||||| ||||| |||||
1101  -ValGlyProValProThrLeuThrLeuAspSerLeuSerGln----- 1114
QY 2932 GGTCCCGCAG-----CGTCTCAGAGTCCCGCTGGCCTCGAGCCACAGCTTTCTGGACC 2985
Db      ||| ||| ||||| ||||| |||||
1115  -ValSerGlnPheValAlaPheGluGluLeuProAlaGlyAlaProGluLeuProGlnAs 1134
QY 2986 TCCACCTCAGACTCAGAGCCCGCTGCTCAGGAGACCTCTGCTCTGAGCCCGCAGCCCT 3045
Db      ||| ||| ||||| ||||| |||||
1134  pGlyProThrArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnProLe 1154
QY 3046 G 3046
Db      |
1154  u 1154
```

```
RESULT 13
KCH2 RABIT
ID KCH2 RABIT STANDARD; PRT; 1161 AA.
AC Q8WNY2; O02731; O19119; O97586; Q9TV06;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go
DE related gene potassium channel 1) (ERG1) (ERG) (ra-erg) (Ether-a-go-
DE go related protein 1) (Eag related protein 1).
GN KCNH2 OR ERG.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Witchel H.J., Hancox J.C., Levi A.J., Meech R.W.;
RT "ERG - rabbit ventricular ERG K+ channel subunit.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE OF 411-571 FROM N.A. (ISOFORM 1/2).
RX MEDLINE=97164986; PubMed=9012748;
RA Wymore R.S., Gintant G.A., Wymore R.T., Dixon J.E., McKinnon D.,
RA Cohen I.S.;
RT "Tissue and species distribution of mRNA for the IKr-like K+ channel,
RT erg.";
RL Circ. Res. 80:261-268(1997).
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated inwardly
CC rectifying potassium channel. Channel properties are modulated by
CC cAMP and subunit assembly. Mediates the rapidly activating
CC component of the delayed rectifying potassium current in heart
CC (IKr) (By similarity).
CC -!- SUBUNIT: The potassium channel is probably composed of a homo- or
CC heterotetrameric complex of pore-forming alpha subunits that can
CC associate with modulating beta subunits. Heteromultimer with
CC KCNH6/ERG2, KCNH7/ERG3, KCNE1 and KCNE2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8WNY2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8WNY2-2; Sequence=VSP_000971;
CC -!- TISSUE SPECIFICITY: Detected in heart, both in atrium and in left
CC ventricle.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -!- PTM: Phosphorylated on serine and threonine residues (By
CC similarity).
CC -!- SIMILARITY: Belongs to the potassium channel family. H (Eag)
CC subfamily.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U87513; AAB68612.1; -.
CC EMBL; AF068736; AAC99425.1; -.
CC EMBL; AF105061; AAD39357.1; -.
CC EMBL; U75212; AAC48723.1; -.
CC InterPro; IPR000595; cNMP binding.
CC InterPro; IPR003967; Erg_channel.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR001622; K+channel_pore.
```





Db 459 LeuIleValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrVal 478  
QY 856 TCCAAAGTCGGGCCAGGTGGTGTGTTTGGCCCAAGTCCATTGTCCTCCACTACGTACCCACC 915  
Db 479 AsnAlaAsnGluGluValSerHisProGlyArgIleAlaValHisTyrPheLysGly 498  
QY 916 TGGTTCCTGCTGGATGTCATCGAGCGCTGCCCTTTGACCTGCTACATGCCCTTCAAGGTC 975  
Db 499 TrpPheLeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 513  
QY 976 AACGTGTACTTCGGGGCC-----CATCTGCTGAAGACGGTGGCCCTG 1017  
Db 514 -----IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeu 531  
QY 1018 CTGGGCTGCTGGCCCTGCTTCGGCGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTG 1077  
Db 532 LeuArgLeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaVal 551  
QY 1078 CTGACACTGCTCATGGCCCGTGTTCGCCCTGCTCGCGCACTGGTGCCTGCTGCTGTTT 1137  
Db 552 LeuLeuLeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyr 571  
QY 1138 TACATTGGCCAGCGGGAGATCGAGAGCAGCGGAATCCGAGTGCCTGAGATTGGTGGCTG 1197  
Db 572 AlaIleGlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTrpLeu 588  
QY 1198 CAGGAGCTGGCCCGCCGACTGGAGACTCCCTACTACCTGTTGGCCGAGGCCAGCTGGA 1257  
Db 589 HisAsnLeuGlyAspGlnMetGlyLysProTyr----- 599  
QY 1258 GGGAAACAGCTCCGGCCAGAGTGACAACCTGCAGCAGCAGCAGCGGCCAACGGGACGGG 1317  
Db 600 ---AsnSerSerGly----- 603  
QY 1318 CTGGAGCTGCTGGCGGCCCGTCTGCTGGCAGCGCCTACATCACCTCCCTCTACTTCGCA 1377  
Db 604 -----LeuGlyGlyProSerIleLysAspLysTyrValThrGlyLeuTyrPheThr 620  
QY 1378 CTCAGCAGCCTCACAGCGTGGCTTCGGCAACGTGTCCGCCAACACGACGACCGAGAAG 1437  
Db 621 PheSerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLys 640  
QY 1438 ATCTTCTCCATCTGCACCATGCTCATCGGCGCCTGATGCACGCGGTGGTGTGTTGGAAAC 1497  
Db 641 IlePheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsn 660  
QY 1498 GTGACGGCCATATCCAGCGCATGTACGCCCGCGCTTCTGTACCACAGCGCGCACGCGC 1557  
Db 661 ValSerAlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeu 680  
QY 1558 GACCTGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTG 1617  
Db 681 ArgValArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGlu 700  
QY 1618 GAGTACTTCCAGGCCACCTGGCGGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAG 1677  
Db 701 GluTyrPheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLys 720  
QY 1678 AGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCTCTGCAG 1737  
Db 721 GlyPheProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGln 740  
QY 1738 ---CTGCCACTGTTTGGCGGGCCAGCGCGGCTGCCTGCGGGCACTGTCTCTGGCCCTG 1794  
Db 741 HisCysLysProPheArgGlyAlaThrLysAspCysLeuArgAlaLeuAlaMetLysPhe 760  
QY 1795 CGGCCCGCCTTCTGTGCACGCGGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCC 1854  
Db 761 LysThrThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuThrAla 780  
QY 1855 CTCTACTTTGTCTGCTCTGGCTCCATGAGGTGCTCAAGGGTGGCACCGTGTCTGCCCATC 1914  
Db 781 LeuTyrPheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIle 800

QY 1915 CTAGGAAGGGCGACCTGATCGGCTGTGTAGCTGCCCGGGGAGCAGGTGGTAAAGGCC 1974  
Db 801 LeuGlyLysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSer 820  
QY 1975 AATGCCACGTGAAGGGGTGACGTACTGCGTCTCGTCTGCAGTGTCTGCAGCTGGCTGGCCTG 2034  
Db 821 AsnGlyAspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeu 840  
QY 2035 CACGACAGCCCTTGCGCTGTACCCCGAGTTTGGCCCGCTTACGTGCTGGCCCTCCGAGGG 2094  
Db 841 LeuGluValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu----- 858  
QY 2095 GAGCTCAGCTACAACCTG-----GGTGTGGGGGAGGCTCTGCAGAG 2136  
Db 859 GluIleThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGlu 878  
QY 2137 GTGACACACAGCTCCCTGAGCGGCGACAATACCTTTATGTCCACGTGGAGGAGAGGAG 2196  
Db 879 TrpGluGlyGlyPheAsnArgGlnArgLysArgLysLeuSerPheArgArgThrAsp 898  
QY 2197 ACAGATGGGAGCAGGGCCCGACCGTCTCCCCAGCCCGCAGCTGATGAGCCCTCCAGCCCC 2256  
Db 899 LysAspThrGluGln----- 903  
QY 2257 CTGCTGTCCCTGGCTGCACCTCCTCATCCTCAGCTGCCAAGCTGTATCCCCACGTCGA 2316  
Db 904 -----ProGlyGluValSerAla-----LeuGlyProGlyArg 914  
QY 2317 ACAGCACCCCGGCTCGTCTAGGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2376  
Db 915 AlaGlyAlaGlyPro-----SerSerArgGlyArgProGlyGlyProTrpGlyGluSer 932  
QY 2377 GCTGAGGCTGGCCCTCTGCTCCCCCA-----CGGCGCCCTA 2412  
Db 933 ProSerSerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSer 952  
QY 2413 GAGGGGTACGGCTG-----CCCCCATGCTCCATGGAATGTGCCCCCAGATCTG 2460  
Db 953 SerProLeuArgLeuValProPheSerSerProArgProProGlyGluProProGlyGly 972  
QY 2461 AGCCCCAGGGTAGTAGTGGCATTTGAAGACGGGTGTGGCTCGGACCAGGCCCAAG----- 2514  
Db 973 GluPro---LeuThrGluAspCysGluLysSerSerAspThrCysAsnProLeuSerGly 991  
QY 2515 -----TTCTCTTTC-----CGCGTGGGC 2532  
Db 992 AlaPheSerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyr 1011  
QY 2533 CAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGCGGCTGTCACT 2592  
Db 1012 GlnGluLeuProArgCys-----ProAlaProAlaProSerLeuLeuAsn 1026  
QY 2593 GTTCCC---CATGGGCCCGAGGAGGCAAGGAACACAGACACA-----CTGGACAAG 2640  
Db 1027 IleProLeuSerSerProSerArgArgProArgGlyAspValGluSerArgLeuAspAla 1046  
QY 2641 CTTCCGAGGCGGTGACAGAGTGTACAGAGCAGGTG---CTGCAGATCGGGAGGACTG 2697  
Db 1047 LeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThrValLeu 1066  
QY 2698 CAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTGGCGCCCCACAGGGAGGGTCCGTGCCCT 2757  
Db 1067 GlnLeuLeuGln-ArgGlnMetThrLeu----- 1075  
QY 2758 CGGGCATCGGAGAGGGGCCCGTGTGCCCGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGT 2817  
Db 1076 -----ValProAlaTyrSerAla-----Va 1083  
QY 2818 GTGACACTGGGGCATCTCTACTGCTCTGACGCCCGCCAGCTGGCTCTGTCTTGTAGTGG 2877  
Db 1083 lThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerProPhe-- 1102

QY 2878 ACTTGGCCACCTCGTCCGGGCTCTCCCTCCCTCATGGCACCTGGCCCTGGGTCC 2937  
Db 1103 -----ProThrLeuThrLeuAspSerLeuSerGln-----Valse 1114  
QY 2938 CCAGCGTCTC-----AGAGCTCCCTGGCTCGAGCCACAGCTTCTGGACCTCC 2988  
Db 1114 rGlnPheMetAlaCysGluGluLeuProGly---AlaProGluLeuProGlnGluGl 1133  
QY 2989 ACCTCAGACTCAGACCCCTCGCTCAGGAGACCTCTGCTCTGAGCCACACCCCTG 3046  
Db 1133 yProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnProLeu 1152  
RESULT 14  
KCH6\_HUMAN  
ID KCH6\_HUMAN STANDARD; PRT; 994 AA.  
AC Q9H252; Q9BRD7;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 6 (Ether-a-go-go  
DE related gene potassium channel 2) (Ether-a-go-go related protein 2)  
DE (Bag related protein 2).  
GN KCNH6 OR ERG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Titus S.A., Ganetzky B.S.;  
RT "Human Bag-related gene member 2 (Herg2) potassium channel.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Amygdala, and Kidney;  
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,  
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamiyama K.,  
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Tanigami A.,  
RA Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F., Wakebe H.,  
RA Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T., Irie R.,  
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,  
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
RT "NED0 human cDNA sequencing project";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Uterus;  
RX MEDLINE=2238257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium  
channel. Elicits a slowly activating, rectifying current (By

similarity). Channel properties may be modulated by cAMP and  
subunit assembly.  
-!- SUBUNIT: The potassium channel is probably composed of a homo- or  
heterotetrameric complex of pore-forming alpha subunits that can  
associate with modulating beta subunits. Heteromultimers with  
KCNH2/ERG1 and KCNH7/ERG3 (By similarity).  
-!- SUBCELLULAR LOCATION: Integral membrane protein.  
-!- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=3;  
Comment=Experimental confirmation may be lacking for some  
isoforms;  
Name=1;  
IsoId=Q9H252-1; Sequence=Displayed;  
Name=2;  
IsoId=Q9H252-2; Sequence=VSP\_000977, VSP\_000978;  
Name=3;  
IsoId=Q9H252-3; Sequence=VSP\_000979, VSP\_000980;  
-!- DOMAIN: The segment S4 is probably the voltage-sensor and is  
characterized by a series of positively charged amino acids at  
every third position.  
-!- SIMILARITY: Belongs to the potassium channel family. H (Bag)  
subfamily.  
-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.  
-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.  
-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; AF311913; AAG40871.1; -;  
DR EMBL; AK090969; BAC03559.1; -;  
DR EMBL; AK091877; BAC03764.1; -;  
DR EMBL; BC006334; AAH06334.1; -;  
DR Genew; HGNC:18862; KCNH6.  
DR InterPro; IPR000595; cNMP binding.  
DR InterPro; IPR003967; Erg\_channel.  
DR InterPro; IPR005821; Ion\_trans.  
DR InterPro; IPR001622; K+channel\_pore.  
DR InterPro; IPR005820; M+channel\_nlg.  
DR InterPro; IPR001610; PAC.  
DR InterPro; IPR000700; PAS-assoc C.  
DR InterPro; IPR000014; PAS domain.  
DR Pfam; PF00027; cNMP binding; 1.  
DR Pfam; PF00520; ion\_trans; 1.  
DR Pfam; PF00785; PAC; 1.  
DR PRINTS; PR01470; ERGCHANNEL.  
DR SMART; SM00100; cNMP; 1.  
DR SMART; SM00086; PAC; 1.  
DR PROSITE; PS00888; cNMP\_BINDING\_1; FALSE\_NEG.  
DR PROSITE; PS00889; cNMP\_BINDING\_2; FALSE\_NEG.  
DR PROSITE; PS50042; cNMP\_BINDING\_3; 1.  
DR PROSITE; PS50113; PAC; FALSE\_NEG.  
DR PROSITE; PS50112; PAS; FALSE\_NEG.  
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
KW Potassium channel; Potassium; Potassium transport; Transmembrane;  
KW Multigene family; Alternative splicing.  
FT DOMAIN 1 261 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 262 282 SEGMENT S1 (POTENTIAL).  
FT TRANSMEM 299 319 SEGMENT S2 (POTENTIAL).  
FT DOMAIN 320 340 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 341 361 SEGMENT S3 (POTENTIAL).  
FT TRANSMEM 371 391 SEGMENT S4 (POTENTIAL).  
FT DOMAIN 392 398 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 399 419 SEGMENT S5 (POTENTIAL).  
FT DOMAIN 464 484 SEGMENT H5 (PORE-FORMING) (POTENTIAL).  
FT TRANSMEM 491 511 SEGMENT S6 (POTENTIAL).  
FT DOMAIN 512 994 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 41 PAS.

FT	DOMAIN	92	144	PAC.
FT	NP BIND	594	711	CNMP.
FT	VARSP LIC	419	472	WYAIGNVERPYLEHKIGWLDLSGLVQLGKRYNGSDPASGPSV
FT				QDKYVTALYFTFS -> C (in isoform 2).
FT				/FTid=VSP 000977.
FT	VARSP LIC	745	780	Missing (in isoform 2).
FT				/FTid=VSP 000978.
FT	VARSP LIC	501	502	SL -> CE (in isoform 3).
FT				/FTid=VSP 000979.
FT	VARSP LIC	503	994	Missing (in isoform 3).
FT				/FTid=VSP 000980.
FT	CONFLICT	925	925	T -> M (IN REF. 2; BAC03764).
FT	CONFLICT	963	963	F -> L (IN REF. 2; BAC03764).
SQ	SEQUENCE	994 AA;	109924 MW;	BE9ECB349A798576 CRC64;
Alignment Scores:				
Pred. No.:		9.03e-60	Length:	
Score:		1509.50	Matches:	
Percent Similarity:		49.04%	Conservative:	
Best Local Similarity:		34.39%	Mismatches:	
Query Match:		24.79%	Indels:	
DB:		1	Gaps:	
US-09-965-830-1_COPY_6_3257 (1-3252) x KCH6_HUMAN (1-994)				
QY	1	ATGCCGGCCATGCGGGCCTCTCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG	60	
Db	1	MetProValArgArgGlyHisValAlaProGlnAsnThrTyrLeuAspThrIleLeArg	20	
QY	61	CGCTTCGACGGCACGCACAGTAACCTTCGTCTGGGCAAGCCCAAGTGGCGGCTCTTC	120	
Db	21	LysPheGluGlyGlnSerArgLysPheLeuIleAlaAsnAlaGlnMetGluAsnCys---	39	
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC	180	
Db	40	AlaIleIleTyrCysAsnAspGlyPheCysGluLeuPheGlyTyrSerArgValGluVal	59	
QY	181	ATGCAGCGGGCTGTGCTGCTCTCTCTCTCTTATGGCCAGACACCAAGTGGCTGATCCTGTAC	240	
Db	60	MetGlnGlnProCysThrCysAspPheLeuThrGlyProAsnThrProSerSerAlaVal	79	
QY	241	CAACAGATCCGCAAGGCCCTGGACGAGCACACAGGATTCAGGCTGAGCTGATCCTGTAC	300	
Db	80	SerArgLeuAlaGlnAlaLeuLeuGlyAlaGluGlyCysLysValAspIleLeuTyrTyr	99	
QY	301	CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAGAATGAGAAA	360	
Db	100	ArgLysAspAlaSerSerPheArgCysLeuValAspValProValLysAsnGluAsp	119	
QY	361	GGGAGGTGGCTCTCTTCCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCCGA---	417	
Db	120	GlyAlaValIleMetPheIleLeuAsnPheGluAspLeuAlaGlnLeuLeuAlaLysCys	139	
QY	417	-----	417	
Db	140	SerSerArgSerLeuSerGlnArgLeuLeuSerGlnSerPheLeuGlySerGluGlySer	159	
QY	418	-----GGGGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCGATAT	465	
Db	160	HisGlyArgProGlyGlyProGly-----ProGlyThrGlyArgGlyLysTyr	175	
QY	466	GGCCGGGCACGATCCAAA-----GGCTTCAATGCCAAC	498	
Db	176	---ArgThrIleSerGlnIleProGlnPheThrLeuAsnPheValGluPheAsnLeuGlu	194	
QY	499	CGGCGGCGGAGCCGGCCGTG-----CTCTACCCTGTCCGGGCAC-----CTGCAG	546	
Db	195	LysHisArgSerSerThrThrGluIleGluIleIleAlaProHisLysValValGlu	214	
QY	547	AAGCAGCCCAAGGGCAAGCACAGCTCAATAAGGGGTGTTTGGGGAGAAACCAACTTG	606	
Db	215	ArgThrGlnAsnValThrGluLysValThrGlnValLeuSerLeuGlyAlaAspValLeu	234	

QY	607	CCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCACTCCTGTGTGCACTGTGGGCA	666	
Db	235	ProGluTyrLysLeuGlnAlaProArgIleHisArgTyrThrIleLeuHisTyrSerPro	254	
QY	667	CTGAGAGCCACCTGGGATGGCTTCATCCTGCTGCTGCCACACTCTATGTGGCTGTCACTGTG	726	
Db	255	PheLysAlaValTyrAspTyrPheLeuLeuValIleTyrThrAlaValPheThr	274	
QY	727	CCCTACAGCGTGTGTGAGCACAGCAGCGGAGCCAGTGCCTGGCCCGCGGC-----	777	
Db	275	ProTyrSerAlaAlaPheLeuLeuSerAspGlnAspGluSerArgArgGlyAlaCysSer	294	
QY	778	-----CCGCCAGCGTCTGTGACCTGGCCGTGGAGTCTCTTTCATCCTTGAC	825	
Db	295	TyrThrCysSerProLeuThrValValAspLeuIleValAspIleMetPheValValAsp	314	
QY	826	ATTGTGCTGAATTTCCGTACCATTCGTGTCCAAGTCGGGCCAGGTGGTGTGGCCCA	885	
Db	315	IleValIleAsnPheArgThrTyrValAsnThrAsnAspGluValValSerHisPro	334	
QY	886	AAGTCCATTGCTCCACTACGTACCCACCTGCTTCCTGCTGGATGTATCGCAGCGCTG	945	
Db	335	ArgArgIleAlaValHisTyrPheLysGlyTyrPheLeuIleAspMetValAlaAlaIle	354	
QY	946	CCCTTTGACCTGCTA-----CATGCTTCAAGGTCAACGTGTACTTCGGGGCC	993	
Db	355	ProPheAspLeuLeuIlePheArgThrGlySerAspGluThrThrThrLeuIleGly---	373	
QY	994	CATCTGCTGAAGACGGTGGCTGCTGCGCTGCTGCGCTGCTTCCCGGGCTGGACCGG	1053	
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QY	1054	TACTGCGAGTACAGCGCGTGGTGTGCTGACACTGCTATGCGCGGTGTTCGCCCTGCTCGG	1113	
Db	393	TyrSerGluTyrGlyAlaAlaValLeuPheLeuLeuMetCysThrPheAlaLeuIleAla	412	
QY	1114	CAC TGGTCCGCTCGCTGCTGTTTATACATTGGCCAGCGGAGATCGAGAGCGCAATCC	1173	
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QY	1174	GAGTGCCTGAGATTGGCTGGCTGAGGAGTGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCT	1233	
Db	433	-----LysIleGlyTrpLeuAspSerLeuGlyValGlnLeu-----	444	
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Db	445	-----GlyLysArgTyrAsnGly-----SerAspProAlaSer---	455	
QY	1294	AGCAGCGAGGCCAACGGGACGGGGCTGGAGCTGCTGGCGGCCCGCTGCTGCTGCTGCTGCTGCT	1353	
Db	456	-----GlyProSerValGlnAspLys	462	
QY	1354	TACATCACTCCCTCTACTTCGCACTCAGCAGCCTCACAGCGGTGGCTTCGGCAACGTG	1413	
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QY	1414	TCCGCCAACACAGGACACCGAGAGATCTTCTCCATCTGCACCATGCTCATCGCGCCCTG	1473	
Db	483	SerProAsnThrAsnSerGluLysValPheSerIleCysValMetLeuIleGlySerLeu	502	
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Db	503	MetTyrAlaSerIlePheGlyAsnValSerAlaIleIleGlnArgLeuTyrSerGlyThr	522	
QY	1534	TTTCTGTACACAGCCGACCGCGGACCTTCGCGGACTACATCCGCATCCACCGTATCCCC	1593	
Db	523	AlaArgTyrHisThrGlnMetLeuArgValLysGluPheIleArgPheHisGlnIlePro	542	
QY	1594	AAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGCGGTGAACAATGGC	1653	
Db	543	AsnProLeuArgGlnArgLeuGluGluTyrPheGlnHisAlaTrpSerTyrThrAsnGly	562	
QY	1654	ATGCACACCCGAGCTGCTGCAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATG	1713	



Db 563 IleAspMetAsnAlaValLeuLysGlyPheProGluCysLeuGlnAlaAspIleCysLeu 582  
QY 1714 CACCTGCACAAGAGGTCTCTGCAG---CTGCCACTGTTTGGCGGCCAGCCGCGGTGC 1770  
Db 583 HisLeuHisArgAlaLeuLeuGlnHisCysProAlaPheSerGlyAlaGlyLysGlyCys 602  
QY 1771 CTGCGGGCAGTCTCTGCGCCTGCGCCGCGCTTCTGCACGCCGGGCGAGTACCTCATC 1830  
Db 603 LeuArgAlaLeuAlaValLysPheLysThrHisAlaProProGlyAspThrLeuVal 622  
QY 1831 CACCAAGCGGATGCCCTGCAGGCCCTCTACTTGTCTGTCTGTGGTCCATGGAGGTGCTC 1890  
Db 623 HisLeuGlyAspValLeuSerThrLeuTyrPheIleSerArgGlySerIleGluIleLeu 642  
QY 1891 AAGGTGGCACCCTGCTGCCATCTTAGGGAAGGCGACCTGATCGGCTGTGAGTGCCTC 1950  
Db 643 ArgAspAspValValAlaIleLeuGlyLysAsnAspIlePheGlyGluProValSer 662  
QY 1951 CGGCGGAGCAGGTGGTAAAGGCCAATGCCGACGCTGAAGGGGCTGACGTACTGCTGCTG 2010  
Db 663 LeuHisAlaGlnProGlyLysSerSerAlaAspValArgAlaLeuThrTyrCysAspLeu 682  
QY 2011 CAGTGTCTGCAGTGGTGGCTGCACGACAGCTTGCCTGTACCCCGAGTTTGCCTCCG 2070  
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QY 2071 CGCTTCAGTCGTGGCTCCGAGGGGAGCTCAGCTACAACTG-----GGTCTGGGGGA 2124  
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QY 2125 -----GGCTCTGCAGAGGTGGACACAGCTCCCTGAGC 2157  
Db 721 LeuHisSerProArgGlnAlaProGlySerGlnAspHisGlnGlyPhePheLeuSer 740  
QY 2158 GCGGACAATACCTTATGTCACGCTGGAGGAGAGGACAGATGGGAGCAGGGGCC 2217  
Db 741 ---AspAsn-----GlnSerGlySerProHisGluLeuGlyPro 752  
QY 2218 ACGGTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGC-----CCCCGTGTCTCCCTGCG 2271  
Db 753 GlnPhe-----ProSerLysGlyTyrSerLeuLeuGlyProGly 765  
QY 2272 TGCACCTCTCATCTCAGTGCACAGCTGCTATCCCGACGTCGAACAGCACCCCGCCT 2331  
Db 766 SerGlnAsnSerMetGlyAla----- 772  
QY 2332 CGTCTAGTGGCAGAGGAGGCGAGGCGAGGCGAGGCTTTGAAGCTGAGGTGGCC 2391  
Db 773 -----GlyProCysAlaProGlyHisProAspAla----- 782  
QY 2392 TCTGTCTCCCGAGGGCCCTA-----GAGGGGCTACGGTGGCCCGCATGCCATGG 2442  
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QY 2443 AATGTGCCCCCAGATCTGAGCCCCCAGGCTAGTAGATGGCATTTGAAGACGGCTGTGGCTCG 2502  
Db 801 GluMetProProArgHisSerProGln----- 809  
QY 2503 GACCAGCCCAAGTCTCTTTCCGCTGGGCGCAGTCTGGCCCGGAATGTAGCAGAGCC 2562  
Db 810 -----SerPro 811  
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Db 812 GlnGluAspProAspCysTrpProLeu----- 820  
QY 2623 ACAGACACACTGGACAAGCTTCGGCAGGCGGTGACAGAGCTGTACAGAGAGGTGCTGCAG 2682  
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QY 2683 ATGCGGGAAGGACTGCAGTCA---CTTCGCCAGGCTGTGCAGTCTGTCTGGCGCCAC 2739

Db 836 LeuGluSerArgValSerSerAspLeuSerArgIleLeuGlnLeuGlnLysProMet 855  
QY 2740 AGGAGGCTCCGTCCCTCGGGCATCGGAGAGGGCGCGTCCCGCAGCAGCACCTCCGGG 2799  
Db 856 ProGlnGly-----HisAlaSerTyrIleLeuGluAlaProAlaSerAsnAspLeu 872  
QY 2800 CTTTGCAGCCTCTGTGTGTGGACACTGGGGCATCTCTCTACTGCTGCAGCCCCCAGCT 2859  
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QY 2860 GGCTCTGTCTGAGTGGGACTTGGCCCCCACCCTCGTCCGGGGCCTCTCTCCCTCATGGCA 2919  
Db 882 -----ThrSerProGlyProArg-----Leu 888  
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QY 2980 TGGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTC-----TGCTCTGAG 3033  
Db 897 -----GlnThrProSerTyrGlyAspLeuAspAspCysSerPro 909  
QY 3034 CCCAGCACCCCTGCTCCCTCTCTCTCTCAGGAAGGGGCTAGGACTGGGCCCCCAGAG 3093  
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QY 3094 CCTGTGAGCCAGGCTGAGGCTACCAGCACTGGAGAGCCCCCAGGAGGTTCAGGGGCGCTG 3153  
Db 930 AlaProSerSerGluGlnGluProGluGlyLeuTrpPro-----Leu 945  
QY 3154 GCCTTGGCCCTGGACCCCCCAGCGCTGGAGATGGTCTATTGGC---TGCCATGGCTCT 3210  
Db 946 AlaSerProLeuHisProLeuGluValGlnGlyLeuIleCysGlyProCysPheSerSer 965

RESULT 15  
KCH6\_RAT  
ID KCH6\_RAT STANDARD; PRT; 950 AA.  
AC O54853;  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Potassium voltage-gated channel subfamily H member 6 (Ether-a-go-go related gene potassium channel 2) (Ether-a-go-go related protein 2)  
DE (Eag related protein 2).  
GN KCNH6 OR ERG2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cervical ganglion;  
RX MEDLINE=98054206; PubMed=9390998;  
RA Shi W., Wymore R.S., Wang H.-S., Pan Z., Cohen I.S., McKinnon D., Dixon J.E.;  
RT "Identification of two nervous system-specific members of the erg potassium channel gene family."  
RL J. Neurosci. 17:9423-9432(1997).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20183472; PubMed=10718922;  
RA Wulfsen I., Hauber H.P., Schiemann D., Bauer C.K., Schwarz J.R.;  
RT "Expression of mRNA for voltage-dependent and inward-rectifying K channels in GH3/B6 cells and rat pituitary."  
RL J. Neuroendocrinol. 12:263-272(2000).  
RN [3]  
RP INTERACTION WITH KCNH2 AND KCNH7, AND MUTAGENESIS OF GLY-480.  
RX MEDLINE=21079731; PubMed=11212207;  
RA Wimmers S., Wulfsen I., Bauer C.K., Schwarz J.R.;  
RT "Erg1, erg2 and erg3 K channel subunits are able to form heteromultimers."  
RL Pflugers Arch. 441:450-455(2001).  
RN [4]

RP	TISSUE SPECIFICITY.	FT	MUTAGEN	480	480	G->S: DOMINANT NEGATIVE MUTANT; ABOLISHES
RX	MEDLINE=21319165; PubMed=11425889;	FT				ERG CURRENT.
RA	Saganich M.J., Machado E., Rudy B.;	SQ	SEQUENCE	950 AA;	105705 MW;	AB5AE674B08776F0 CRC64;
RT	"Differential expression of genes encoding subthreshold-operating					
RT	voltage-gated K+ channels in brain.";					
RL	J. Neurosci. 21:4609-4624(2001).					
CC	-!- FUNCTION: Pore-forming (alpha) subunit of voltage-gated potassium					
CC	channel. Elicits a slowly activating, rectifying current. Channel					
CC	properties may be modulated by cAMP and subunit assembly.					
CC	-!- SUBUNIT: The potassium channel is probably composed of a homo- or					
CC	heterotetrameric complex of pore-forming alpha subunits that can					
CC	associate with modulating beta subunits. Heteromultimer with					
CC	KCNH2/ERG1 and KCNH7/ERG3.					
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.					
CC	-!- TISSUE SPECIFICITY: Highly expressed in celiac and superior					
CC	mesenteric ganglia, but not detected in brain or in heart.					
CC	Detected at low levels in retina. Also found in pituitary.					
CC	According Ref.4 found in olfactory bulb (granular and mitral cell					
CC	layers).					
CC	-!- DOMAIN: The segment S4 is probably the voltage-sensor and is					
CC	characterized by a series of positively charged amino acids at					
CC	every third position.					
CC	-!- SIMILARITY: Belongs to the potassium channel family. H (Eag)					
CC	subfamily.					
CC	-!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.					
CC	-!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.					
CC	-!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -					
CC	the European Bioinformatics Institute. There are no restrictions on its					
CC	use by non-profit institutions as long as its content is in no way					
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CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>					
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).					
CC	-----					
DR	EMBL; AF016192; AAB94742.1; --					
DR	InterPro; IPR000595; CNMP binding.					
DR	InterPro; IPR003967; Erg_Channel.					
DR	InterPro; IPR005821; Ion_trans.					
DR	InterPro; IPR001622; K+channel_pore.					
DR	InterPro; IPR005820; M+channel_nlg.					
DR	InterPro; IPR001610; PAC.					
DR	InterPro; IPR000700; PAS-assoc_C.					
DR	InterPro; IPR000014; PAS_domain.					
DR	Pfam; PF00027; CNMP_binding; 1.					
DR	Pfam; PF00520; ion_trans; 1.					
DR	Pfam; PF00785; PAC; 1.					
DR	PRINTS; PR01470; ERGCHANNEL.					
DR	SMART; SM00100; CNMP; 1.					
DR	SMART; SM00086; PAC; 1.					
DR	PROSITE; PS00888; CNMP_BINDING_1; FALSE_NEG.					
DR	PROSITE; PS00889; CNMP_BINDING_2; FALSE_NEG.					
DR	PROSITE; PS50042; CNMP_BINDING_3; 1.					
DR	PROSITE; PS50113; PAC; FALSE_NEG.					
DR	PROSITE; PS50112; PAS; FALSE_NEG.					
KW	Transport; Ion transport; Ionic channel; Voltage-gated channel;					
KW	Potassium channel; Potassium; Potassium transport; Transmembrane;					
KW	Multigene family.					
FT	DOMAIN 1 261					
FT	TRANSMEM 262					
FT	TRANSMEM 299					
FT	DOMAIN 320					
FT	TRANSMEM 341					
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FT	TRANSMEM 392					
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FT	DOMAIN 464					
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FT	TRANSMEM 262				</	





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QY      2974 GCTTTCTGGACCTCCACCTCAGACTC-----AGAGCCCCCTGCCTCA 3015
Db      862 lyAspLeuAspAspHisIleGlnThrProArgAsnPheSerProArgThrProHisValA 882
QY      3016 GGAGACCTCTGCTCTGAGCCCCAGCACCCCTGCCTCCCTCCTCTCTGTGAGGAAGGGCT 3075
Db      882 laMetAlaMet-AspLysThrLeuValProSerSerGluGlnGluProGlyGlyLeu 901
QY      3076 AGGACTGGGCGCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCACTGAGAGAGCCCCCA 3135
Db      902 LeuSerProLeuAlaSerProLeuArgProLeuGluVal----- 914
QY      3136 CCAGGTCAGGGGGCCTGGCCTTGCCCTGGGACCCCCACAGCCTGGAGATGGTG 3189
Db      915 ProGlyLeuGlyGlySerArgPheProSerLeuProGluHisLeuSerSerVal 932
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Search completed: September 1, 2004, 15:54:29  
Job time : 195 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2004, 15:52:14 ; Search time 345 Seconds  
(without alignments)  
5931.137 Million cell updates/sec

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Perfect score: 6089  
Sequence: 1 atgcggccatgcggggcct.....aagaagggcacaggggtctga 3252

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 2594344

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
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Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	5704	93.7	1083	9	US-09-965-830-2	Sequence 2, Appli
2	5698	93.6	1083	14	US-10-160-224-1	Sequence 1, Appli
3	5675	93.2	1083	14	US-10-185-867-2	Sequence 2, Appli
4	5659	92.9	1080	9	US-09-119-855-2	Sequence 2, Appli
5	5649.5	92.8	1082	14	US-10-121-746-20	Sequence 20, Appli
6	2529.5	41.5	1107	14	US-10-185-867-16	Sequence 16, Appli
7	2515	41.3	1102	14	US-10-185-867-36	Sequence 36, Appli
8	2461.5	40.4	1017	9	US-09-965-830-6	Sequence 6, Appli
9	1901	31.2	1284	9	US-09-119-855-11	Sequence 11, Appli
10	1901	31.2	1284	14	US-10-160-224-9	Sequence 9, Appli
11	1901	31.2	1284	14	US-10-185-867-11	Sequence 11, Appli
12	1835.5	30.1	542	9	US-09-119-855-5	Sequence 5, Appli
13	1835.5	30.1	542	14	US-10-185-867-5	Sequence 5, Appli
14	1551	25.5	1159	9	US-09-735-995-2	Sequence 2, Appli
15	1551	25.5	1159	9	US-09-735-995-4	Sequence 4, Appli
16	1551	25.5	1159	9	US-09-119-855-10	Sequence 10, Appli
17	1551	25.5	1159	14	US-10-000-151B-3	Sequence 3, Appli
18	1551	25.5	1159	14	US-10-193-692-5	Sequence 5, Appli
19	1551	25.5	1159	14	US-10-185-867-10	Sequence 10, Appli
20	1551	25.5	1159	14	US-10-174-613-49	Sequence 49, Appli
21	1551	25.5	1159	16	US-10-696-708-2	Sequence 2, Appli
22	1551	25.5	1159	16	US-10-696-708-4	Sequence 4, Appli
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24	1551	25.5	1159	16	US-10-483-617-2	Sequence 2, Appli
25	1509.5	24.8	994	14	US-10-192-440-8	Sequence 8, Appli
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45	1384.5	22.7	1196	15	US-10-391-399-82	Sequence 82, Appli

ALIGNMENTS

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; Sequence 2, Application US/09965830  
; Patent No. US20020177201A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/965,830  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 09/600,776  
; PRIOR FILING DATE: 2001-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1083  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-965-830-2

Alignment Scores: 1.05e-285 Length: 1083  
Pred. No.: 1083



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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	93.68%	Indels:	0
DB:	9	Gaps:	0
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QY	61	CGCTTCGACGGCAGCAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGGGCTCTTC	120
Db	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe	40
QY	121	CCCCTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC	180
Db	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal	60
QY	181	ATGCAGCGGGCTGTGCTGCTCCTTCTCTTTATGGGCCAGACACCATGAGCTCGTCCGC	240
Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg	80
QY	241	CAACAGATCCGAAGGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC	300
Db	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr	100
QY	301	CGGAAGAGCGGGCTCCCGTTCTGCTGCTCCTGGATGTGATACCCATAAAGAAATGAGAAA	360
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QY	361	GGGAGGTGGCTCTCTCCTAGTCTCTCACAGGACATCAGCGCAACCAAGAACCGAGGG	420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCCGACAGATGGAAGGAGACAGTGGTGGCGCGCGCGATATGGCCGGCCAGATCC	480
Db	141	GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer	160
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Db	201	AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys	220
QY	661	GGGGCACTGAGAGCCACTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC	720
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Db	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
QY	781	CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTTCATCCTTGACATTGCTGAATTC	840
Db	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
QY	841	CGTACCACATTCTGTCCAAGTCGGGCCAGGTGGTGTGTTGCCCAAGTCCATTGCGCTC	900
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QY	901	CAC TACGTCAACCACCTGGTTCCTGCTGGATGTCTATCGCAGCGCTGCCCTTTGACCTGCTA	960
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QY	1081	ACACTGCTCATGGCGGTGTTCCGCTGCTCGGCACCTGGGTGCCTGCGTCTGGTTTAC	1140
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Db	381	IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln	400
QY	1201	GAGTGGCCCCGACTGGAGACTCCCTACTACTTGGTGGCCGAGGCCAGCTGGAGGG	1260
Db	401	GluLeuAlaArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGCTCCGGCCAGAGTGAACACTGCAGCAGCAGCAGCGGCAACCGGACGGGCTG	1320
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QY	1381	AGCAGCCTCACCGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGACACCGAGAATC	1440
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Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla	660
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QY	2041	AGCCTTGGCTGTACCCCGAGTTTGCCCGCGCTTCAGTGTGGCTCCGAGGGGAGCTC	2100

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Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACATAACCTTATGTCCACGCTGGAGGAGAAGGAGACAGATGGGAGCAGGGCCCCACG 2220  
Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCGAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTGTCCTGGTGCACCTCC 2280  
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QY 2281 TCATCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGACACCCCGCCTCGTCTAGGT 2340  
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QY 2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCCTATGCCATGCCATGTGCCCCCAGATCG 2460  
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QY 2461 AGCCCCAGGCTAGTAGATGGCAATTGAAGACGGCTGTGGCTCGACCCAGCCCCAAGTTCTCT 2520  
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; Sequence 1, Application US/10160224  
; Publication No. US20030077731A1  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: Wickenden, Alan  
; APPLICANT: ICAGEN, Incorporated  
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit  
; FILE REFERENCE: 018512-001320US  
; CURRENT APPLICATION NUMBER: US/10/160,224  
; CURRENT FILING DATE: 2002-05-28  
; PRIOR APPLICATION NUMBER: US/09/343,494  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1083  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Elk (hElk; Eag (ether a go-go)-like K+ gene)  
; OTHER INFORMATION: potassium channel monomer protein  
US-10-160-224-1

Alignment Scores:  
Pred. No.: 2.13e-285 Length: 1083  
Score: 5698.00 Matches: 1082  
Percent Similarity: 99.91% Conservative: 0  
Best Local Similarity: 99.91% Mismatches: 1  
Query Match: 93.58% Indels: 0  
DB: 14 Gaps: 0

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QY 61 CGCTTCGACGGCACCGCACAGTAACTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC 120  
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QY 121 CCCGTGGTCTACTGCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGTTC 180  
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QY 181 ATGCAGCGGGGTGTGCTGTCTCCTTCTTATGGGCCAGACACCAGTGAGCTCGTCCGC 240  
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QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAGGATTCAGGCTGAGCTGATCCTGTAC 300  
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QY 301 CGGAAGAGCGGGTCCCGTTCTGGTGTCTCTCGATGTATACCCATAAAGATGAGAAA 360  
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QY 361 GGGGAGGTGGCTCTCTTCCCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGG 420  
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QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGGCCCGATATGGCCGGCACGATCC 480

141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 160  
481 AAAGGCTTCAATGCCAACCGCGCGGAGCGCGCGTGTCTTACCACCTGTCCGGGCAC 540  
161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
541 CTGCAGAAGCAGCCCAAGGCAACACCAAGCTCAATAAGGGGGTGTGGGAGAAACCA 600  
181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCATGT 660  
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901 CACTACGTCAACACCTGGTTCTCTGCTGGATGTTCATCGCAGCGCTGCCCTTTGACCTGCTA 960  
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961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCCATCTGCTGAACAGGTGCGCTGCTG 1020  
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1021 CGCCTGTGCGCCTGCTTCCGCGGTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTG 1080  
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1081 ACACGTGCTCATGGCCGTGTTCCGCCCTGCTCGGCACGTGGTGCCTCGCTGTGTTTAC 1140  
361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGTGGCTGCAG 1200  
381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400  
1201 GAGTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGCGCGAGCGCCAGCTGGAGGG 1260  
401 GluLeuAlaArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420  
1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACCGGACCGGGCTG 1320  
421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440  
1321 GAGCTGTGGCGGCCCGTTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTTCGCACTC 1380  
441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
1381 AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGACACCGAGAAGATC 1440  
461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480  
1441 TTCTCCATCTGCACCATGTCTCATCGCGCGCCTGATGCACGCGGTGGTGTGTTGGAAACGTG 1500  
481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500  
1501 ACGGCCATCATCAGCGCATGTACGCCCGCGCTTCTGTACCACAGCGCGCACCGCGGAC 1560

501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520  
1561 CTGCGCGACTACATCCGCGCATCCACCGTATCCCCAAGCCCCCTCAAGCAGCGCATGTGGAG 1620  
521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540  
1621 TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGC 1680  
541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560  
1681 CTCCCTGACGAGCTGCGCGGAGACATCGCCATGCACCTGCACAAAGGAGGTCTCTGCAGCTG 1740  
561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580  
1741 CCACTGTTTGAGCGGCCAGCGCGGTGCCTGCGGGCACTGTCTGTGGCCCTGCGGCC 1800  
581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600  
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601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
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641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
1981 GACGTGAAGGGGTGACGTACTGCGTCTCTGCAGTGTCTGCAGTGGCTGGCCTGCACGAC 2040  
661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680  
2041 AGCCTTCCGCTGTACCCCGAGTTTGCCTCCGCGCTTCAGTCTGTGGCTCCGAGGGGAGCTC 2100  
681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700  
2101 AGCTACAACCTGGTGTCTGGGGAGGTCTGCAGAGGTGGACACAGCTCCCTGAGCGGC 2160  
701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
2161 GACATACCCCTTATGTCCACGCTGGAGGAGAAGGAGACAGATGGGAGCAGGCCCCCAG 2220  
721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
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741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760  
2281 TCATCTCAGCTGCCAAGCTGTATTCCTCCACGTTCGAACAGCACCCCGGCTCTGTAGGT 2340  
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2521 TTCCGGCTGGCCAGTCTGGCCCCGGAATGTAGCAGCAGCCCCCTCCCTCTGGACCAGAGAC 2580  
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2581 GGCCTGTCTACTGTTCCCCATGGGCCCGCAGCAGGCAAGGAACACAGACACACTGGACAAG 2640  
861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880



QY 2641 CTTGGCGAGGGGTGACAGAGCTGTCTCAGAGCAGGTCTGCAGATGCGGGAGGACTGCAG 2700  
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Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920  
  
QY 2761 GCATCGGAGAGGGCCGTGCCCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
| | | | |  
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QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCCAGC 3120  
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QY 3121 ACTGAGAGCCCCCACCAGGGTACGGGGGCCTGGCCTTGGCCTGGGACCCCCACAGCCTG 3180  
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Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060  
  
QY 3181 GAGATGGTGCTTATTGGTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC 3240  
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Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080  
  
QY 3241 ACAGGGGTC 3249  
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Db 1081 ThrGlyVal 1083

RESULT 3  
US-10-185-867-2  
; Sequence 2, Application US/10185867  
; Publication No. US20030104429A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/10/185,867  
; CURRENT FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: US/09/358,383  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1083  
; TYPE: PRT  
; ORGANISM: Macaca sp.  
US-10-185-867-2

Alignment Scores:  
Pred. No.: 3.26e-284 Length: 1083  
Score: 5675.00 Matches: 1078  
Percent Similarity: 99.63% Conservative: 1  
Best Local Similarity: 99.54% Mismatches: 4  
Query Match: 93.20% Indels: 0

DB: 14 Gaps: 0  
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QY 61 CGCTTCGACGGCACGCACAGTAATCTCTGTCTGGGCAACGCCCAGGTGGGGGCTCTTC 120  
| | | | |  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
  
QY 121 CCCGTGGTCTACTGCTCTGTATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180  
| | | | |  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
  
QY 181 ATCAGCGGGCTGTGCCTGCTCCTTCTCTTATGGGCCAGACACCATGAGCTCGTCCGC 240  
| | | | |  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
  
QY 241 CAACAGATCCGCAAGGCCCTGGACGACACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
| | | | |  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
  
QY 301 CGGAAGACGGGCTCCCGTTCTGGTGTCTCTCTGGATGTATACCCATAAAGAATGAGAAA 360  
| | | | |  
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
  
QY 361 GGGAGGTGGCTCTCTTCTTAGTCTCTCACAAAGGACATCAGCGAAAACCAAGACCGAGGG 420  
| | | | |  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
  
QY 421 GGCCCGACAGATGGAAGGACAGGTGGTGGCGCGCGCGATATGGCCGGCACGATCC 480  
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Db 141 GlyProAspArgTrpLysGluThrGlySerGlyArgArgArgTyrGlyArgAlaArgSer 160  
  
QY 481 AAAGCTTCAATGCCAACCCGGCGGAGCCGGCCGTCTTACCACCTGTCCGGGCAC 540  
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Db 161 LysGlyPheAsnAlaAsnArgArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
  
QY 541 CTCAGAAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600  
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QY 601 AACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTGTTGCACCTGT 660  
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Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220  
  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTGCCACACACTCTATGTGGCTGC 720  
| | | | |  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
  
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGAGAGCCAGTGCCGCCCGCGGCCCCG 780  
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Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCCTTTCATCCTTGACATTGTGCTGAATTTC 840  
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Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
  
QY 841 CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTGTTGCCCAAAGTCCATTGCTCCTC 900  
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Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
  
QY 901 CACTACGTCACCACTGGTTCCTGCTGGATGTTCATCGCAGCGCTGCCCTTTGACCTGCTA 960  
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Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320  
  
QY 961 CATGCCCTTCAAGTCAACGTGTACTTCGGGGCCCATCTGTCTGAAGACGGTGGCCTGCTG 1020  
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Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340  
  
QY 1021 CGCCTGCTGCGCCTGCTTCCCGGGCTGGACCGGTACTGCGCAGTACAGCCCGTGGTGCTG 1080

Db	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360	Db	701	SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
QY	1081	AACTGCTCATGGCGGTTCGCGCTGCTCGCGCAGCTGGGTGCCTGCGTCTGGTTTAC	1140	QY	2161	GACAAATACCCCTTATGTCACACGCTGGAGGAGAGAGAGAGAGATGGGAGCAGGCCCCACG	2220
Db	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380	Db	721	AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr	740
QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG	1200	QY	2221	GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCTCCCTGGCTGCACCTCC	2280
Db	381	IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln	400	Db	741	ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer	760
QY	1201	GAGCTGGCCCGCGAGCTGAGACTCCCTACTACTACCTGGTGGCGGAGGCCAGCTGAGGG	1260	QY	2281	TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGACACACACCCCCCGCTCGTCTAGGT	2340
Db	401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420	Db	761	SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
QY	1261	AACAGCTCCGCGCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAAACGGGCGGTG	1320	QY	2341	GGCAGAGGAGGCCAGGCAGGCGAGGGGCTTTGAAGCTGAGGCTGGCCCTCTGTCTCCC	2400
Db	421	AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440	Db	781	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	800
QY	1321	GAGCTGTGGCGCGCGCTGCTGCGCAGCGCCTACATCACCTCCCTCTACTTTCGCATC	1380	QY	2401	CCACGGGCCCTAGAGGGCTACGGCTGCCCTGCCCTCCCATGCGATGGAATGTCCCCCAGATCTG	2460
Db	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460	Db	801	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu	820
QY	1381	AGCAGCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACACGACACCGAGAATC	1440	QY	2461	AGCCCCAGGGTAGTAGTGCGATTGAAGACGGCTGGCTCGGCTCGGACCCCAAGTTCTCT	2520
Db	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle	480	Db	821	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	840
QY	1441	TTCTCCATCTGCACCATGCTCATCGCGCGCCTGATGCACGGGTGGTGTGGGAACGTG	1500	QY	2521	TTCCGCTGGCGCCAGTCTGGCCCCGGAATGTAGCAGCAGCCCCCTCCCTGGACGAGAGC	2580
Db	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal	500	Db	841	PheArgMetGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer	860
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Db	501	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520	Db	861	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	880
QY	1561	CTGCGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGTGGAG	1620	QY	2641	CTTCGGCAGCGGTGACAGAGCTGTACAGCAGGTGTGCAGATGCGGGAAGGACTGCAG	2700
Db	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540	Db	881	LeuArgGlnAlaValMetGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	900
QY	1621	TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACACCGAGCTGTGCAGAGC	1680	QY	2701	TCACTTCGCCAGCGCTGTGCAGTTGTCTCTGGCGCCCCACAGGGAGGGTCCGTGCCCTCGG	2760
Db	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560	Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
QY	1681	CTCCCTGACGAGCTGGCGCAGACATCGCCATGCACCTGCACAAGGAGTCTCTGCAGCTG	1740	QY	2761	GCATCGGAGAGGGCCGTGCCCGCAGCCACACCTCCGGCTTCCTGCAGCCTCTGTGTGTG	2820
Db	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu	580	Db	921	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal	940
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Db	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600	Db	941	AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr	960
QY	1801	GCCTTCTGCACGCGCGGAGTACCTCATCCCAAGCGCATGCCCTGCAGGCCCTCTAC	1860	QY	2881	TGGCCCCACCTCGTCCGGGGCCTCTCTCCCTCATGGCACCTGGCCCTGGGGTCCCCCA	2940
Db	601	AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620	Db	961	TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro	980
QY	1861	TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTCGCCATCCTAGGG	1920	QY	2941	GCCTCTCAGAGTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA	3000
Db	621	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640	Db	981	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	1000
QY	1921	AAGGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGGCCAATGCC	1980	QY	3001	GAGCCCCCTGCCTCAGAGACCTCTGCTCTGAGCCAGCACCCCTGCCTCCCTCCTCCT	3060
Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla	660	Db	1001	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1020
QY	1981	GACGTGAAGGGGTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2040	QY	3061	TCTGAGGAAGGGGTAGACTGGGCCCCGAGAGCTGTGAGCCAGGCTGAGGCTACCAGC	3120
Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680	Db	1021	SerGluGluGlyAlaArgThrGlyProProGluProValSerGlnAlaGluAlaThrSer	1040
QY	2041	AGCCTTGCCTGTATCCCCAGTTTCCCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG	2100	QY	3121	ACTGAGAGCCCCCACCAGGGTCAGGGGGCTGGCTTGGCTTGGACCCCCACAGCCTG	3180
Db	681	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700	Db	1041	ThrGlyGluProProProValSerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu	1060
QY	2101	AGCTACAACTGGGTGCTGGGGAGGCTCTGCAGAGTGGACACAGCTCCCTGAGCGGC	2160	QY	3181	GAGATGGTGTATTGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC	3240
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RESULT 4  
US-09-119-855-2  
; Sequence 2, Application US/09119855  
; Patent No. US20020099197A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: mni-055  
; CURRENT APPLICATION NUMBER: US/09/119,855  
; CURRENT FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1080  
; TYPE: PRT  
; ORGANISM: Monkey  
US-09-119-855-2

Alignment Scores:  
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Query Match: 92.94% Indels: 0  
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QY 250 CGCAAGGCCCTGGACGAGCACAGGAGTTCAAGCTGAGCTGATCCTGTACCGGAAGC 309  
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QY 490 AATGCCAACCGCGCGGAGCCGGCCGCTGCTCTACCACTGTCCGGGCACCTGCAGAAG 549  
Db 161 AsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHisLeuGlnLys 180

QY 550 CAGCCCAAGGGCAAGCAAGCTCAATAAGGGGTGTTTGGGAGAAACCAAACTTGCCT 609  
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QY 610 GAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCTGTTGCACTGTGGGGCACTG 669  
Db 201 GluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCysGlyAlaLeu 220

QY 670 AGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTCACTGTGCC 729  
Db 221 ArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaValThrValPro 240

QY 730 TACAGCGTGTGTGAGCACAGCACGGGAGCCAGCCAGTCGCCCGCCCGCCAGCGTC 789  
Db 241 TyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyProProSerVal 260

QY 790 TGTGACCTGGCCGTGGAGTCTCTTCATCTCTGACATTGTGCTGAATTTCCTGACCACA 849  
Db 261 CysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPheArgThrThr 280

QY 850 TTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTTTGCCTCCAAAGTCCATTTGCCCTCCACTACGTC 909  
Db 281 PheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeuHisTyrVal 300

QY 910 ACCACCTGGTTCCTGCTGGATGTTCATCGCAGCGCTGCCCTTTGACCTGTACATGCCTTC 969  
Db 301 ThrThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeuHisAlaPhe 320

QY 970 AAGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCTGCTGCGCCTGCTG 1029  
Db 321 LysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeuArgLeuLeu 340

QY 1030 CGCCTGCTTCGCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTGACACTGCTC 1089  
Db 341 ArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeuThrLeuLeu 360

QY 1090 ATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCCTTGCCTGCTGCTTTTACATTGGCCAG 1149  
Db 361 MetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyrIleGlyGln 380

QY 1150 CGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAGGAGCTGGCC 1209  
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QY 1210 CGCCGACTGGAGACTCCCTACTACTGCTGGTGGCCGGAGCCAGCTGGAGGGAACAGCTCC 1269  
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QY 1270 GGCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTGGAGCTGCTG 1329  
Db 421 GlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeuGluLeuLeu 440

QY 1330 GGGCGCCCGTGCCTGCGCAGCGCCTACATCACCTCCCTCTACTTTCGCACTCAGCAGCCTC 1389  
Db 441 GlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeuSerSerLeu 460

QY 1390 ACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATCTTCTCCATC 1449  
Db 461 ThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIlePheSerIle 480

QY 1450 TGCACCATGCTCATCGCGCCCTTGATGCACGCGGTGGTGTGTTGGGAACGTGACGGCCATC 1509  
Db 481 CysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrAlaIle 500

QY 1510 ATCCAGCGCATGTACGCCCGCGCTTCTGTATCACACAGCCGCACGCGCGACCTGCGCGAC 1569  
Db 501 IleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAspLeuArgAsp 520

QY 1570 TACATCCGATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAG 1629  
Db 521 TyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGluTyrPheGln 540

QY 1630 GCCACCTGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGCCTCCCTGAC 1689  
Db 541 AlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSerLeuProAsp 560

QY 1690 GAGCTGCGCGCAGACATCGCCCATGCACCTGCACAAGGAGTCTCTGAGTGCCACTGTTT 1749





QY	61	CGCTTCGACGGCACAGTAAC	120
Db	21	ArgPheAspGlyThrHisSerAsn	39
QY	121	CCCGTGGTCTACTGCTGATGG	180
Db	40	ProValValTyrCysSerAspGly	59
QY	181	ATGCAGCGGGGCTGCTCCTCT	240
Db	60	MetGlnArgGlyCysAlaCysSer	79
QY	241	CAACAGATCCGGAAGCCCTGG	300
Db	80	GlnGlnIleArgLysAlaLeuAsp	99
QY	301	CGGAAGAGCGGGTCCCGTTCT	360
Db	100	ArgLysSerGlyLeuProPheTrp	119
QY	361	GGGGAGGTGGCTCTCTTCTCT	420
Db	120	GlyGluValAlaLeuPheLeuVal	139
QY	421	GGCCCCGACAGATGGAAGGAC	480
Db	140	GlyProAspArgTrpLysGluThr	159
QY	481	AAAGGCTTCAATGCCAACCGG	540
Db	160	LysGlyPheAsnAlaAsnArgArg	179
QY	541	CTGCAGAAAGCAGCCCAAGGG	600
Db	180	LeuGlnLysGlnProLysGlyLys	199
QY	601	AACTTGCCTGAGTACAAAGTAG	660
Db	200	AsnLeuProGluTyrLysValAla	219
QY	661	GGGGACTGAGAGCCACCTGGG	720
Db	220	GlyAlaLeuArgAlaThrTrpAsp	239
QY	721	ACTGTGCCCTACAGCGTGTGTG	780
Db	240	ThrValProTyrSerValCysVal	259
QY	781	CCGAGCTGTGTGACCTGGCGCT	840
Db	260	ProSerValCysAspLeuAlaVal	279
QY	841	CGTACCAATTCGTTGCCAAGTC	900
Db	280	ArgThrThrPheValSerLysSer	299
QY	901	CAC	960
Db	300	HisTyrValThrTrpPheLeuLeu	319
QY	961	CATG	1020
Db	320	HisAlaPheLysValAsnValTyr	339
QY	1021	CGCTGTGCGCCTGCTCCGGGCT	1080
Db	340	ArgLeuLeuArgLeuLeuProArg	359
QY	1081	ACACTGCTCATGGCGGTTCGGCC	1140
Db	360	ThrLeuLeuMetAlaValPheAla	379

QY	1141	ATTGGCCAGCGGGAGATCGAGAG	1200
Db	380	IleGlyGlnArgGluIleGluSer	399
QY	1201	GAGCTGGCCCGCCGACTGGAGAC	1260
Db	400	GluLeuAlaArgLeuGluThrPro	419
QY	1261	AACAGCTCCGGCCAGAGTGACAA	1320
Db	420	AsnSerSerGlyGlnSerAspAsn	439
QY	1321	GAGCTGTGGGCGGCCGTGCTGCT	1380
Db	440	GluLeuLeuGlyGlyProSerLeu	459
QY	1381	AGCAGCCTCACAGCGTGGGCTTC	1440
Db	460	SerSerLeuThrSerValGlyPhe	479
QY	1441	TTCTCCATCTGCACCATGCTCAT	1500
Db	480	PheSerIleCysThrMetLeuIle	499
QY	1501	ACGGCCATCATCCAGCGCATGTAC	1560
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QY	1561	CTGCGGACTACATCCGCATCCAC	1620
Db	520	GlnArgAspTyrIleArgIleHis	539
QY	1621	TACTTCCAGGCCACCTGGCGGTGA	1680
Db	540	TyrPheGlnAlaThrTrpAlaVal	559
QY	1681	CTCCCTGACGAGCTGCGCGCAGAC	1740
Db	560	LeuProAspGluLeuArgAlaAsp	579
QY	1741	CCACTGTTTGAGGGCGCCAGCCG	1800
Db	580	ProLeuPheGluAlaAlaSerArg	599
QY	1801	GCCTTCTGCACCGCGCGAGTACCT	1860
Db	600	AlaPheCysThrProGlyGluTyr	619
QY	1861	TTTGTCTGTCTGGCTCCATGGAG	1920
Db	620	PheValCysSerGlySerMetGlu	639
QY	1921	AAGGGCAGCTGATCGGCTGTGAG	1980
Db	640	LysGlyAspLeuIleGlyCysGlu	659
QY	1981	GACGTGAAGGGGCTGACGTACTG	2040
Db	660	AspValLysGlyLeuThrTyrCys	679
QY	2041	AGCCTTGGCTGTACCCGAGTTTGC	2100
Db	680	SerLeuAlaLeuTyrProGluPhe	699
QY	2101	AGCTACAACCTTGGTGTGGGGAG	2160
Db	700	SerTyrAsnLeuGlyAlaGlyGly	719
QY	2161	GACAATACCCCTTATGTCCACGCT	2220
Db	720	AspAsnThrLeuMetSerThrLeu	739
QY	2221	GTCTCCCCAGCCCGAGCTGATGAG	2280

Db 740 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 759  
QY 2281 TCATCCTCAGCTGCCAAGCTGTATCCCCACGTCGAACACACACCCCGGCTCGTCTAGCT 2340  
Db 760 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 779  
QY 2341 GGACAGGGAGGCCAGGCAGGGGCTTTGAAGGCTGAGCTGGCCCTCTGCTCCC 2400  
Db 780 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 799  
QY 2401 CCACGGGCCCTAGAGGGGTACGGCTGCCCCCCCCTATGCCATGGAATGTGCCCCCAGATCTG 2460  
Db 800 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu 819  
QY 2461 AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCCCAAGTTCTCT 2520  
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QY 2521 TTCCCGCTGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGC 2580  
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QY 2581 GGCCTGCTCACTGTTCCCATGGGCCAGCGAGGCAAGGAACACACACACTGGACAAG 2640  
Db 860 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 879  
QY 2641 CTTCCGGCAGCGGTGACAGAGCTGTTCAGACAGGTGCTGCAGATGCGGGAAGGACTGCAG 2700  
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QY 2701 TCACCTTCGCAGAGCTGTGCAGCTTGTCTGGCGCCCCCAGAGGAGGTCCGTGCCCTCGG 2760  
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QY 2881 TGGCCCCACCTCGTCCGGGGCCTCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA 2940  
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; TYPE: PRT  
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Alignment Scores:  
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Score: 2529.50 Matches: 559  
Percent Similarity: 60.24% Conservative: 150  
Best Local Similarity: 47.49% Mismatches: 267  
Query Match: 41.54% Indels: 201  
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QY 61 CGCTTCGACGGCACGACAGTAACCTCGTGTCTGGCAACGCCCGAGGTGGCGGCTCTTC 120  
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QY 121 CCCGTGGTCTACTGCTCTGTATGGTCTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60  
QY 181 ATGACAGCGGGCTGTGCCTCTCTGATGGTCTCTGTCATGGCCAGACACCATGAGTCTGTC 240  
Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACCAAGAGTTCAAGGCTGAGTCTGATCTGTAC 300  
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QY 301 CGGAAGAGCGGGCTCCGTTCTGTGTCTCTCTGATGTGATACCCATAAAGATGAGAAA 360  
Db 101 LysLysAsnGlySerProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120  
QY 361 GGGGAGGTGGTCTCTCTTCTCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCCGAGGG 420  
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QY 421 GGGCCCGACAGATGGAAGGAGACAGGTGTGGTGGCGGCGCGGATATGGCCGGGACGATCC 480  
Db 141 ThrProGluAspLysLysGluAsp-----LysValLysGlyArgSerArgAla 156  
QY 481 ---AAAGGCTTCAATGCCAACCCGGCGGAGCGCGGCTCTCTGATGTGATACCCATAAAGATGAGAAA 537  
Db 157 GlyThrHisPheAspSerAlaArgArgArgSerArgAlaValLeuTyrHisIleSerGly 176  
QY 538 CACCTGCAGAAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAA 597  
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QY 598 CCAAACTTGCCTGAGTACAAAGTAGCCGCCATCCGGGAGTCCGCCCTTTCATCCTGTTGCAC 657  
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 QY 718 GTCACCTGTGCCCTACAGCGTGTGTGTGAGCAGACAGCGGAGCCAGTCGCGCCCGCGGC 777  
 Db 237 ValThrValProTyrAsnValCysPheIleGlyAsnAspLeuSerThrThrArgSer 256  
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 Db 257 ---ThrThrValSerAspIleAlaValGluLeuPheIleAspIleLeuAsn 275  
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 Db 296 IleHisTyrValThrThrTrpPheIleAspLeuIleAlaLeuPropheAspLeu 315  
 QY 958 CTACATGCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCTG 1017  
 Db 316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu 335  
 QY 1018 CTGCGCTGCTGCGCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCGTGGTG 1077  
 Db 336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355  
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 QY 1258 GGGAAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGGAGGCCAACGGGACGGGG 1317  
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 QY 1318 CTGGAGCTGTGGCGGCGCGCTGCTGCGCAGCGCCTATCATCACCTCCCTCTACTTCGCA 1377  
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 Db 429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys 448  
 QY 1438 ATCTTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACGCGGTGGTGTGTTGGGAAC 1497  
 Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468  
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 Db 489 AspLeuLysAspPheIleArgValHisHisLeuProGlnGlnLeuLysGlnArgMetLeu 508  
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 QY 1678 AGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGACCTGCACAAGGAGTCTGCAG 1737  
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QY 1738 CTGCCACTGTTTGAGGGCGGCCAGCCGCGGCTGCCTGCGGGCACCTGTCTCTGGCCCTGCGG 1797  
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 QY 1918 GGGAAAGGCGACCTGATCGGCTGTGAGTGCCTCCGCGGAGCAGGTGTTAAAGGCCAAT 1977  
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 QY 2098 CTCAGCTACAACCTGGGTGCTGGG-----GGAGGCTCT 2130  
 Db 669 LeuThrTyrAsnLeuArgGluGlyHisGluSerAspValIleSerArgLeuSerAsnLys 688  
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 Db 709 IleValGluAspGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 726  
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 Db 738 -----Arg 738  
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 QY 2397 ----- 2397  
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Db 986 TyrHisSerProSerLeuAspTyrSerProSerHisTyrGlnValGlnGluHis 1005  
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QY 3154 GCCTTGCCCTGGGACCCCGACAGCCTGAGATGGTGTATTGGCTGCCATGGCTCTGGC 3213  
Db 1045 ValLeuPro-----SerArgSerGluGlu-----GlySerPheSerGlnGly 1058  
QY 3214 ACAGTC-----CAGTGGACCCAGGAA 3234  
Db 1059 ThrValSerSerPheSerLeuGluAsnLeuProGlySerTrpAsnGlnGlu 1075

RESULT 7  
US-10-185-867-36  
; Sequence 36, Application US/10185867  
; Publication No. US20030104429A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, RORY A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/10/185,867  
; CURRENT FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: US/09/358,383  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 1102  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-185-867-36

Alignment Scores: 1.73e-121 Length: 1102  
Pred. No.: 2515.00 Matches: 551  
Score: 62.00% Conservative: 149  
Percent Similarity:

Best Local Similarity: 48.80% Mismatches: 295  
Query Match: 41.30% Indels: 134  
DB: 14 Gaps: 24  
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QY 1 ATGCGGGCCATGCGGGCCTCCTGGCGCCTCAGAACACACCTTCTTGACACCATCGTACG 60  
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCACGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGTC 180  
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60  
QY 181 ATGACGCGGGCTGTGCTGCTCCTTCTCTTATGCGGACAGACACAGTGAGCTGCTCCG 240  
Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80  
QY 241 CAACAGATCCGCAAGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 81 LeuGlnIleGluLysSerLeuGluLysValGluPheLysGlyGluIleMetPheTyr 100  
QY 301 CGGAAGAGCGGGCTCCCGTCTCTGCTGCTCTCTGATGTATACCCATAAAGAATGAGAAA 360  
Db 101 LysLysAsnGlyAlaProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120  
QY 361 GGGAGGTGGCTCTCTTCTCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGA--- 417  
Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140  
QY 418 GGGGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCCGATATGCGCGGCACGA 477  
Db 141 ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly----- 157  
QY 478 TCCAAAGGCTTCAATGCCAACCGCGGGGAGCGCGCGTGTCTTACACCTGTCCGGG 537  
Db 158 ---SerHisPheAspSerAlaArgArgArgSerArgAlaValLeuTyrHisIleSerGly 176  
QY 538 CACCTGCAGAAGCAGCCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTGGGAGAAA 597  
Db 177 HisLeuGlnArgArgGluLysAsnLysLeuLysIleAsnAsnAsnValPheValAspLys 196  
QY 598 CCAAACCTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCCGCTTCTATCTGTGCAC 657  
Db 197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216  
QY 658 TGTGGGCACTGAGAGCCACCTGGGATGGTTCATCTGCTCGCCACACTCTATGTGGCT 717  
Db 217 PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAla 236  
QY 718 GTCACCTGTCCCTACAGCGTGTGTGTGAGCAGCAGCGGAGCCCGAGTCCCGCGCGGC 777  
Db 237 ValThrValProTyrAsnValCysPheIleGlyAsnGluAspLeuSerThrThrArgSer 256  
QY 778 CCGCCCGAGCTCTGTGACCTGGCGGTGGAGGTCTCTTCTTCTTGTGACATGTGTGAAT 837  
Db 257 ---ThrThrValSerAspIleAlaValGluIleLeuPheIleAspIleIleLeuAsn 275  
QY 838 TTCCGTACCCACATTCGTGTCCAAGTCCGGGCCAGGTGGTGTGTCGCCCAAGTCCATTGC 897  
Db 276 PheArgThrThrThrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295  
QY 898 CTCCACTACGTCACCACTGGTTCCTGCTGGATGTGATGTCATCGCAGCGTGCCTTTGACCTG 957  
Db 296 IleHisTyrValThrThrTrpPheIleIleAspLeuIleAlaLeuProPheAspLeu 315  
QY 958 CTACATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGTGAAGACGGTGGCGCTG 1017  
Db 316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu 335

QY	1018	CTGCGCCTGCTGCGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCCGCTGGTG	1077
Db	336	LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal	355
QY	1078	CTGACACTGCTCATGGCCGTGTTTCGCCCTGCTCGCGCACTGGTGCCTGCGTCTGGTTT	1137
Db	356	LeuThrLeuLeuMetSerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleTrpTyr	375
QY	1138	TACATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTG	1197
Db	376	ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu	395
QY	1198	CAGGAGCTGGCCCGCACTCGAGACTCCCTACTACTGTTGGCCGGAGGCCAGCTGGA	1257
Db	396	HisGluLeuGlyLysArgLeuGluSerProTyrTyr	407
QY	1258	GGGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGGCGCAACGGGACGGGG	1317
Db	408	GlyAsnAsnThr	411
QY	1318	CTGGAGCTGCTGGGGCGCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCA	1377
Db	412	-----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr	428
QY	1378	CTCAGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGGACACCGAGAAG	1437
Db	429	LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys	448
QY	1438	ATCTTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGTGGTGTGGGAAC	1497
Db	449	IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn	468
QY	1498	GTGACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTCTGTACCACAGCGCACGCGC	1557
Db	469	ValThrAlaIleIleGlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys	488
QY	1558	GACCTGGCGGACTACATCCGATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTG	1617
Db	489	AspLeuLysAspPheIleArgValHisHisLeuProGlnGlnLeuLysGlnArgMetLeu	508
QY	1618	GAGTACTTCCAGGCCACCTGGCGGTGAACAATGCATCGACACCCAGCTGCTGCAG	1677
Db	509	GluTyrPheGlnThrThrTrpSerValAsnAsnGlyIleAspSerAsnGluLeuLys	528
QY	1678	AGCCTCCCTGACGAGTGCAGCAGACATCGCCATGCACCTGCACAAGGAGTCTCTGCAG	1737
Db	529	AspPheProAspGluLeuArgSerAspIleThrMetHisLeuAsnLysGluIleLeuGln	548
QY	1738	CTGCCACTGTTTGAAGCGGCCAGCCGGCTGCTGCGGGCACTGTCTCTGSCCTGCGG	1797
Db	549	LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuSerLeuHisIleLys	568
QY	1798	CCCGCCTTCTGACGCCCGGGCGAGTACCTCATCCACCAAGCGGATGCCCTGCAGGCCCTC	1857
Db	569	ThrSerPheCysAlaProGlyGluTyrLeuLeuArgGlnGlyAspAlaLeuGlnAlaIle	588
QY	1858	TACTTTGTCTGCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTGCCCATCCTA	1917
Db	589	TyrPheValCysSerGlySerMetGluValLeuLysAspSerMetValLeuAlaIleLeu	608
QY	1918	GGGAAGGGCGACCTGATCGGCTGTGAGTGCCTCCCGCGGGAGCAGGTGTTAAGGCCAAT	1977
Db	609	GlyLysGlyAspLeuIleGlyAlaAsnLeuSerIleLysAspGlnValIleLysThrAsn	628
QY	1978	GCCGACGTGAAGGGGTGACGTACTCGTCTCTGCAGTGTCTGCAGCTGGCTGGCCTGCAC	2037
Db	629	AlaAspValLysAlaLeuThrTyrCysAspLeuGlnCysIleIleLeuLysGlyLeuPhe	648
QY	2038	GACAGCCTTGGCGTGTACCCCGAGTTTGGCCCGCGCTTCAGTCTGGCTCCGAGGGGAG	2097
Db	649	GluValLeuGlyLeuTyrProGluTyrAlaHisLysPheValGluAspIleGlnHisAsp	668

QY	2098	CTCAGCTACAACCTGGGTGCTGGG-----GGAGGCTCT	2133
Db	669	LeuThrTyrAsnLeuArgGluGlyHisGluSerAspValIleSerArgLeuSerAsnLys	688
QY	2131	GCAGAGGTGGACACCACTCCCTGAGCGGCGACAATACCCCTTATGTCCACGCTG-----	2184
Db	689	SerThrValProGlnAlaGluProLysGlyAsnGlySerIleLysLysArgLeuProSer	708
QY	2185	-----GAGGAGAAGGAGACAGATGGGAGACAGGGCCCCACGGTCTCCCGAGCCCCA	2235
Db	709	IleValGluAspGluGluGluGluValGluGluGluThrThrSerLeuSerPro	728
QY	2236	GCTGATGAGCCCTCCAGCCCCCTGTGTCCCGCTGGCTGCACCTCCTCATCCTCAGCTGCC	2295
Db	729	IleTyrThrArgGlySerSerValSerHisSerLysLysThrGlySerSerLysSerTyr	748
QY	2296	AAGCTGCTATCCCCACGTCGA-----ACAGCACCC-----CGGCCT---CGT	2334
Db	749	LeuGlyLeuSerLeuLysGlnLeuThrSerGlyThrValProPheHisSerProIleArg	768
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QY	2506	CAGCCCAAG---TTCTCTTTCCGCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCC	2562
Db	825	GluThrGlnThrPheAspPheGlySerGluGlnIleArgProGluProArgIleSerPro	844
QY	2563	TCCCTGGACCAAGAG-----AGCGGCGCTGCTCACTGTTCGCCATGGGCCCAGCGAG	2613
Db	845	SerLeuGlyGluSerGluIleGlyAlaAlaPheLeuPheIle-----Lys	859
QY	2614	GCAAGGAACACA--GACACACTGGACAAGCTTCGGCAGCGGCTGACAGAGCTGTCCAGAG	2670
Db	860	AlaGluGluThrLysGlnGlnIleAsnLysLeuAsnSerGluValThrThrLeuThrGln	879
QY	2671	CAGGTGCTGCAGATCGCGGAAGGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTGT	2730
Db	880	GluValSerGlnLeuGlyLysAspMetArgSerIleMetGlnLeuLeuGluAsnIleLeu	899
QY	2731	CGCCCCACAGGAGGGTCCGTGCCCTCGGGCATCGGGAGAGGGGCGGTGCCAGCCAGC	2790
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Db	920	GluSerPheGlnThrArg-----ValSerTyrSerAlaHisGlnProCysLeuHis	936
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Db	937	LeuGlnAlaAsnGlyAlaHisLeuTyrHisGlyAsnValThrSerAspIleTrp-----	954
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QY	2959	-----TGGCCTCGAGCCACA	2973
Db	993	CysGlnValIleGlnGluGlyHisLeuGlnPheLeuArgCysIleSerProHisSerAsp	1012
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QY 3082 GGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGACTGGAGAGCCCCCACCAGGG 3141
Db 1053 GlyProValSerSerPheSerLeu-----GluAsnLeuProGly 1065
QY 3142 TCAGGGGGCCTGGCCTTGCCCTGGGGAC 3168
Db 1066 Ser-----TrpAsp 1068
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RESULT 8

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US-09-965-830-6
; Sequence 6, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965,830
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-830-6
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Pred. No.: 9.77e-119 Length: 1017
Score: 2461.50 Matches: 538
Percent Similarity: 59.19% Conservative: 119
Best Local Similarity: 48.47% Mismatches: 245
Query Match: 40.43% Indels: 208
DB: 9 Gaps: 23

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QY 61 CGTTTCGACGGCAGCACAGTAACCTTCGTGCTGGGCAACGCCAGTCGGGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyThrArgGlyPhe 40
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuThrGlyTyrGlyArgThrGluVal 60
QY 181 ATGACGGGGCTGTGCCTGCTCCTTCCTTTATGGCCAGACACCAAGTGAGCTCGTCGC 240
Db 61 MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGluThrSerGluProAlaLeu 80
QY 241 CAACAGATCCCAAGGCCCTGGACGAGCAACAAGGATTCAAGGCTGAGTGCCTGTATC 300
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QY 301 CGGAAGAGCGGGCTCCGTTCTGGTGTCTCTGATGTGATACCCATAAGAATGAGAAA 360
Db 101 ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetMetProIleLysAsnGluMet 120
QY 361 GGGGAGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
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Db 141 LeuGlyProGln-----GlyGlyArgGlyAspSerAsnHisGluAsn 154
QY 478 TCCAAAGGC-----TTCAATGCCAACCCGCGCGGAGCCGGGCC 516
Db 155 SerLeuGlyArgArgGlyAlaThrTrpLysPheArgSerAlaArgArgSerArgThr 174
QY 517 GTGCTCTACACCTGTCCGGGCACCTGCAGAAGCAGCCCAAGGGCAAGCAACAAGCTCAAT 576
Db 175 ValLeuHisArgLeuThrGlyHisPheGlyArgGlyGlnGlyMetLysAlaAsn 194
QY 577 AAGGGGTGTTTGGGAGAAACAAACTTGCTGAGTACAAAGTAGCCGCCATCCGGAAG 636
Db 195 AsnAsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGly 214
QY 637 TCGCCCTTCATCCTGTTCACCTGTGGGCACCTGAGAGCCACCTGGGATGGCTTCATCCTG 696
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Db 275 IleLeuAspIleIleLeuAsnPheArgThrThrTyrValSerGlnSerGlyGlnValIle 294
QY 877 TTTGCCCAAGTCCATTTGCTCCACTACGTACCAACCTGGTTCCTGTGGATGTATC 936
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QY 937 GCAGCGTGCCTTTGACCTGTACATGCCTTCAAGTCAACGCTACTTCGGGGGCCAT 996
Db 315 AlaAlaLeuProPheAspLeuLeuTyrIlePheAsnIleThrValThrSerLeuValHis 334
QY 997 CTGCTGAAGACGGTGGCCTGTGCTGCGCTGTGCGCTGCTTCCGGGCTGGACCGGTAC 1056
Db 335 LeuLeuLysThrValArgLeuLeuArgLeuLeuArgLeuLeuLysLeuGluArgTyr 354
QY 1057 TCGAGTACAGCGCCGTGGTGTGCTGACACTGCTCATGGCCGTTCGCCCTGCTCGGCAC 1116
Db 355 SerGlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHis 374
QY 1117 TGGTTCGCTGCTGTGTTTACATTTGGCCAGCGGAGATCGAGAGCAGCAATCCGAG 1176
Db 375 TrpMetAlaCysIleTyrTyrValIleGlyArgArgGluMetGluAlaAsnAspProLeu 394
QY 1177 CTGCTGAGATTGGCTGGCTGCAGGAGTGGCCCGCCGACTGGAGACTCCCTACTACCTG 1236
Db 395 LeuTrpAspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluValProTyr----- 412
QY 1237 GTGGCCCGGAGGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGC 1296
Db 412 ----- 412
QY 1297 AGCAGGCCAACGGGACGGGGCTGGAGCTGGGGCGGCCGCTGCTGGCCAGCGCCTAC 1356
Db 413 -----ValAsnGlySer-----ValGlyGlyProSerArgArgSerAlaTyr 426
QY 1357 ATCACCTCCCTCTACTTCGACACTCAGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCC 1416
Db 427 IleAlaAlaLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCys 446
QY 1417 GCCAACACGACACCGAGAAAGATCTTCTCCATCTGCACCATGTCTCATCGGCCCTGTATG 1476
Db 447 AlaAsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet 466
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QY 1477 CACGGGTGGTGTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCGCTTT 1536  
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467 HisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgSer 486  
QY 1537 CTGTACCACAGCGCGACCGCGACCTGCGCGACTACATCCGCATCCACCGGTATCCCCAAG 1596  
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527 AspAlaAsnGluLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHis 546  
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QY 1837 GCGGATGCCCTGCGAGCCCTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGT 1896  
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587 GlyAspAlaLeuGlnAlaHisTyrTyrValCysSerGlySerLeuGluValLeuArgAsp 606  
QY 1897 GGCACCGTGTGCGCCATCCTAGGAAGGGGACCTGATCGGCTGTGAGTGCCTCCCGCGG 1956  
Db |||||  
607 AsnMetValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspIleProGluPro 626  
QY 1957 GAGCAG-----GTGGTAAAGGCCAATGCCGACGTG 1986  
Db |||||  
627 GlyGlnGluProGlyLeuGlyAlaAspProAsnPheValLeuLysThrSerAlaAspVal 646  
QY 1987 AAGGGGTGACGTACTCGTCTGCAGTGTCTGCAGCTGGCTGGCTGCACGACGCTT 2046  
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647 LysAlaLeuThrTyrCysGlyLeuGlnLeuSerSerArgGlyLeuAlaGluValLeu 666  
QY 2047 GCGCTGTACCCCGAGTTTGCCCCGCGCTTCAGTCGTGGCCTCCGAGGGGAGCTCAGCTAC 2106  
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667 ArgLeuTyrProGluTyrGlyAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPhe 686  
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687 AsnLeuArgGlnGlySer-----AspThrSerGlyLeuSerArgPheSer 701  
QY 2155 -----AGCGGCGACAATACC 2169  
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702 ArgSerProArgLeuSerGlnProArgSerGluSerLeuGlySerSerAspLysThr 721  
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QY 2230 GCGCCAGCTGATGAGCCCTCCAGCCCTGCTGTCCCTGGCTGCACCTCCTCATCCTCA 2289  
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735 GlyGlyGlyProArgProArgProLeuLeuProAsnLeuSerProAlaArgPro 754  
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QY 2302 -----CTATCCCCACGTTCGAACAGCACCCCGGCTCGTCTAGGTGGCAGAGGAGG 2352  
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775 SerProSerLeuSerProSerLeuSer-----ProAlaLeuAlaGlyGlnGlyHis 791  
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792 -----SerAlaSerProHisGlyProProArgCysSer 802

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803 AlaAlaTrpLysProProGlnLeuLeuIleProLeuGlyThrPheGlyProProAsp 822  
QY 2458 CTGAGCCCCAGGGTAGTAGTGGCATTGAAGAC---GGCTGTGGCTCGGACCCAGCCCAAG 2514  
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899 gGluLeuArgHisIleMetGlyLeuLeu----- 908  
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909 -----GlnAlaArgLeuGlyProPro----- 915  
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916 -----GlyHisProAlaGlySer----- 921  
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QY 2932 GGTCCCCCAGCGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACC 2991  
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QY 2992 TCAGACTCAGAGC----- 3004  
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946 oSerLeuGlnAspThrThrLeuAlaGluValHisCysProAlaSerValGlyThrMetGl 966  
QY 3005 -----CCCCTGCCTCAGGAGAC 3021  
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966 uThrGlyThrAlaLeuLeuAspLeuArgProSerIleLeuProProTyrProSerGluPr 986  
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RESULT 9  
US-09-119-855-11  
; Sequence 11, Application US/091119855  
; Patent No. US20020099197A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: mni-055  
; CURRENT APPLICATION NUMBER: US/09/119,855  
; CURRENT FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 1284  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-119-855-11

Alignment Scores:  
Pred. No.: 7.28e-90 Length: 1284  
Score: 1901.00 Matches: 455

Percent Similarity: 53.85% Conservative: 146  
Best Local Similarity: 40.77% Mismatches: 273  
Query Match: 31.22% Indels: 242  
DB: 9 Gaps: 31

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QY 301 CGGAAGAGCGGGCTCCCGTCTCTGCTGCTCTCTCAAGGACATCAGCGAAACCAAG--- 411
Db 100 LysLysGluGlyAlaProPheTrpCysLeuPheAspIleValProIleLysAsnGluLys 119
QY 361 GGGGAGGTGGCTCTCTCTAGTCTCTCAAGGACATCAGCGAAACCAAG--- 411
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QY 412 -----AACCGAGGG 420
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RESULT 10  
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; Sequence 9, Application US/10160224  
; Publication No. US20030077731A1  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: Wickenden, Alan  
; APPLICANT: ICAGEN, Incorporated  
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit  
; FILE REFERENCE: 018512-001320US  
; CURRENT APPLICATION NUMBER: US/10/160,224  
; CURRENT FILING DATE: 2002-05-28  
; PRIOR APPLICATION NUMBER: US/09/343,494  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 1284  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Drosophila Elk (dElk; Eag (ether a go-go)-like K+  
; OTHER INFORMATION: gene) protein  
US-10-160-224-9  
Alignment Scores:  
Pred. No.: 7.28e-90 Length: 1284  
Score: 1901.00 Matches: 455  
Percent Similarity: 53.85% Conservative: 146  
Best Local Similarity: 40.77% Mismatches: 273  
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; Sequence 5, Application US/10185867  
; Publication No. US20030104429A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: US/10/185,867  
; PRIOR FILING DATE: US/09/358,383  
; PRIOR APPLICATION NUMBER: 1999-07-21  
; PRIOR FILING DATE: USSN 09/119,855  
; PRIOR APPLICATION NUMBER: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 542  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-185-867-5

Alignment Scores:  
Pred. No.: 1.59e-86 Length: 542  
Score: 1835.50 Matches: 352  
Percent Similarity: 77.64% Conservative: 82  
Best Local Similarity: 62.97% Mismatches: 92  
Query Match: 30.14% Indels: 33  
DB: 14 Gaps: 5  
US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-10-185-867-5 (1-542)  
QY 1 ATGCCGGCCATCGGGCCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60  
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCAGCAGTAACTTCGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40  
QY 121 CCGTGGTCTACTGCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGGCTGAGTTC 180  
Db 41 ProfileValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60  
QY 181 ATGCAGCGGGCTGTGCCTGCTCCTTCCTTTATGGGCCAGACACCATGAGTCTGCTCCG 240  
Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80  
QY 241 CAACAGATCCGCAAGCCCTCGGACGAGCACAAGGAGTTCAAGGTGAGCTGATCCTGTAC 300  
Db 81 LeuGlnIleGluLysSerLeuGluGluLysThrGluPheLysGlyGluIleMetPheTyr 100  
QY 301 CGGAAGACGGGCTCCCGTTCTGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360  
Db 101 LysLysAsnGlySerProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120  
QY 361 GGGAGGTGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCCGAGGG 420  
Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140  
QY 421 GGCCCGCAGATGGAAGGAGACAGGTGGTGGCCGCGCGATATGCGCGGCGCAGATCC 480  
Db 141 ThrProGluAspLysLysGluAsp-----LysValLysGlyArgSerArgAla 556

QY 481 ---AAAGGCTTCAATGCCAACCCGGCGGCGGAGCCGGCGCTGTCTACCACTGTCCGGG 537  
Db 157 GlyThrHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176  
QY 538 CACCTGCAGAAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTGGGAGAAA 597  
Db 177 HisLeuGlnArgArgGluLysAsnLysLeuLysIleAsnAsnValPheValAspLys 196  
QY 598 CCAAACTTGCCTGAGTACAAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTCAC 657  
Db 197 ProAlaPheProGluTyrLysValSerAspAlaLysSerLysPheIleLeuLeuHis 216  
QY 658 TGTGGGCACCTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGCT 717  
Db 217 PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAla 236  
QY 718 GTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTCGCCGCCGGC 777  
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QY 778 CCGCCAGCGTCTGTGACCTGGCGGTGAGGTCTCTTCATCCTGACATTTGCTGAAT 837  
Db 257 ---ThrThrValSerAspIleAlaValGluIleLeuPheIleIleAspIleIleLeuAsn 275  
QY 838 TTCCGTACCACTTCGTGTCCAAGTCGGGCCAGGTGGTGTTCGCCCCAAAGTCCATTTGC 897  
Db 276 PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295  
QY 898 CTCCACTACGTCACACCTGGTTCCTGCTGATGTATCATCGCAGCGTCCCTTTGACCTG 957  
Db 296 IleHisTyrValThrThrTrpPheIleIleAspLeuIleAlaLeuPropheAspLeu 315  
QY 958 CTACATGCCTTCAAGTCAACGTGTACTTCGGGGCCCATCTGCTGAACAGCGTCCGCTG 1017  
Db 316 LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuLysThrValArgLeu 335  
QY 1018 CTGCGCCTGCTGCGCCTGCTTCCCGGGTGGACCGGTACTCGCAGTACAGCGCGCTGTG 1077  
Db 336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355  
QY 1078 CTGACACTGCTCATGGCGCGTGTTCGCCCTGCTGCGGCACCTGGTGCCTGCTGCTTT 1137  
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QY 1138 TACATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTG 1197  
Db 376 ValIleGlyLysMetGluArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu 395  
QY 1198 CAGGAGTGGCCCGCCTGAGACTCCCTACTACTGCTGGTGGCGGAGGCCAGCTGGA 1257  
Db 396 HisGluLeuGlyLysArgLeuGluSerProTyrTyr----- 407  
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Db 408 GlyAsnAsnThr----- 411  
QY 1318 CTGGAGCTGTGGGCGGCGCGTCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCA 1377  
Db 412 -----LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr 428  
QY 1378 CTCAGCAGCCTCACCGCGTGGCTTCGGCAACGTCGTCCGCAACACCGACCCGAGAAAG 1437  
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QY 1438 ATCTTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGTGTGGGAAC 1497  
Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468  
QY 1498 GTGACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTGTACACAGCCGCGCGC 1557  
Db 469 ValThrAlaIleIleGlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys 488





Db 512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531  
QY 1024 CTGCTGGCGCTCTCCGCGCTGGACCGGTACTCGCAGTACAGCGCGTGGTGTGCTGACA 1083  
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QY 1084 CTGCTCATGGCCGCTTCCGCTCTGCTCGGCACCTGGGTGGCTGCTGCTGTTTACATT 1143  
Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIle 571  
QY 1144 GGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAGAG 1203  
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QY 1204 CTGGCCCGCGACTGGAGACTCCCTACTACTCTGTGGCGCGAGGCCAGCTGGAGGGAAC 1263  
Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598  
QY 1264 AGCTCCGCGCAGAGTGACAACTGCAGCAGCAGCAGCGAGCGCAACGGGACGGGCTGGAG 1323  
Db 599 SerSerGly----- 601  
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QY 1504 GCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTATCCACAGCGCGCAGCGGACCTG 1563  
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QY 1564 CGCGACTACATCCGCTCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTAC 1623  
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QY 1801 GCCTTCTGCACCGCGCGAGTACCTCATCCACCAAGCGCATGCCCTGCAGGCCCTCTAC 1860  
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QY 1861 TTTGTCTGCTCTGGCTCCATGGAGTGTCAAGGTGGACCGTGTCTGCCATCCTAGGG 1920  
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QY 2041 AGCCTTGGCTGTACCCCGAGTTTGGCCCGCTTACGTGCTGGCTCCGAGGGGAGCTC 2100  
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QY 2143 ACCAGCTCCCTGAGCGCGCAATAACCTTATGTCACCGTGGAGGAGGAGACAGAT 2202  
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QY 2323 CCGCGGCTCTAGTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2382  
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Db 1099 oLeu-----ProThrLeuThrLeuAspSerLeuSerGln----- 1110  
QY 2932 GGTCCCCCAGCGTCTC-----AGAGCTCCCCCTGGCCTCGAGCCACAGCTTCTG 2982  
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QY 2983 ACCTCCACTCAGACTCAGAGCCCTCCCTGCTCAGGAGACCTCTGCTCTGAGCCCGCACC 3042  
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QY 3043 CCTG 3046  
Db 1149 oLeu 1150

RESULT 15  
US-09-735-995-4  
; Sequence 4, Application US/09735995  
; Patent No. US20010034024A1  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
; TITLE OF INVENTION: SYNDROME GENE  
; FILE REFERENCE: 2323-136  
; CURRENT APPLICATION NUMBER: US/09/735,995  
; CURRENT FILING DATE: 2000-12-14  
; PRIOR APPLICATION NUMBER: 09/226,012  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1159  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-995-4

Alignment Scores:  
Pred. No.: 7.61e-72 Length: 1159  
Score: 1551.00 Matches: 424  
Percent Similarity: 44.86% Conservative: 143  
Best Local Similarity: 33.54% Mismatches: 337  
Query Match: 25.47% Indels: 360  
DB: 9 Gaps: 38

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-735-995-4 (1-1159)

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QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGTC 180  
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QY 181 ATGACGGGGCTGTGCCTGCTCCTCTTATGGCCAGACACCATGAGCTCGTCCGC 240  
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgArgAlaAla 79

QY 241 CAACAGATCCGAAGGCCCTGGACGACACAAGGATTCAAGGCTGAGCTGATCCTGTAC 300  
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QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360  
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QY 603 ----- 603  
Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338  
QY 603 ----- 603  
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QY 802 GTGAGGTCTCTTTCATCCTTGACATTTGCTGAATTCGTACCACATTCGTGTCCAAG 861  
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Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511  
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QY 504 -----GCGGAGCCGGCCGTGCTCTA----- 524  
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QY 525 --CCACCTGTCCGGGCACCTGCAGAAGCAGCCCAAGGCAAG---CACAGCTCAAT--- 576  
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QY 576 ----- 576  
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QY 577 -----AAGGGGGTGTTTGGGGAG 594  
Db 279 ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro 298  
QY 595 AAACCCAAAC----- 603  
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QY 604 -----TTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTC 645  
Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp 398  
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QY 706 CTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTG-----AGCACAGCACGG 756  
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QY 862 TCGGGCCAGGTGGTGTTCGCCCAAGTCCATTTGCCCTCCACTACGTCAACACCTGGTTC 921  
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Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511  
QY 982 TACTTCGGGGCC-----CATCTGCTGAAGACGGTGCCTGCTGCTGCGC 1023  
Db 512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531  
QY 1024 CTGCTGCGCCTGCTTCGCGGGCTGGACCGGTACTCGCAGTACAGCGCGTGGTGGTGTGACA 1083



Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551  
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Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598  
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Db 599 SerSerGly----- 601  
QY 1324 CTGCTGGCGGCGCGCTGCTGCGTGGCGAGCGGCTACATCACCTCCCTCTACTTCGCACTCAGC 1383  
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Thu Sep 2 12:18:20 2004

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Search completed: September 1, 2004, 16:23:36  
Job time : 470 secs





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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2004, 15:37:55 ; Search time 61 Seconds  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5704	93.7	1083	4	US-09-600-776-2
2	5698	93.6	1083	4	US-09-343-494-1
3	5675	93.2	1083	4	US-09-358-383C-2
4	5649.5	92.8	1082	4	US-09-336-643A-20
5	2529.5	41.5	1107	4	US-09-358-383C-16
6	2515	41.3	1102	4	US-09-358-383C-36
7	2461.5	40.4	1017	4	US-09-600-776-6
8	1901	31.2	1284	4	US-09-343-494-9
9	1901	31.2	1284	4	US-09-358-383C-11
10	1835.5	30.1	542	4	US-09-358-383C-5
11	1551	25.5	1159	2	US-08-956-242-13
12	1551	25.5	1159	3	US-09-351-215-13

13	1551	25.5	1159	3	US-09-226-012-2	Sequence 2, Appli
14	1551	25.5	1159	3	US-09-226-012-4	Sequence 4, Appli
15	1551	25.5	1159	4	US-09-358-383C-10	Sequence 10, Appli
16	1551	25.5	1159	4	US-09-275-252A-12	Sequence 12, Appli
17	1487	24.4	290	4	US-09-358-383C-8	Sequence 8, Appli
18	1378.5	22.6	962	4	US-09-694-777A-24	Sequence 24, Appli
19	1378	22.6	960	4	US-09-694-777A-21	Sequence 21, Appli
20	1370.5	22.5	989	4	US-09-694-777A-23	Sequence 23, Appli
21	1370	22.5	962	4	US-09-614-480-9	Sequence 9, Appli
22	1369	22.5	962	4	US-09-694-777A-3	Sequence 3, Appli
23	1367.5	22.5	987	4	US-09-694-777A-22	Sequence 22, Appli
24	1358.5	22.3	989	4	US-09-694-777A-4	Sequence 4, Appli
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C 42	409	6.8	1065	1	US-08-642-255-72	Sequence 72, Appli
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ALIGNMENTS

RESULT 1  
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; Sequence 2, Application US/09600776  
; Patent No. 6326168  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/600,776  
; CURRENT FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-011434  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1083  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-600-776-2

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Best Local Similarity:	100.00%		Mismatches:	0
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QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCCTGTGAGCCAGGCTGAGGCTACCAGC 3120  
Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040  
QY 3121 ACTGAGAGCCCCCACCAGGTCAGGGGCTGGCCCTGGCCCTGGGACCCCGACAGCCTG 3180  
Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060  
QY 3181 GAGATGGTGTATTGGTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAAGGC 3240  
Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080  
QY 3241 ACAGGGGTC 3249  
Db 1081 ThrGlyVal 1083

RESULT 2

US-09-343-494-1

; Sequence 1, Application US/09343494

; Patent No. 6413741  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: Wickenden, Alan  
; APPLICANT: ICAGEN, Incorporated  
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit  
; FILE REFERENCE: 018512-001320US  
; CURRENT APPLICATION NUMBER: US/09/343,494  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: US 60/091,469  
; EARLIER FILING DATE: 1998-07-01  
; EARLIER APPLICATION NUMBER: US 60/116,621  
; EARLIER FILING DATE: 1999-01-21  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1083  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Elk (hElk; Eag (ether a go-go)-like K+ gene)  
; OTHER INFORMATION: potassium channel monomer protein  
US-09-343-494-1

Alignment Scores:

Pred. No.: 0 Length: 1083  
Score: 5698.00 Matches: 1082  
Percent Similarity: 99.91% Conservative: 0  
Best Local Similarity: 99.91% Mismatches: 1  
Query Match: 93.58% Indels: 0  
DB: 4 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-343-494-1 (1-1083)

QY 1 ATCCCGGCATCGGGGCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60  
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCACGCACAGTAACCTCGTGTGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGTCTCCCGGGCTGAGGTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGAGCGGGGCTGTGCTGTCTCCTTCCTTTATGGGCCACAGCAGGAGTCAAGGCTGATCCTGTAC 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTCAAGGCTGAGCTGATCCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuLeuTyr 100  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGATGTGATACCCATAAAGATGAGAAA 360  
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGGAGGTGGCTCTCTCCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGGGCGGCGGCTATGGCCGCGCACGATCC 480  
Db 141 GlyProAspArgTrpLysGluThrGlyGlyGlyArgArgTyrGlyArgAlaArgSer 160  
QY 481 AAAGGCTTCAATGCCAACCCGGCGGGAGCGGGCGGCGGCTCTACCTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAAGCAGCCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200



601	QY	AACTTGCCCTGAGTACAAAGTAGCCGCCATCGGGAAGTCGCCCTTATCCTGTTGCACTGT	660
201	Db	AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys	220
661	QY	GGGCACTGAGAGCCACCTGGGATGGCTTCATCTCCTCGCCACACTCTATGTGGTGT	720
221	Db	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
721	QY	ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCAGTCGCCCGCGCGCCG	780
241	Db	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
781	QY	CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCATCTCCTTGACATTGTGCTGAATTC	840
261	Db	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
841	QY	CGTACCACATTTCGTGTCCAAAGTCGGCCAGGTGGTGTTCGCCCAAGTCCATTTGCCTC	900
281	Db	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300
901	QY	CACTACGTCACCACCTGGTTCCTGTGATGTATCGCAGCGCTGCCCTTTGACCTGCTA	960
301	Db	HisTyrValThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	320
961	QY	CATGCCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGTGAAGACGGTGGCCCTGCTG	1020
321	Db	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
1021	QY	CGCTGTCTGGCCTGCTTCCGGGTGGACCGGTACTCGCAGTACAGCGCCGTGGTGTCTG	1080
341	Db	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360
1081	QY	ACACTGCTCATGGCCGTGTTCCGCTCTCGGCACCTGGTGGCTGCGTCTGGTGTTC	1140
361	Db	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
1141	QY	ATTGGCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTGGTGGTGGCAG	1200
381	Db	IleGlyGlnArgGluIleGluSerSerGluLeuProGluIleGlyTrpLeuGln	400
1201	QY	GAGCTGGCCGCGGACTGGAGACTCCCTACTACTCCTGTGGCGCGGAGGCCAGCTGGAGG	1260
401	Db	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgProAlaGlyGly	420
1261	QY	AACAGCTCCGCGCAGAGTGACAACTGCAGCAGCAGCAGCGGCAACGCGGAGCGGGCTG	1320
421	Db	AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440
1321	QY	GAGCTGTGGCGCGCGCTGCTGCGCAGCGCTACATCACCTCCCTCTACTTCGCACCTC	1380
441	Db	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
1381	QY	AGCAGCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGGACACCGAGAAGATC	1440
461	Db	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle	480
1441	QY	TTCTCCATCTGCACCATGCTCATCGCGGCCCTGATGCAGCGGTGGTGTGGGAACGTG	1500
481	Db	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal	500
1501	QY	ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCACAGCCGCGCAGCG	1560
501	Db	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520
1561	QY	CTGGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGTGGAG	1620
521	Db	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540
1621	QY	TACTTCCAGGCCACTGGCGCGGTGAACAAATGGCATCGACACCGAGCTGCTGCAGAGC	1680
541	Db	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560

Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940  
QY 2821 GACACTGGGGCATCCTCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTTGTAGTGGACT 2880  
Db 941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValIleuSerGlyThr 960  
QY 2881 TGGCCCCACCTCGTCCGGGGCCTCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA 2940  
Db 961 TrpProHisProAlaProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980  
QY 2941 GCGTCTCAGACTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000  
Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000  
QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCGAGCACCCCTGCCCTCCCTCCTCCT 3060  
Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020  
QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCCGAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC 3120  
Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaThrSer 1040  
QY 3121 ACTGGAGACCCCCACCAGGTCAGGGGCTGGGCGCTGGCCTGGCCTGGACCCCCACAGCCTG 3180  
Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060  
QY 3181 GAGATGGTCTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGGC 3240  
Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGluGly 1080  
QY 3241 ACAGGGGTC 3249  
Db 1081 ThrGlyVal 1083

RESULT 3

US-09-358-383C-2  
; Sequence 2, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358,383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1083  
; TYPE: PRT  
; ORGANISM: Macaca sp.  
US-09-358-383C-2

Alignment Scores:

Pred. No.: 0 Length: 1083  
Score: 5675.00 Matches: 1078  
Percent Similarity: 99.63% Conservative: 1  
Best Local Similarity: 99.54% Mismatches: 4  
Query Match: 93.20% Indels: 0  
DB: 4 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-358-383C-2 (1-1083)

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QY 61 CGCTTCGACGGCACGACAGTAACCTTGTGTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAenAlaGlnValAlaGlyLeuPhe 40

QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 180  
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QY 181 ATGCAGCGGGGCTGTGCCTGCTCCTTCTCTTATGGGCCAGACACCAGTACGCTCGTCCGC 240  
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QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGAGTTCAAGGTGAGCTGATCCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCTCTGATGTGATACCCCATAAAGAATGAGAA 360  
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGAGGTGGCTCTCTTCTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCGATATGGCCGGCAGCATCC 480  
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QY 481 AAAGGCTCAATGCCAACCCGGCGGAGCCGGCCGTCTTACACCTGTCCGGGCAC 540  
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QY 541 CTGCAAGACAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 660  
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QY 661 GGGCACTGAGAGCCACCTGGGATGGCTTTCATCCTGTCTGCCACACTCTATGTGGCTGTC 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCAAGTCCCGCCCGGCGCCG 780  
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QY 781 CCCAGCGTCTGTGACCTGGCGTGGAGGTCTCTTTCATCTTGACATTGTGTAATTTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTCTGTGCCAAGTCGGGCCAGGTGGTGGTGGCCCAAGTCCATTTCCTC 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
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QY 1081 ACACCTGCTCATGGCCGTGTTCGCCCTGTCTCGCGCATGGGTGGCTGCGCTGCTGTTTAC 1140  
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG 1200  
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QY 1201 GAGCTGGCCCCGCGACTGGAGACTCCCTACTACTCTGGTGGGCGGAGGCCAGCTGGAGGG 1260

Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGGAGGCCAAACGGGACGGGCTG 1320  
Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440  
QY 1321 GAGTGTCTGGGGCCCGCTCGTGGCGCAGCGCTACATCACCTCCCTCTACTTGGCACTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGCAGCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGACACCGAGAAGATC 1440  
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QY 1441 TTCTCCATCTGCACCATGTCTACGGCGCCCTGATGCACGGGTGGTGTGGGAACGTG 1500  
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QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTTCTGTACACAGCCGCGCGAC 1560  
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Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisGlyGluValLeuGlnLeu 580  
QY 1741 CCACGTGTTGAGGGCGCCAGCGCGGTGCGCTGCGGCACTGCTCTGCGCCCTGCGGCC 1800  
Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600  
QY 1801 GCCTTCTGCACCGCGGCGAGTACCTCATCCACCAAGCGGATGCCCTGCAGGCCCTCTAC 1860  
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QY 1861 TTTGTCTGCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTCGCCATCTAGGG 1920  
Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640  
QY 1921 AAGGGGACCTGATCGGCTGTGAGTGCCTGGCGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGGTGACGTACTGCTCCTGAGTGTCTGAGTGGCTGGCTGCACGAC 2040  
Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680  
QY 2041 AGCCTTGCGTGTACCCCGAGTTTGGCCCGGCTTCAGTCGTGGCTCCGAGGGGAGCTC 2100  
Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700  
QY 2101 AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACAGCTCCCTGAGCGGC 2160  
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QY 2161 GACAATACCTTTATGTCCACGCTGGAGGAGAGGACAGATGGGGAGCAGGSCCCACG 2220  
Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCCAGCCCCAGTGTATGAGCCCTCCAGCCCCCTGTGTCCCTGGCTGCACCTCC 2280  
Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760  
QY 2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTGCAACAGCACCCCGGCTCTAGGT 2340

Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780  
QY 2341 GGCAGAGGGAGGCCAGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCCCTCTGTCTCC 2400  
Db 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800  
QY 2401 CCACGGGCCCTAGAGGGGTACGGGTACGGCTGCCCGCCCATGCGAATGTGCCCCAGATCTG 2460  
Db 801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTyrAsnValProProAspLeu 820  
QY 2461 AGCCCCAGGTAGTAGTGGCATTTGAAGACGGCTGTGGTTCGGACCGCCCAAGTTCTCT 2520  
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QY 2521 TTCCGCTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGC 2580  
Db 841 PheArgMetGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860  
QY 2581 GGCCTGCTCACTGTTCCCATGCGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2640  
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QY 2641 CTTCGGCAGCGGTGACAGAGCTGTTCAGAGCAGGTGTCTGCAGATCGGGAAGGACTGCAG 2700  
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QY 2761 GCATCGGAGAGGGCGCGTGTCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
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Db 1081 ThrGlyVal 1083

RESULT 4  
US-09-336-643A-20  
; Sequence 20, Application US/09336643A  
; Patent No. 6399761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward



; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; CURRENT FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 1082  
; TYPE: PRT  
; ORGANISM: H. sapiens  
US-09-336-643A-20

Alignment Scores:  
Pred. No.: 0 Length: 1082  
Score: 5649.50 Matches: 1076  
Percent Similarity: 99.35% Conservative: 0  
Best Local Similarity: 99.35% Mismatches: 6  
Query Match: 92.78% Indels: 1  
DB: 4 Gaps: 1

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-336-643A-20 (1-1082)

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QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
Db 40 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 59  
QY 181 ATGCAGCGGGCTGTGCTGCTCCCTTCCTTTATGGCCAGACACCATGAGCTGATCCTGTAC 240  
Db 60 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 79  
QY 241 CAACAGATCCGAAGGCCCTGGACGACCAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 80 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 99  
QY 301 CGGAAGAGCGGCTCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAATGAGAA 360  
Db 100 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 119  
QY 361 GGGAGGTGGCTCTCTTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 120 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 139  
QY 421 GGGCCCGACAGATGGAAGGAGCAGGTGGTGGCCCGCGCCGATATGGCCGGGCACGATCC 480  
Db 140 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 159  
QY 481 AAAGCTTCAATGCCAACCGGGCGGAGCGCGGCTCTACACCTGTCCGGGCAC 540  
Db 160 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 179  
QY 541 CTGCAGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600  
Db 180 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 199  
QY 601 AACTTGCCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTTCATCCTGTTGACTGT 660

Db 200 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 219  
QY 661 GGGGCACCTGAGAGCCACCTGGGATGGCTTCATCTCTGCTCGCCACACTCTATGTGGTGTG 720  
Db 220 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 239  
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGCGGAGCCAGTGCCTCCGCGGCCG 780  
Db 240 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 259  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGTCCCTTCATCTTACATTTGACATTTGCTGAATTC 840  
Db 260 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 279  
QY 841 CGTACCACATTCTGTCTCAAGTCGGGCCAGGTGTTTGTCCCAAAAGTCCATTTGCCTC 900  
Db 280 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 299  
QY 901 CACTACGTCCACACCTGGTTCTCTGCTGGATGTTCATCGCAGCGCTGCCCTTTGACCTGCTA 960  
Db 300 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 319  
QY 961 CATGCCCTTCAAGGTCAACGTGTACTTCGGGGCCCCATCTGCTGAAGACGGTGCCTGCTG 1020  
Db 320 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 339  
QY 1021 CGCCTGTGCGCCTGCTTCCGGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGTG 1080  
Db 340 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 359  
QY 1081 ACCTGTCTATGGCCGTGTTTCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTTTGTAC 1140  
Db 360 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 379  
QY 1141 ATTGGCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGTGCAG 1200  
Db 380 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 399  
QY 1201 GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGCGCGAGCCAGCTGGAGGG 1260  
Db 400 GluLeuAlaArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 419  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGGCTG 1320  
Db 420 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 439  
QY 1321 GAGCTGTGGCGGCCCTGCTGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC 1380  
Db 440 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 459  
QY 1381 AGCAGCTCACAGCGGTGGCTTCGGCAACGTGTCCGCCAACACGACACCGAGAAGATC 1440  
Db 460 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 479  
QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGTCACCGGTGGTGTGGGAACCTG 1500  
Db 480 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal 499  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCCGACCGCGGAC 1560  
Db 500 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 519  
QY 1561 CTGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 520 GlnArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 539  
QY 1621 TACTTCCAGGCCACTTGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGC 1680  
Db 540 TyrPheGlnAlaThrTrpAlaValAlaAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 559  
QY 1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATCGCCTGTGCACAGGAGGTCTCTGCAGCTG 1740  
Db 560 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 579

QY 1741 CCACTGTTTGGAGGGCCAGCCGGCTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCC 1800  
Db 580 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 599  
QY 1801 GCCTTCTGCACGCCGGGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1860  
Db 600 AlaPheCysThrProGlyGluPheLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 619  
QY 1861 TTTTGTCTGCTCTGGCTCCATGGAGTGTCTCAAGGTGGCACCGTGTCTGCCATCCTAGG 1920  
Db 620 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 639  
QY 1921 AAGGGCGACCTGATCGGCTGTGAGCTGCTCCCGGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 640 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValVallysAlaAsnAla 659  
QY 1981 GACGTGAAGGGCTGACGTACTGCTGCTGAGTGTCTGCAGTGTCTGCGCTGGCTGCACGAC 2040  
Db 660 AspVallysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 679  
QY 2041 AGCCTTGGCTGTACCCCGAGTTTGGCCCGCTTCAGTCGTGGCTCCGAGGGAGCTC 2100  
Db 680 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 699  
QY 2101 AGCTACAACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAAGTCCCTGAGCGGC 2160  
Db 700 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 719  
QY 2161 GACAATACCTTATGTCCAGCTGGAGGAGAGAGACAGATGGGGAGAGGGCCCCACG 2220  
Db 720 AspAsnThrLeuMetSerThrLeuGluGlyGluThrAspGlyGluGlnGlyProThr 739  
QY 2221 GTCTCCCCAGCCAGCTGATGAGCCCTCCAGCCCTGCTGTCTCCCTGGGTGCACCTCC 2280  
Db 740 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 759  
QY 2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACCTGCAACAGCACCCCGCTGCTTAGGT 2340  
Db 760 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 779  
QY 2341 GGCAGAGGGAGGCCAGCAGGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCTGCTGCTCC 2400  
Db 780 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 799  
QY 2401 CCACGGGCCCTAGAGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCATGCTG 2460  
Db 800 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTyrAsnValProProAspLeu 819  
QY 2461 AGCCCCAGGGTAGTAGTGGCATTTGAAGACGGCTGCGCTCGGACCAAGTCTCT 2520  
Db 820 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 839  
QY 2521 TTCCGGCTGGCCAGTCTGGCCCGGAATGTAGCAGAGCCCTCCCTGGACCAAGAGC 2580  
Db 840 PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 859  
QY 2581 GGCCTGCTCACTGTTCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2640  
Db 860 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 879  
QY 2641 CTTCCGAGGGCTGACAGAGTGTGACAGCAGGTGCTGCAGATGCGGGAAGGACTGCAG 2700  
Db 880 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 899  
QY 2701 TCACCTGCCAGGCTGTGAGCTGTCTGGCGCCCCACAGGAGGGTCCGTGCCCTCGG 2760  
Db 900 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 919  
QY 2761 GCATCGGAGAGGGCCGTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTG 2820  
Db 920 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 939

QY 2821 GACACTGGGGCATCTCTACTGCTGCAGCCCCCAGCTGGCTGTGTAGTGGGACT 2880  
Db 940 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 959  
QY 2881 TGGCCCCACCTCGTCCGGGSCCTCTCCCTCATGGCACCTGGCCCTGGGGTCCCCCA 2940  
Db 960 TrpProHisProArgProGlyProProProLeuMetAlaProArgProTrpGlyProPro 979  
QY 2941 GCGTCTCAGAGCTCCCTGGCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000  
Db 980 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 999  
QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCCAGCACCTCCCTCCCTCCT 3060  
Db 1000 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1019  
QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCAGGCTGAGGCTACCAGC 3120  
Db 1020 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1039  
QY 3121 ACTGGAGAGCCCCCAGGAGGTGAGGGGCTGGCCCTGGCCCTGGGACCCCCACAGCCTG 3180  
Db 1040 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1059  
QY 3181 GAGATGCTGCTTATTGGCTGCCATGGCTGTGGCAGTCCAGTCCAGTCCAGGAAGAAGC 3240  
Db 1060 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1079  
QY 3241 ACAGGGGTC 3249  
Db 1080 ThrGlyVal 1082

RESULT 5  
US-09-358-383C-16  
; Sequence 16, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rofy A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358,383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 1107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-358-383C-16

Alignment Scores:  
Pred. No.: 2,92e-157 Length: 1107  
Score: 2529.50 Matches: 559  
Percent Similarity: 60.24% Conservative: 150  
Best Local Similarity: 47.49% Mismatches: 267  
Query Match: 41.54% Indels: 201  
DB: 4 Gaps: 27

US-09-965-830-1\_copy\_6\_3257 (1-3252) x US-09-358-383C-16 (1-1107)

QY 1 ATCCCGCCCATGCGGGGCTCTCGCGCCTCAGAACACCTTCTGGACACCATCGGTACG 60  
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCACGCACAGTAACCTTCGTGTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40  
QY 121 CCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 180  
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60









		4	Gaps:	23
DB:				
US-09-965-830-1_COPY_6_3257 (1-3252) x US-09-600-776-6 (1-1017)				
QY	1	ATGCCGGCCATCGGGGCTCTCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG	60	
Db	1	MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20	
QY	61	CGCTTCGACGGCAGCACAGTAACCTTCGTGCTGGCAACGCCAGGTGGCGGCTCTTC	120	
Db	21	ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyThrArgGlyPhe	40	
QY	121	CCGCTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC	180	
Db	41	ProIleValTyrCysSerAspGlyPheCysGluLeuThrGlyTyrGlyArgThrGluVal	60	
QY	181	ATGCAGCGGGCTGTGCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	240	
Db	61	MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGluThrSerGluProAlaLeu	80	
QY	241	CAACAGATCCGCAAGCCCTCGACGACGACCAAGAGTTCAAGGCTGAGCTGATCCTGTAC	300	
Db	81	GlnArgLeuHisLysAlaLeuGluGlyHisGlnGluHisArgAlaGluIleCysPheTyr	100	
QY	301	CGGAGAGCGGGCTCCCGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	360	
Db	101	ArgLysAspGlySerAlaPheTyrCysLeuLeuAspMetMetProIleLysAsnGluMet	120	
QY	361	GGGAGGTGGCT	420	
Db	121	GlyGluValValLeuPheLeuPheSerPheLysAspIleThrGlnSerGlySerProGly	140	
QY	421	---GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGCGATATGCGCGGCACGA	477	
Db	141	LeuGlyProGln-----GlyArgGlyAspSerAsnHisGluAsn	154	
QY	478	TCCAAAGGC-----TTCAATGCCAACCGCGCGCGCGAGCCGGGCC	516	
Db	155	SerLeuGlyArgArgGlyAlaThrTyrLysPheArgSerAlaArgArgArgSerArgThr	174	
QY	517	GTGCTCTACACCTGTCGGGCACCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	576	
Db	175	ValLeuHisArgLeuThrGlyHisPheGlyArgGlyGlnGlyGlyMetLysAlaAsn	194	
QY	577	AAGGGGTGTTTGGGAGAAACCAACTTGCCTGAGTACAAAGTAGCCGCGCATCCGGAAG	636	
Db	195	AsnAsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGly	214	
QY	637	TGCGCCCTTCATCTCTGCTGCTGGGCACTGAGAGGACCTGGGATGGTTCATCTCTG	696	
Db	215	SerArgCysLeuLeuLeuHisTyrSerValSerLysAlaIleTyrAspGlyLeuIleLeu	234	
QY	697	CTCGCCACACTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	756	
Db	235	LeuAlaThrPheTyrValAlaValThrValProTyrAsnValCysPheSerGlyAspAsp	254	
QY	757	GAGCCAGTCCG	816	
Db	255	AspThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPhe	274	
QY	817	ATCCTTGACATGCTGTAATTTCCGTACCATTCATTCATTCATTCATTCATTCATTCATTC	876	
Db	275	IleLeuAspIleIleLeuAsnPheArgThrThrTyrValSerGlnSerGlyGlnValIle	294	
QY	877	TTTGCCCAAGTCCATTTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	936	
Db	295	SerAlaProArgSerIleGlyLeuHisTyrLeuAlaThrTyrPhePheIleAspLeuIle	314	
QY	937	GCAGCGCTGCCCTTTGACCTGCTACATGCTTCAAGGTCAACGCTGCTGCTGCTGCTGCTG	996	
Db	315	AlaAlaLeuProPheAspLeuLeuTyrIlePheAsnIleThrValThrSerLeuValHis	334	
QY	997	CTGCTGAAGACGGTGGCGCTGCTGCGCCTGCTGCGCCTGCTGCGCCTGCTGCGCCTGCTG	1056	

QY	2671	CAGGTGCTGCAGATCGGGAAGGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTG	2730	
Db	880	GluValSerGlnLeuGlyLysAspMetArgSerIleMetGlnLeuLeuGluAsnIleLeu	899	
QY	2731	CGGCCCCACAGGAGGGTCCGTCCCTCGGGCATCGGAGAGGGCGCTGCCAGCCAGC	2790	
Db	900	SerProGlnGlnProSerGlnPheCysSerLeuHisProThrSerIleCysProSerArg	919	
QY	2791	ACCTCCGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGCGATCCTCTACTGCTGCGAG	2850	
Db	920	GluSerPheGlnThrArg-----ValSerTyrSerAlaHisGlnProCysLeuHis	936	
QY	2851	CCCCAGCT-----GGCTCTGCTTGTAGTGGGACTTGGCCCCAC	2889	
Db	937	LeuGlnAlaAsnGlyAlaHisLeuTyrHisGlyAsnValThrSerAspIleTyr	954	
QY	2890	CCTCGTCGGGGCTCTCTCCCTCATGGCACCTGGCGCTGGGGTCCCCCAGCTCTCAG	2949	
Db	955	-----SerValAspProSerLeuValGlySerAsnProGlnArgThrGluAlaHisGlu	972	
QY	2950	AGCTCCCC-----TGGCCTCGAGCCACA	2973	
Db	973	GlnSerProValAspSerGluLeuHisHisSerProAsnLeuAlaTyrSerProSerHis	992	
QY	2959	-----TGGCCTCGAGCCACA	2973	
Db	993	CysGlnValIleGlnGluGlyHisLeuGlnPheLeuArgCysIleSerProHisSerAsp	1012	
QY	2974	GCTTCTGAGCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGAGACCTCTGCTCTGAG	3033	
Db	1013	ThrThrLeuThrProLeuGlnSerIleSerAlaThrLeuSerSerValCysSerSer	1032	
QY	3034	CCCAGCACCCCT-----GCCTCCCTCCTCTCTGAGGAAGGGCTAGGACT---	3081	
Db	1033	SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGlySerIleThrHis	1052	
QY	3082	GGGCCCCGAGAGCCTGTGAGCCAGGCTGAGGCTACCAGCACTGGAGAGCCCCCACCAGGG	3141	
Db	1053	GlyProValSerSerPheSerLeu-----GluAsnLeuProGly	1065	
QY	3142	TCAGGGGGCCTGGCCTTGGCCTGGGAC	3168	
Db	1066	Ser-----TrpAsp	1068	

RESULT 7  
US-09-600-776-6  
; Sequence 6, Application US/09600776  
; Patent No. 6326168  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/600,776  
; CURRENT FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-011434  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1017  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-600-776-6  
Alignment Scores:  
Pred. No.: 7.86e-153 Length: 1017  
Score: 2461.50 Matches: 538  
Percent Similarity: 59.19% Conservative: 119  
Best Local Similarity: 48.47% Mismatches: 245  
Query Match: 40.43% Indels: 208





QY 3005 -----CCCCTGCCTCAGGAGAC 3021  
Db 966 uThrGlyThrAlaLeuLeuAspLeuArgProSerIleLeuProProTyrProSerGluPr 986  
QY 3022 CTCTGCTCTGAGCCCGCAGCACCCCTGCCT 3049  
Db 986 oAspProLeuGlyProSerProValPro 995

RESULT 8  
US-09-343-494-9  
; Sequence 9, Application US/09343494  
; Patent No. 6413741  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: Wickenden, Alan  
; APPLICANT: ICAGEN, Incorporated  
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit  
; FILE REFERENCE: 018512-001320US  
; CURRENT APPLICATION NUMBER: US/09/343,494  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: US 60/091,469  
; EARLIER FILING DATE: 1998-07-01  
; EARLIER APPLICATION NUMBER: US 60/116,621  
; EARLIER FILING DATE: 1999-01-21  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 1284  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Drosophila Elk (dElk; Bag (ether a go-go)-like K+  
; OTHER INFORMATION: gene) protein  
US-09-343-494-9

Alignment Scores:  
Pred. No.: 3.44e-116 Length: 1284  
Score: 1901.00 Matches: 455  
Percent Similarity: 53.85% Conservative: 146  
Best Local Similarity: 40.77% Mismatches: 273  
Query Match: 31.22% Indels: 242  
DB: 4 Gaps: 31

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-343-494-9 (1-1284)

QY 1 ATGCCGGCCATCGGGGCTCTCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60  
Db 1 MetProAlaArgLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCACGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn 39  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGTTC 180  
Db 40 ProfileValTyrCysSerAspGlyPheValAspLeuThrGlyTyrSerArgAlaGlnIle 59  
QY 181 ATGACGGGGGTGTGCTGCT 240  
Db 60 MetGlnLysGlyCysSerCysHisPheLeuTyrGlyProAspThrLysGluGluHisLys 79  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCAACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 80 GlnGlnIleGluLysSerLeuSerAsnLysMetGluLeuLysLeuGluValIlePheTyr 99  
QY 301 CGGAAGAGCGGCTCCCGTTCTGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
Db 100 LysLysGluGlyAlaProPheTyrCysLeuPheAspIleValProIleLysAsnGluLys 119  
QY 361 GGGGAGGTGGTCT 411  
Db 120 ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGlu 139

QY 411 ----- 411  
Db 140 MetAsnValAsnGluGluCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGlyAla 159  
QY 412 -----AACCGAGGG 420  
Db 160 ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyGlyLeuProGlyLeuGly 179  
QY 421 GGCCCG-----GACAGATGGAAGGAGACAGGTGGTGGCGCGCGCATATGGCCGG 471  
Db 180 GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspValPro 199  
QY 472 GCACGATCCAAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCGGTGCTCTTACCACCTG 531  
Db 200 Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValLeuTyrGlnLeu 216  
QY 532 TCCGGGCACCTGCAGAACGACGCCCAAGGGC---AAGCACAAAGCTCAATAAGGGG----- 582  
Db 217 SerGlyHisTyrLysProGluLysGlyGlyValLysThrLysLeuLysLeuGlyAsnAsn 236  
QY 583 ---GTGTTGGGGAGAAACCAACTTCCTGAGTACAAAGTAGCCGCGCATCCGGAAGTCG 639  
Db 237 PheMetHisSerThrGluAlaProPheProGluTyrLysThrGlnSerIleLysLysSer 256  
QY 640 CCCTTCATCCTGTGCACTGTGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTC 699  
Db 257 ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleTyrAspTyrValIleLeuVal 276  
QY 700 GCCACACTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGAGCACAGCAGGGAG 759  
Db 277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg 296  
QY 760 CCCAGTCCCGCGCGCGCCAGCGCTGTGTGACCTGGCCGTGGAGTCTCTTCATC 819  
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Db 369 HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuLeuGlnLysIle 388  
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; Sequence 11, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358,383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 1284  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-358-383C-11  
Alignment Scores:  
Pred. No.: 3.44e-116 Length: 1284



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QY	181	ATGACGGGGCTGTGCT	240
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QY	241	CAACAGATCCGCAAGGCCCTGGACGACGACAAAGGATTCAAGGCTGAGCTGATCCTGTAC	300
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; Sequence 5, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-358-383C-5
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Db 276 PheArgThrThrTyrValSerLysSerGlyGlnValIlePheGluAlaArgSerIleCys 295  
QY 898 CTCCACTACGTACCACTGGTTCCTGCTGGATGTCATCGCAGCGCTGCCCTTGCCTG 957  
Db 296 IleHisTyrValThrThrTrpPheIleIleAspLeuIleAlaLeuProPheAspLeu 315  
QY 958 CTACATGCTTCAAGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGCGGTGCGCCTG 1017  
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QY 1018 CTGCGCTGTGCGCTGCTTCCGGGTGGACCGGTACTCGCAGTACAGCGCGTGGTG 1077  
Db 336 LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal 355  
QY 1078 CTGACACTGCTCATGGCCGTGTTCGCCCTGCTCGGCACTGGGTGCGCTGCTGTGTTT 1137  
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QY 1138 TACATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTG 1197  
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QY 1198 CAGGAGCTGGCCCGCAGTGGAGACTCCCTACTACCTGGTGGCGGAGGCCAGCTGGA 1257  
Db 396 HisGluLeuGlyLysArgLeuGluSerProTyrTyr----- 407  
QY 1258 GGGAAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGGCGCAACGGGACGGGG 1317  
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QY 1378 CTCAGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGGCAACACGACACCGAGAAG 1437  
Db 429 LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys 448  
QY 1438 ATCTTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCAAGCGGTGGTGTGGGAAC 1497  
Db 449 IlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaLeuValPheGlyAsn 468  
QY 1498 GTGACGGCCATCATCCAGCGCATGTACCGCCCGCTTCTGTACCAAGCCGCGCAGCGC 1557  
Db 469 valThrAlaIleIleGlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys 488

QY 1558 GACTGCGCGCACTACATCCGATCCACCGTATCCCAAGCCCCCTCAAGCAGCGCATGCTG 1617  
Db 489 AspLeuLysAspPheIleArgValHisHisLeuProGlnLeuLysGlnArgMetLeu 508  
QY 1618 GAGTACTTCCAGGCCACCTGGCGGTGAACAATGGCATGCACACACCGAGCTGCTG 1674  
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RESULT 11  
US-08-956-242-13  
; Sequence 13, Application US/08956242C  
; Patent No. 5986081  
; GENERAL INFORMATION:  
; APPLICANT: Ganetzy, Barry S.  
; APPLICANT: Titus, Steven A.  
; TITLE OF INVENTION: Polynucleotides Encoding Herg-3  
; FILE REFERENCE: 960296.94550  
; CURRENT APPLICATION NUMBER: US/08/956,242C  
; CURRENT FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 1159  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-08-956-242-13  
Alignment Scores:  
Pred. No.: 2,41e-93 Length: 1159  
Score: 1551.00 Matches: 424  
Percent Similarity: 44.86% Conservative: 143  
Best Local Similarity: 33.54% Mismatches: 337  
Query Match: 25.47% Indels: 360  
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QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 180  
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QY 181 ATGACGCGGGCTGTGCTGCTCTCTCTCTTATGGGCCAGACACCATGAGCTCGTCCGC 240  
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGAGTCAAGGCTGAGCTGATCCTGTAC 300  
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QY 361 GGGGAGGTGGCTCTCTCTCTA-----GTCTCTCACAGGACATC----- 399  
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QY 400 -----AGCGAAACCAAGAACCGAGGGGGCCCGACAGATGG----- 435  
Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159  
QY 435 ----- 435  
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 QY 490 AATGCCAAACCGCG----- 503  
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 QY 577 -----AAGGGGTGTTGGGGAG 594  
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2467 AGGGTACTAGATGGCATTTGAAGACGGCTGTGGCTCGGACCGCCCAAG----- 2514
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; Sequence 13, Application US/09351215
; Patent No. 6087488
; GENERAL INFORMATION:
; APPLICANT: Ganetzky, Barry S.
; APPLICANT: Titus, Steven A.
; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
; FILE REFERENCE: 960296.94550
; CURRENT APPLICATION NUMBER: US/09/351,215
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 08/956,242
; EARLIER FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1159
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-351-215-13

Alignment Scores:
Pred. No.: 2,41e-93 Length: 1159
Score: 1551.00 Matches: 424
Percent Similarity: 44.86% Conservative: 143
Best Local Similarity: 33.54% Mismatches: 337
Query Match: 25.47% Indels: 360
DB: 3 Gaps: 38

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QY 1741 CCACCTGTTGAGCGGCCAGCGCGCTGCCTGCGGGCACTGTCTCTGCGCCCTGCGGCC 1800  
Db 741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760  
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QY 1861 TTTGTCTGTCTGTGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTCGCCATCCTAGG 1920  
Db 781 PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly 800  
QY 1921 AAGGCGCACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820  
QY 1981 GACGTGAAGGGGTGAGTACTCGTCTCGTCTCGAGTGTCTGCAGCTGGCTGGCTGCACGAC 2040  
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QY 2041 AGCCTTGGCTGTACCCGAGTTTGGCCCGCGCTTCAGTCTGTGGCTCCGAGGGGAGCTC 2100  
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QY 2101 AGCTACAAACCTG-----GGTGTGGGGAGGCTCTGCAGAGGTGGAC 2142  
Db 859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu 878  
QY 2143 ACCAGCTCCCTGAGCGCGCACAATACCTTATGTCCACGCTGGAGGAGGAGACAGAT 2202



Db 879 GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp 898  
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Db 899 ThrGluGln----- 901  
QY 2263 TCCCTGGCTGCACCTCTCATCTCCTCAGCTGCCAAGCTGCTATCCCCACGTGCAACAGCA 2322  
Db 902 ---ProGlyGluValSerAla-----LeuGlyProGlyArgAlaGly 914  
QY 2323 CCCCCGCTCGTCTAGTGGCAGAGGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCTGAG 2382  
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QY 2383 GCTGGCCCTCTGCTCCCCA-----CGGGCCCTAGAGGGG 2418  
Db 933 SerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerPro 952  
QY 2419 CTACGGCTG-----CCCCCATGCCATGGAATGTGCCCCCATGATCTGAGCCCC 2466  
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QY 2515 -----TTCTCTTTC-----CGCGTGGGCCAGTCT 2538  
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QY 2596 -----CCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTG 2634  
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QY 2692 GGACTGCAGTCACTTCGCGCAGGCTGTGCAGCTTGTCTGTGGCGCCCCACAGGAGGTCCG 2751  
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QY 2932 GGTCCCCCAGCGTCTC-----AGAGCTCCCCCTGGCTCGAGCCACAGCTTCTGG 2982  
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QY 2983 ACCTCCACCTCAGACTCAGAGCCCGCTCCTCAGGAGACCTCTGCTCTGAGCCCCAGACC 3042  
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RESULT 13

US-09-226-012-2

; Sequence 2, Application US/09226012

; Patent No. 6207383  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
; TITLE OF INVENTION: SYNDROME GENE  
; FILE REFERENCE: 2323-136  
; CURRENT APPLICATION NUMBER: US/09/226,012  
; CURRENT FILING DATE: 1999-01-06  
; EARLIER APPLICATION NUMBER: 09/122,847  
; EARLIER FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1159  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-226-012-2  
Alignment Scores: 2.41e-93 Length: 1159  
Pred. No.: 1551.00 Matches: 424  
Score: 44.86% Conservative: 143  
Percent Similarity: 33.54% Mismatches: 337  
Best Local Similarity: 25.47% Indels: 360  
Query Match: 3 Gaps: 38  
DB:  
US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-226-012-2 (1-1159)  
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QY 61 CGCTTCGACGCGCACAGTAACCTCTGCTGGCAACGCCAGTGGCGGGCTCTTC 120  
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QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGGCTTCTCCGGGCTGAGGTC 180  
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QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGAGTTCAAGCTGAGCTGATCTGTAC 300  
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QY 301 CGGAAGAGCGGGCTCCGCTTCTGTGTCTCTGATGTATACCCATAAAGATGAGAAA 360  
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Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139  
QY 400 -----AGCGAAACCAAGAACCGAGGGGGCCCGACAGATGG----- 435  
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QY 435 ----- 435  
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QY 504 -----GCGGAGCCGGCGCTGCTCTA----- 524  
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QY 525 --CCACCTGTCCGGGCACCTGCAGAAGCAGCCCAAGGCGAAG---CACAAGCTCAAT--- 576  
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QY 802 GTGGAGGTCTCTTCATCCTTGACATGTGTGAATTTCCGTACCACATTCGTGTCCAAG 861  
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Db 499 LeuIleAspMetValAlaAlaIlePropheAspLeuLeu----- 511  
QY 982 TACTTCGGGGCC-----CATCTGTGAAGACGGTGCCTGCTGCTGCGC 1023  
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QY 1024 CTGCTGCGCCTGCTTCGCGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTCTGACA 1083  
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QY 1624 TTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCACCGAGCTGTCAGAGCCTC 1683  
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Db 741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760  
QY 1801 GCCTTCTGCACCGCGCGGAGTACCTCATCCACCAAGCGGATGCCCTGCAGGCCCTCTAC 1860  
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QY 1861 TTTGTCTGTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTCGCCATCCTAGGG 1920  
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QY 1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGCGGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820  
QY 1981 GACGTGAAGGGGTGACGTACTGCTGCTCCTGCTGAGTGTCTGAGCTGGCTGGCCTGCACGAC 2040  
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QY 2041 AGCCTTGGCTGTACCCCGAGTTTGCCTCCCGCTTCAGTGTGGCTCCGAGGGGAGCTC 2100  
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QY 2143 ACCAGTCCCTGAGCGCGCACAAATACCTTATGTCCACGCTGGAGGAGAAGACAGAT 2202  
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QY 595 AAACCAAAC----- 603  
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QY 2515 -----TTCTCTTTC-----CGCGTGGGCCAGTCT 2538  
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Db 1074 -----ValProProAlaTyrSerAla-- 1080  
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QY 2872 AGTGGGACTTGGCCCCACCCTCGTCCGGGGCTCTCTCCCTCATGCGACCCCTGGCCCTGG 2931  
Db 1099 oLeu-----ProThrLeuThrLeuAspSerLeuSerGln----- 1110  
QY 2932 GGTCCCCCAGCGTCTC-----AGAGCTCCCGCTGGCCTCGAGCCACAGCTTTCTGG 2982  
Db 1111 -ValSerGlnPheMetAlaCysGluGluLeuProProGly---AlaProGluLeuProGl 1129  
QY 2983 ACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCAGCACCC 3042  
Db 1129 nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149  
QY 3043 CCTG 3046  
Db 1149 oLeu 1150

RESULT 15  
US-09-358-383C-10  
; Sequence 10, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358,383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855

; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1159  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-358-383C-10  
Alignment Scores: 2.41e-93 Length: 1159  
Pred. No.: 1551.00 Matches: 424  
Score: 44.86% Conservative: 143  
Percent Similarity: 33.54% Mismatches: 337  
Best Local Similarity: 25.47% Indels: 360  
Query Match: 4 Gaps: 38  
DB: 4  
US-09-965-830-1\_COPY\_6\_3257 (1-3252) x US-09-358-383C-10 (1-1159)  
QY 1 ATGCGGCCCATGCGGGCCCTCTCTGGCGCCTCAGAACACCTTCTCTGGACACCATCGCTACG 60  
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QY 61 CGTTTCAGCGGCACGCACAGTAATCTGCTGGGCAACGCCCGAGTGGCGGCTCTTC 120  
Db 21 LysPheGluGlyGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys--- 39  
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180  
Db 40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59  
QY 181 ATGACAGCGGGCTGTGCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Db 60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79  
QY 241 CAACAGATCCGCAAGCCCTCGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99  
QY 301 CGGAAGAGCGGGCTCCCGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp 119  
QY 361 GGGAGGTGGCT 399  
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139  
QY 400 -----AGCGAAACCAAGAACCGAGGGGCGCCCGACAGATGG----- 435  
Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerThrLeuAlaProGlyArg 159  
QY 435 ----- 435  
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179  
QY 436 ---AAGGAGACAGGTGGTGGCGCGCGCGATATGGCCGGGC---ACGATCCAAAGGCTTC 489  
Db 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValValAspValA 199  
QY 490 AATGCCAACCGGCG----- 503  
Db 199 spLeuThrProAlaAlaProSerSerGluSerLeuLeuAspGluValThrAlaMetA 219  
QY 504 -----GCGAGCGCGCGCGCTCTCTA----- 524  
Db 219 spAsnHisValAlaGlyLeuGlyProAlaGluGluArgAlaLeuValGlyProGlyS 239  
QY 525 --CCACCTGTCCGGGCACTGCAGAGCAGCCCAAGGCAAG---CACAAGCTCAAT--- 576  
Db 239 erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258  
QY 576 ----- 576

Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278  
QY 577 -----  
Db 279 ValArgArgAlaSerSerAlaAspAlaMetArgAlaGlyValLeuProPro 298  
QY 595 AAACCAAC----- 603  
Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318  
QY 603 ----- 603  
Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338  
QY 603 ----- 603  
Db 339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358  
QY 603 ----- 603  
Db 359 IleAlaProLysIleLysGluAlaArgThrHisAsnValThrGluLysValThrGlnValLeu 378  
QY 604 -----TTGCCTGAGTACAAAGTAGCCGCGCATCCGGAAGTCGCCCTTC 645  
Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp 398  
QY 646 ATCCTGTTGCACACTGTGGGGACTGAGAGCCACCTGGATGGCTTCATCCTGCTCGCCACA 705  
Db 399 ThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuVal 418  
QY 706 CTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTG-----AGCACAGCACGG 756  
Db 419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu 438  
QY 757 GAGCCACAGTGCC-----GCCCGCGCGCGCCGCGCTGTGTGACCTGTGACCTGGCC 801  
Db 439 GlyProProAlaThrGluCysGlyTyrAlaCysGlnProLeuAlaValAspLeuIle 458  
QY 802 GTGAGAGTCCCTTCATCCTTGACATTGTGCTGAATTTCCGTACCAATTCGTGTCTCCAAG 861  
Db 459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsnAla 478  
QY 862 TCGGGCCAGGTGGTGTTCGCCCAAAGTCCATTGCTCCCTCCACTACGTACACACCTGGTTC 921  
Db 479 AsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrpPhe 498  
QY 922 CTGCTGGATGTCAATCGCAGCGCTGCCCTTTGACCTGTACATGCTTCAAGTCAACGTG 981  
Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511  
QY 982 TACTTCGGGGCC-----CATCTGTGAAGACGGTGGCGCTGTGCGC 1023  
Db 512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLysThrAlaArgLeuLeuArg 531  
QY 1024 CTGCTGCGCTGCTTCCGCGGCTGGACCGTACTCGCAGTACAGCGCGCTGGTGCTGACA 1083  
Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551  
QY 1084 CTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCGCTGCTGCTGCTTTACATT 1143  
Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIle 571  
QY 1144 GGCCAGCGGGAGATCGAGAGCAGCGGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAGGAG 1203  
Db 572 GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTrpLeuHisAsn 588  
QY 1204 CTGGCCCGCGACTGGAGACTCCCTACTACTGCTGGTGGCGGAGGCCAGCTGGAGGGAAC 1263  
Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598  
QY 1264 AGTCCGGCCAGAGTGACAACACTGCAGCAGCAGCAGCGAGGCCAACGGGCGGTGGAG 1323  
Db 599 SerSerGly----- 601

QY 1324 CTGCTGGGGCGCCGCTCGCTGCGCAGCGCTACATCACCTCCCTCTACTTCGCACTCAGC 1383  
Db 602 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 620  
QY 1384 AGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGGACACCGAGAAGATCTTC 1443  
Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640  
QY 1444 TCCATCTGCACCATGCTCATCGCGCGCCTGATGCACCGGTGGTGTGGAAACGTGACG 1503  
Db 641 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 660  
QY 1504 GCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCACAGCGCGCAGCCGACCTG 1563  
Db 661 AlaIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680  
QY 1564 CGCACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTAC 1623  
Db 681 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGluTyr 700  
QY 1624 TTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCAACCGAGCTGTCGAGAGCCTC 1683  
Db 701 PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720  
QY 1684 CCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGAGGTCTCTGCAG---CTG 1740  
Db 721 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys 740  
QY 1741 CCACTGTTTGAGGGCGCAGCCGCGCTGCCCTGCGGCACTGTCTCTGGCCCTGCGGCCC 1800  
Db 741 LysProPheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760  
QY 1801 GCCTTCTGCACGCGCGCGAGTACCTCATCCACCAAGCGCATGCCCTGCAGGCCCTCTAC 1860  
Db 761 ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr 780  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTCGCCATCTAGGG 1920  
Db 781 PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly 800  
QY 1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGCCCAATGCC 1980  
Db 801 LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820  
QY 1981 GACGTGAAGGGCTGACGTACTGCGTCTCTGCAAGTGTCTGAGCTGGCTGGCTGCACGAC 2040  
Db 821 AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu 840  
QY 2041 AGCCTTGGCGTGTACCCCGAGTTTGCCTGCGCGCTTCAGTCTGCGCTCCGAGGGAGCTC 2100  
Db 841 ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle 858  
QY 2101 AGCTACACCTG-----GGTGTGGGGAGGCTCTGCAGAGGTGGAC 2142  
Db 859 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu 878  
QY 2143 ACCAGCTCCTGAGCGCGCACATACCTTATGTCCACGCTGGAGGAGAGGAGACAGAT 2202  
Db 879 GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgThrAspLysAsp 898  
QY 2203 GGGAGACAGGGCCCCACGGTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTG 2262  
Db 899 ThrGluGln----- 901  
QY 2263 TCCCTGGCTGCACCTCTCATCTCTCAGTGCCTGCAAGTGTCTATCCCCACGTGCAACACA 2322  
Db 902 ---ProGlyGluValSerAla-----LeuGlyProGlyArgAlaGly 914  
QY 2323 CCCCAGGCTCGTCTAGGTGGCAGAGGGAGGCCAGGCGAGGGCTTTGAAGGCTGAG 2382  
Db 915 AlaGlyPro-----SerSerArgGlyArgProGlyGlyProTrpGlyGluSerProSer 932



QY 2383 GCTGGCCCTCTGCTCCCCA-----CGGGCCCTAGAGGGG 2418  
Db SerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerPro 952  
QY 2419 CTACGGCTG-----CCCCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCC 2466  
Db LeuArgLeuValProPheSerSerProArgProGlyGluProProGlyGlyGluPro 972  
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QY 2515 -----TTCTCTTTC-----CGCGTGGGCCAGTCT 2538  
Db SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyrGlnGlu 1011  
QY 2539 GGCCCGGAATGACAGCAGCCCCCTCCCTGGACAGAGAGCGGCTGCTCACTGTT--- 2595  
Db LeuProArgCys-----ProAlaProThrProSerLeuLeuAsnIlePro 1026  
QY 2596 -----CCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTG 2634  
Db LeuSerSerProGlyArgArgProArgGlyAspValGluSerArg-----Leu 1042  
QY 2635 GACAAGCTTCGGCAGCGGTGACAGAGCTGTACAGCAGGTG---CTGCAGATCGGGAA 2691  
Db AspAlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThr 1062  
QY 2692 GGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTGGCGCCCCACAGGGAGGTCGG 2751  
Db ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu----- 1073  
QY 2752 TGCCCTCGGGCATCGGAGAGGGCGCGTGCCAGCCAGCACCCTCCGGGCTTCTGCAGCCT 2811  
Db ValProProAlaTyrSerAla-- 1080  
QY 2812 CTGTGTGTGACACTGGGCATCCTCTACTGCTGAGCCCCCAGCTGGCTCTGTCTTG 2871  
Db ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr 1099  
QY 2872 AGTGGGACTTGGCCCCCACCCTCGTCCGGGGCCCTCCTCCCTCATGGCACCCCTGGCCCTGG 2931  
Db oLeu-----ProThrLeuThrLeuAspSerLeuSerGln----- 1110  
QY 2932 GGTCCCCCAGCGTCTC-----AGAGCTCCCCCTGGCCTCGAGCCACAGCTTTCTGG 2982  
Db ValSerGlnPheMetAlaCysGluGluLeuProProGly--AlaProGluLeuProGl 1129  
QY 2983 ACCTCCACCTCAGACTCAGAGCCCCCTGCTCAGGAGACCTCTGCTGTGAGCCCCAGCACC 3042  
Db nGluGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149  
QY 3043 CCTG 3046  
Db oLeu 1150

Search completed: September 1, 2004, 16:07:05  
Job time : 188 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2004, 15:01:21 ; Search time 315.5 Seconds  
(without alignments)  
5824.688 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257  
Perfect score: 6089  
Sequence: 1 atgcgcgcatgcggggcct.....aagaaggcacaggggtctga 3252

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US09965830/runat\_01092004\_160109\_4789/app\_query.fasta\_1.3399  
-DB=A\_Geneseq\_29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09965830 @CGN 1 1 480 @runat\_01092004\_160109\_4789 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5704	93.7	1083	2	AAY22426 Human bra
2	5704	93.7	1083	7	ADC47040 BECl pota
3	5704	93.7	1083	7	ADE55604 Human Pro
4	5698	93.6	1083	3	AAY44778 Human Elk
5	5697	93.6	1083	3	AAY44779 Human Elk
6	5696	93.5	1083	3	AAY44780 Human Elk
7	5695	93.5	1083	3	AAY44781 Human Elk
8	5695	93.5	1083	3	AAY84835 Herg4, a
9	5688	93.4	1080	3	AAY77738 Human ESK
10	5675	93.2	1083	3	AAY44904 Monkey po

11	5675	93.2	1083	6	ABU61670	Abu61670 Monkey ER
12	5675	93.2	1083	7	ADB66795	Adb66795 Monkey ER
13	5649.5	92.8	1082	2	AAY34128	Aay34128 Human pot
14	5428	89.1	1087	7	ADE55602	Ade55602 Rat Prote
15	2529.5	41.5	1107	3	AAY44907	Aay44907 Human pot
16	2529.5	41.5	1107	6	ABU61677	Abu61677 Human ful
17	2529.5	41.5	1107	7	ADB66804	Adb66804 Human ERG
18	2515	41.3	1102	3	AAY83028	Aay83028 Rat Elk1
19	2515	41.3	1102	6	ABU61692	Abu61692 Rat Relk1
20	2515	41.3	1102	7	ADB66823	Adb66823 Potassium
21	2461.5	40.4	1017	2	AAY22427	Aay22427 Human bra
22	2347	38.5	457	3	AAY77739	Aay77739 Human ESK
23	1901	31.2	1284	6	ABU61674	Abu61674 Drosophil
24	1901	31.2	1284	7	ADB66801	Adb66801 Drosophil
25	1901	31.2	1311	4	ABB61234	Abb61234 Drosophil
26	1835.5	30.1	542	6	ABU61671	Abu61671 Human ERG
27	1835.5	30.1	542	7	ADB66797	Adb66797 Partial h
28	1832.5	30.1	542	3	AAY44905	Aay44905 Human pot
29	1551	25.5	1159	2	AAY32020	Aay32020 Human cat
30	1551	25.5	1159	3	AAY85405	Aay85405 Long Qt s
31	1551	25.5	1159	4	AAB70939	Aab70939 Human eag
32	1551	25.5	1159	4	AAM51812	Aam51812 Human pot
33	1551	25.5	1159	5	AAU99167	Aau99167 Human eth
34	1551	25.5	1159	6	ABP71697	Abp71697 Human HER
35	1551	25.5	1159	6	ABU61673	Abu61673 Human ERG
36	1551	25.5	1159	6	ABP71255	Abp71255 Human HER
37	1551	25.5	1159	7	ADB66800	Adb66800 Human ERG
38	1551	25.5	1159	7	ADD02769	Add02769 Human HER
39	1550	25.5	1159	3	AAY85406	Aay85406 Long Qt s
40	1537.5	25.3	1163	7	ADD45069	Add45069 Rat Prote
41	1533.5	25.2	1163	3	AAY83031	Aay83031 Rat Ergl
42	1509.5	24.8	994	7	ADB68018	Adb68018 Human Eag
43	1508.5	24.8	994	5	ABG31253	Abg31253 Human erg
44	1487	24.4	290	6	ABU61672	Abu61672 Human ERG
45	1487	24.4	290	7	ADB66799	Adb66799 Partial h

ALIGNMENTS

RESULT 1

AAY22426

ID AAY22426 standard; protein; 1083 AA.

XX

AC AAY22426;

XX

DT 28-SEP-1999 (first entry)

XX

DE Human brain specific potassium channel protein sequence.

XX

KW Brain specific potassium channel; human; central nervous system disorder;  
KW dementia; cerebral ischaemic sclerosis; therapy.

XX

OS Homo sapiens.

XX

PN WO9937677-A1.

XX

PD 29-JUL-1999.

XX

PF 20-JAN-1999; 99WO-JP000190.

XX

PR 23-JAN-1998; 98JP-00011434.

PR

PR 04-DEC-1998; 98JP-00346198.

XX

PA (YAMA ) YAMANOUCHI PHARM CO LTD.

XX

PI Miyake A, Mochizuki S, Yokoi H;

XX

DR WPI; 1999-458683/38.

DR

DR N-PSDB; AAX84910.

XX

PT Potassium channel protein expressed specifically in brain tissue and

PT method for its production.

XX

PS Claim 1; Page 33-39; 63pp; English.

XX This sequence is the potassium channel protein of the invention, that is expressed specifically in brain tissue. The protein is used to treat and investigate disorders of the central nervous system such as dementia and cerebral ischaemic sclerosis

XX

SQ Sequence 1083 AA;

Alignment Scores:

Pred. No.:	0	Length:	1083
Score:	5704.00	Matches:	1083
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	93.68%	Indels:	0
DB:	2	Gaps:	0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x AAY22426 (1-1083)

QY	1	ATGCCGGCCATCGGGCCCTCCTGGCGCTCAGAACACCTTCCTGGACACCATCGCTACG	60
Db	1	MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CGCTTCGACGGCAGCACAGTAACTTCGTCTGGCAACGCCAGGTGGCGGCTCTTC	120
Db	21	ArgPheaspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe	40
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCGTGACCTCACGGGCTTCCTCCGGGCTGAGTC	180
Db	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal	60
QY	181	ATGCAGCGGGGTGTCCTGCTCCTTCCTTTATGGCCAGACACCAAGTGCCTCGCCG	240
Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg	80
QY	241	CAACAGATCCGCAAGGCCCTGGACGAGCAAGAGATTCAAGGCTGAGTGCCTGTAC	300
Db	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr	100
QY	301	CGGAAGAGCGGGTCCCGTTCTGGTGTCTCTCGATGTGATACCCATAAAGAATGAGAA	360
Db	101	ArgLysSerGlyLeuProPheTyrCysLeuLeuAspValIleProIleLysAsnGluLys	120
QY	361	GGGAGGTGGCTCTCTTCCTAGTCTCTCAAGGACATCAGCGAAACCAAGACCGAGGG	420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGGATATGGCGGCGACGATCC	480
Db	141	GlyProAspArgTyrLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer	160
QY	481	AAAGGTTCAATGCCAACCGGCGGAGCGCGCGCTCTACACCTGTCCGGGCAC	540
Db	161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
QY	541	CTGCAGAAGCAGCCCAAGGGCAAGCACAGTCAATAAGGGGTGTTTGGGAGAAACCA	600
Db	181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro	200
QY	601	AACTTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTGCACTGT	660
Db	201	AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys	220
QY	661	GGGGCACTGAGAGCCACTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC	720
Db	221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240
QY	721	ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGGAGCCCAAGTCCCGCCCGCGGCCCG	780
Db	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260
QY	781	CCCAGCGTCTGTGACCTGGCGGTGAGGTCTCTTCATCCTTGACATTGTGCTGAATTC	840

Db	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280
QY	841	CGTACCACATTCTGTCCAAAGTCGGGCCAGGTGGTGTTCGCCCAAGTCCATTGCTC	900
Db	281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300
QY	901	CATTACGTCAACCACTGGTTCTGTCTGGATGTTCATCGCAGCGTGCCTTTGACCTGCTA	960
Db	301	HisTyrValThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	320
QY	961	CATGCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGTGAAGACGGTGGCTGCTG	1020
Db	321	HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu	340
QY	1021	CGCTGTGCTGCGCTGCTTCGCGGCTGGACCGGTACTCGCAGTACAGCCGCTGGTGTG	1080
Db	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValLeu	360
QY	1081	ACACTGCTCATGGCCGTGTTCCGCTCTGCTCGGCACCTGGGTGCTGCTGCTTTTAC	1140
Db	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380
QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCCGTGAGATTGGCTGGCTG	1200
Db	381	IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln	400
QY	1201	GAGTGGCCCGGACTGGAGACTCCCTACTACTGTTGGGCGGAGCCAGCTGGAGGG	1260
Db	401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly	420
QY	1261	AACAGTCCGGCCAGAGTGACAACCTGCAGCAGCAGCAGGAGGCCAACGGGACGGGCTG	1320
Db	421	AsnSerSerGlyGlnSerAspAsnAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu	440
QY	1321	GAGTGTGGCGGCCGCTCGCTCGCTCGCAGCGCTACATCACCTCCCTCTACTTCGCACTC	1380
Db	441	GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu	460
QY	1381	AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGACACCGAGAAATC	1440
Db	461	SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle	480
QY	1441	TTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGTTGGGAAACGTG	1500
Db	481	PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal	500
QY	1501	ACGGCCATATCCAGCGCATGTACGGCCCGCTTCTGTACACAGCCCGCAGCGCGAC	1560
Db	501	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Db	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540
QY	1621	TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGCCATCGACACCCAGCTGCTG	1680
Db	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560
QY	1681	CTCCCTGACGAGTTCGCGCAGACATCGCCCATGCAACATGGCATCGACACCCAGCTG	1740
Db	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu	580
QY	1741	CCACTGTTTGAGCGCCAGCCGCGCTGCTCGGGCACTGTCTCTGCGCCCTCGGCC	1800
Db	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GCCTTCTGACGCGCGGAGTACCTCATCCCAAGGCGATGCCCTGCAGGCCCTCTAC	1860
Db	601	AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTGCCCATCCTAGG	1920
Db	621	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640



QY 1921 AAGGGGACCTGATCGGCTGTGAGCTGGCCCCGGGAGCAGGTGTAAGGCCAATGCC 1980  
Db |||||  
641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGGTGACGTACTGCTCCTGCGTGTGAGTGTCTGCAGTGTGCTGGCTGGCTGCACGAC 2040  
Db |||||  
661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680  
QY 2041 AGCCTTGCCTGTATACCCCGAGTTTGCCCCCGCTTCAGTCTGGCTCCGAGGGGAGTCTC 2100  
Db |||||  
681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700  
QY 2101 AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACAGCTCCCTGAGCGGC 2160  
Db |||||  
701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACAATACCTTATGTCCACGCTGGAGGAGAAGGACAGATGGGGAGCAGGCCCCACG 2220  
Db |||||  
721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTCTCCCTGGCTGCACCTCC 2280  
Db |||||  
741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760  
QY 2281 TCATCCTCAGCTGCCAAGCTGTATCCCCACGTCGAACAGCACCCCCGGCCTCGTCTAGGT 2340  
Db |||||  
761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780  
QY 2341 GGCAGAGGGAGGCCAGGCAGGGCAGGGGGCTTGAAGGCTGAGGCTGGCCCTCTGCTCCC 2400  
Db |||||  
781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800  
QY 2401 CCACGGGCCCTAGAGGGGCTACGGTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2460  
Db |||||  
801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu 820  
QY 2461 AGCCCCAGGTAGTAGATGGCATTTGAAGCGCTGTGGCTCGGACCGCCCAAGTTCTCT 2520  
Db |||||  
821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840  
QY 2521 TTCCGGTGGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCCCTCCCTGGACCAGAGC 2580  
Db |||||  
841 PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860  
QY 2581 GGCTTGCTCACTGTTCCCCATGGGCCAGCGCTGTGGCTCGGACCGCCCTCTGTGTTCT 2640  
Db |||||  
861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880  
QY 2641 CTTCCGCGAGCGGTGACAGAGCTGTACAGCAGGTGTGAGATCGGGGAAGACTGCAG 2700  
Db |||||  
881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900  
QY 2701 TCATTTCGCCAGGCTGTGCAGCTGTCTGGCGCCCCACAGGAGGGTCCGTGCCCTCGG 2760  
Db |||||  
901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920  
QY 2761 GCATCGGAGAGGGCCGTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
Db |||||  
921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940  
QY 2821 GACACTGGGGCATCCTCCTACTGCTGCAGCCCCCAGCTGGCTGTCTGTGAGTGGACT 2880  
Db |||||  
941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960  
QY 2881 TGGCCCCACCTCGTCCGGGGCCTCTCCCTCATGGCACCTGGCCCTGGGGTCCCCCA 2940  
Db |||||  
961 TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980  
QY 2941 GCGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000  
Db |||||  
981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000

QY 3001 GAGCCCCCTGCCTCAGGAGACCTTGTCTGTAGCCCCAGCACCCCTGCCTCCCTCCTCCT 3060  
Db |||||  
1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020  
QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC 3120  
Db |||||  
1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040  
QY 3121 ACTGGAGAGCCCCCACCAGGTCAGGGGCGCTTGGCCTTGGACCCCGGACCCCTG 3180  
Db |||||  
1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060  
QY 3181 GAGATGGTGTATTGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGC 3240  
Db |||||  
1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080  
QY 3241 ACAGGGGTC 3249  
Db |||||  
1081 ThrGlyVal 1083  
RESULT 2  
ADC47040  
ID ADC47040 standard; protein; 1083 AA.  
XX  
AC ADC47040;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE BEC1 potassium channel inhibitor #SEQ ID 2.  
XX  
KW BEC1 potassium channel inhibitor; nootropic; neuroprotective;  
KW brain-specific eag-like channel 1; dementia; learning disability;  
XX  
OS Homo sapiens.  
XX  
PN WO2003066099-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 03-FEB-2003; 2003WO-JP001065.  
XX  
PR 05-FEB-2002; 2002JP-00028844.  
XX  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
XX  
PI Kubota H, Suzuki T, Miura M, Nakai E, Yahiro K, Miyake A;  
PI Mochizuki S, Nakatou K;  
XX  
DR WPI; 2003-697418/66.  
DR N-PSDB; ADC47039.  
XX  
PT Antidementia agents comprise new and known brain-specific eag-like  
PT channel 1 (BEC1) potassium channel inhibitors.  
XX  
PS Claim 3; Page 83-89; 95pp; Japanese.  
XX  
CC The invention relates to an antidementia agent that comprises a brain-  
CC specific eag-like channel 1 (BEC1) potassium channel inhibitor. Agents of  
CC the invention are used as BEC1 potassium channel inhibitors for treating  
CC and preventing dementia and learning disabilities. The current sequence  
CC represents the BEC1 potassium channel inhibitor amino acid sequence.  
XX  
SQ Sequence 1083 AA;  
Alignment Scores:  
Pred. No.: 0 Length: 1083  
Score: 5704.00 Matches: 1083  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.68% Indels: 0  
DB: 7 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x ADC47040 (1-1083)

QY 1 ATGCCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGGTACG 60  
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGCTTCGACGGCAGCCACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40

QY 121 CCCGTGGTCTACTGCTCTGATGGCTCTGTGACCTCACGGGCTTCCTCCGGGCTGAGGTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60

QY 181 ATGCAGCGGGCTGTGCCTGCTCCTTCCTTATGGCCAGACACAGTGAGCTCGTCCGC 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80

QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGTGAGCTGATCCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100

QY 301 CGGAAGAGCGGGTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360  
Db 101 ArgLysSerGlyLeuProPheThrCysLeuLeuAspValIleProIleLysAsnGluLys 120

QY 361 GGGGAGGTGGCTCTCTCCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140

QY 421 GGCCCCGACAGATGAAGGAGACAGGTGGTGGCGCGCCGATATGGCGGCGACGATCC 480  
Db 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 160

QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCGGGCGGTGCTCTACCACTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180

QY 541 CTGCAGAAGCAGCCCAAGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200

QY 601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTGCCTTCATCCTGTTGCACTGT 660  
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220

QY 661 GGGGCACTGAGAGCCACCTGGATGGCTTCATCCTGCTCGCACACACTCTATGTGGCTGTC 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240

QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCAGTCCCGCCCGCGGCCCG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260

QY 781 CCCAGCTCTGTGACCTGGCCGTGAGGTCTCTTCATCCTTCACATTGTGCTGAATTTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280

QY 841 CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTGTTGCCCAAGTCCATTGGCCTC 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300

QY 901 CACTACGTCACACCTGGTTCCTGCTGGATGTTCATCGCAGCGTGCCTTTGACCTGCTA 960  
Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320

QY 961 CATGCCCTTCAAGTCAACGTGTACTTCGGGGCCCCATCTGCTGAAGACGGTGCCTGCTG 1020  
Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340

QY 1021 CGCCTGCTGGCCTGCTTCCGGCGGTGACCGGTACTCGCAGTACAGCGCGGTGGTGTG 1080  
Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360

QY 1081 AACTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTTTAC 1140  
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380

QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGGCTGCAG 1200  
Db 381 IleGlyGlnArgGluIleGluSerSerGluLeuProGluIleGlyTrpLeuGln 400

QY 1201 GAGCTGGCCCCGACTGGAGACTCCCTACTACTCCTGTGGCCGGAGCCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgLeuGluThrProTyrTyrLeuValGlyArgProAlaGlyGly 420

QY 1261 AACAGTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCAACCGGACGGGCTG 1320  
Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440

QY 1321 GAGCTGCTGGCGGCCCTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460

QY 1381 AGCAGCTCACAGCGTGGCTTCGGCAACGTGTCCGCCAACACCGGACCCGAGAAGATC 1440  
Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480

QY 1441 TTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACCGGTGGTGTGGAAACGTG 1500  
Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500

QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCACAGCCCGCAGCGGAC 1560  
Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520

QY 1561 CTGCGGCACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540

QY 1621 TACTTCCAGGCCCTGGCGGTGAACAATGGCATCGACACCCAGCTGCTGCAGAGC 1680  
Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560

QY 1681 CTCCCTGACGAGTGGCGCAGACATCGCCCATGCACTGCACAGGAGGTCTTCGACGTG 1740  
Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580

QY 1741 CCACCTGTTGAGCGGCCAGCGCGGTGCCTGCGGGCACTGTCTCTGCGCCCTGCGGCC 1800  
Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600

QY 1801 GCCTTCTGCACCGCGCGAGTACCTCATCCACCAAGCGCATGCCCTGCAGGCCCTCTAC 1860  
Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620

QY 1861 TTTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTGCCATCCTAGGG 1920  
Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640

QY 1921 AAGGCGACCTGATCGGCTGTGAGCTGCCCGGCGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660

QY 1981 GACGTGAAGGGGCTGACGTACTGCTCCTGCAGTGTCTGCAGCTGGCTGGCTGCACGAC 2040  
Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680

QY 2041 AGCCTTGGCTGTACCCCGAGTTTCCCGCGCTTCAGTCGTGGCTCCGAGGGGAGCTC 2100  
Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700

QY 2101 AGCTACAACTGGGTGCTGGGGAGGCTCTGCAGGTGGACACCGAGCTCCCTGAGCGGC 2160  
Db 701 SerTyrAsnLeuGlyAlaGlyGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720

QY 2161 GACAATACCTTATGTCCACGCTGGAGGAGAAGGAGACAGATGGGAGCAGGGCCCCACG 2220  
Db |||||||  
721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCGAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCTGGCTGCACCTCC 2280  
Db |||||||  
741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760  
QY 2281 TCATCTCAGCTGCCAAGCTGTATCCCTCCACCGTCGACAGCACCCCGCCTCGTCTAGGT 2340  
Db |||||||  
761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780  
QY 2341 GGCAGAGGAGGCCAGGCAGGGCAGGGGCTTTGAAGCTGAGGCTGGCCCTCTGCTCCC 2400  
Db |||||||  
781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800  
QY 2401 CCACGGGCCCTAGAGGGCTACGGCTGCCCCCTCCATGCCATGGAATGTGCCCCCGATCTG 2460  
Db |||||||  
801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu 820  
QY 2461 AGCCCCAGGGTAGTAGTGGCATTTGAAGACGGCTGTGGCTCGGACCGCCCAAGTTCTCT 2520  
Db |||||||  
821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840  
QY 2521 TTCCCGCTGGCCAGTCTGGCCCGGAATGTAGCAGAGCCCCCTCCCTGGACGAGAGC 2580  
Db |||||||  
841 PheArgValGlyGlnSerGlyProGluCysSerSerProSerProGlyProGluSer 860  
QY 2581 GGCCTGCTCACTGTTCCTCCATGGGCCCGCAGCGAAGGAACACAGACACTGGACAAG 2640  
Db |||||||  
861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880  
QY 2641 CTTCGGCAGGCGGTGACAGAGCTGTGAGAGAGGTGTGAGATGCGGAGGAGGACTGCAG 2700  
Db |||||||  
881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900  
QY 2701 TCACCTTCGCGAGGCTGTGAGCTTGTCTGGCGCCCCACAGGAGGGTCCGTGCCCTCGG 2760  
Db |||||||  
901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920  
QY 2761 GCATCGGAGAGGGCGGTGCCAGCCAGCACCTCCGGGCTTCTGAGCCTCTGTGTGTG 2820  
Db |||||||  
921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940  
QY 2821 GACACTGGGGCATCTCCTACTGCTGCAGCCCCCAGCTGGCTGTGTGTGAGTGGGACT 2880  
Db |||||||  
941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960  
QY 2881 TGSCCCACCCCTCGTCCGGGGCTCCTCCCTCATGGCACCTCGCCCTGGGGTCCCCCA 2940  
Db |||||||  
961 TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980  
QY 2941 GCGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCA 3000  
Db |||||||  
981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000  
QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTGTGAGCCCGACACCCCTGCCTCCCTCCTCCT 3060  
Db |||||||  
1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020  
QY 3061 TCTGAGGAAGGGCTAGGACTGGCCCGCCGAGAGCCTGTGAGCCAGGCTGAGGCTPACCAGC 3120  
Db |||||||  
1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040  
QY 3121 ACTGGAGAGCCCCACAGGGTCAGGGGCTGGGCTGGCTGGGACCCCGACAGCCTG 3180  
Db |||||||  
1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060  
QY 3181 GAGATGGTGTATTGGCTGCCATGGCTCTGGCAGAGTCCAGTGGACCCAGGAAGAGC 3240  
Db |||||||  
1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080  
QY 3241 ACAGGGGTC 3249

Db |||||||  
1081 ThrGlyVal 1083

RESULT 3

ADE55604

ID ADE55604 standard; protein; 1083 AA.

XX ADE55604;

XX 29-JAN-2004 (first entry)

DE Human Protein XP\_035483, SEQ ID NO 1423.

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

PD 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

WPI; 2003-268312/26.

GENBANK; XP\_035483.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1083 AA;

Alignment Scores:



Pred. No.: 0 Length: 1083  
Score: 5704.00 Matches: 1083  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.68% Indels: 0  
DB: 7 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x ADE55604 (1-1083)

QY 1 ATGCGGCGCATGCGGGCCTCTGCGGCTCTCAGAACACCTCTCTGGACACCATCGCTACG 60  
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGTTTCAGCGCAGCACAGTAACTTCGTCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGACGCGGCTGTGCT 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCAACAAGAGTTCAAGGCTGAGTGTATCTGTAC 300  
Db 81 GlnGlnIleArgGlyAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGAGGTGGCT 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGCCCCGACAGATGGAAGACAGGTGGTGGCGGCGGATATGGCGGCGGACGATCC 480  
Db 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgTyrGlyArgAlaArgSer 160  
QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCT 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGCTGAGTACAAAGTAGCCCGCATCCGGAAGTCGCGCTCTCTCTCTCTCTCTCTCT 660  
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220  
QY 661 GGGGACTGAGAGCCACCTGGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCAGCAGGAGGCCAGTGGCGGCGGCGGCGGCGG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
QY 781 CCCAGCGTCTGTGACCTGGCGGTGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTCTGTCTCAAGTCGGGCGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
QY 901 CACTACGTCAACCGTCT 960  
Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320

QY 961 CATGCCTTCAAGGTCAACGTGTACTTCCGGGGCCCATCTGTGAAGACCGTGGCCTGTCTG 1020  
Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340  
QY 1021 CGCCTGTGCGCCTGCTTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGTGTCTG 1080  
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Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
QY 1141 ATTGCCAGCGGAGATCGAGACGAGCAATCCGAGCTGCCGTGAGATTGGCTGGCTGCAG 1200  
Db 381 IleGlyGlnArgGluIleGluSerSerGluLeuProGluIleGlyTrpLeuGln 400  
QY 1201 GAGTGGCCCCGCGACTGGAGACTCCCTACTACTCTGGTGGGCGGAGCCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCAGCGAGGCCAACCGGGCTG 1320  
Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 440  
QY 1321 GAGTGTGGCGCGCGCTCGCTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACCTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGCAGCCTCACGCGCTGGGCTTCGGAACCTGTCCGCCAACACGACCGCAGAGATC 1440  
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QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCGCTGATGACCGGTGGTGTGGGAACGTG 1500  
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QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCACAGCGCGCGCGGAC 1560  
Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520  
QY 1561 CTGCGGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGTGTGAG 1620  
Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540  
QY 1621 TACTTCCAGGCCACCTGGCGGTGAACAANGCATCGACACCGAGCTGCTGCAGAC 1680  
Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560  
QY 1681 CTCCTGACGAGCTGCGCGCAGACATCGCCATGCATCCCTGCACCAAGGAGGTCTGTGAG 1740  
Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580  
QY 1741 CCCTGTTTGGCGGCGGCGCTGCTCGCGGCACTGTCTCTGGCCCTGCGGCGC 1800  
Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600  
QY 1801 GCCTTCTGCACCGCGGCGAGTACCTCATCCACCAAGCGCATGCCCTGCAGGCCCTCTAC 1860  
Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
QY 1861 TTTGTCTGTCTGGCTCCANGGAGGTGCTCAAGGTGGCACCGTGTCTGCGCATCTAGGG 1920  
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QY 1921 AAGGGCGACCTGATCGGCTGTGAGTGGCGGCGGAGCGAGGTGTAAGGCCAATGCC 1980  
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGCTGACGTACTCGCTCCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040  
Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680  
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Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700  
QY 2101 AGCTAACACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCACTCCCTGAGCGGC 2160  
Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACAAATACCTTATGTCCACGCTGGAGGAGAAGAGACAGATGGGAGCAGGCCCAACG 2220  
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QY 2281 TCATCTCAGCTGCCAAGCTGTATCCCCACGTCGAACAGACCCCGCCTCGTCTAGGT 2340  
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QY 2521 TTCCCGCTGGGCCAGTCTGGCCCCGGAATGTAGCAGACCCCTCCCTGGACAGAGAGC 2580  
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QY 2581 GGCCTGCTCACTGTTCCTCCATGGGCCCGCAGCGAGGCAAGCAACACAGACACTGGACAAG 2640  
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QY 2641 CTTCCGCGAGCGGTGACAGAGCTGTGACAGCAGGTGTGACATGCGGGAAGACTGCAG 2700  
Db 881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuMetArgGluGlyLeuGln 900  
QY 2701 TCACCTCGCCAGGTGTGACAGCTTGTCTGGCGCCCCACAGGAGGTCCGTGCCCTCGG 2760  
Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920  
QY 2761 GCATCGGGAGAGGGCGGTGCCCCAGCCAGCACTCCGGGCTTCTGACGCTCTGTGTGTG 2820  
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Db 961 TrpProHisProArgProGlyProProProLeuMetAlaProTyrProTyrProPro 980  
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Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020  
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QY 3121 ACTGAGAGCCCCCACCAGGTCAGGGGGCTGGCCCTTGGCTGGGACCCCGCAGGCTG 3180

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QY 3241 ACAGGGGTC 3249  
Db 1081 ThrGlyVal 1083  
RESULT 4  
AAY44778  
ID AAY44778 standard; protein; 1083 AA.  
XX  
AC AAY44778;  
XX  
DT 04-MAY-2000 (first entry)  
XX  
DE Human Elk voltage gated potassium channel subunit monomer.  
XX  
KW Voltage gated potassium channel subunit; VGPCs; helk; human; stroke;  
KW Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;  
KW chromosome 12q13; resting potential; cell excitability; seizure; CNS;  
KW migraine; psychotic; anticonvulsant; neuroprotective; ion flux disorder;  
KW reporter molecule; detection; gene therapy; antimigrane;  
KW neuroprotective; antipsychotic.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
Region 452..710  
FT /label= Extended P-S6 region  
FT /note= "Extended\_Pore-S6 region with conserved amino  
FT acids"  
FT  
FT Region 452..514  
FT /label= P-S6 region  
FT /note= "Pore-S6 region with conserved amino acids"  
FT Misc-difference 965  
FT /note= "Encoded by CGT"  
XX  
PN WO200001819-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 30-JUN-1999; 99WO-US014944.  
XX  
PR 01-JUL-1998; 98US-0091469P.  
PR 21-JAN-1999; 99US-0116621P.  
XX  
PA (ICAG-) ICAGEN INC.  
XX  
PI Jegla TJ, Wickenden A;  
XX  
DR WPI; 2000-182114/16.  
DR N-PSDB; AAZ50119.  
XX  
PT Novel polynucleotides and polypeptides of human ELK, a voltage-gated  
PT potassium channel subunit useful for treating ELK miss-expression and to  
PT screen for inhibitors and activators of such channels.  
XX  
PS Claim 13; Page 62; 79pp; English.  
XX  
CC The present sequence is the human ELK (hElk) polypeptide monomer,  
CC comprising an alpha subunit of the voltage-gated potassium channel  
CC (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily,  
CC Eag (ether a go-go) family and Elk subfamily of potassium channel  
CC monomers. hElk gene is mapped to chromosome 12q13. It is isolated from  
CC brain and maintains the resting potential and controls excitability of  
CC the cell. It has antimigrane, cerebroprotective, antipsychotic,  
CC neuroprotective and anticonvulsant activity. The hElk polypeptide can be  
CC used to screen for modulators of VGPCs, that are useful for treating  
CC abnormal ion flux disorders, CNS disorders such as migraines, hearing and  
CC vision problems, seizures, psychotic disorders and to prevent strokes. It

CC can be used as a marker for diagnosis of diseases linked to this gene and  
CC also as reporter molecule in detection systems. The polynucleotide is  
CC useful for gene therapy, to rectify ELK expression  
XX  
SQ Sequence 1083 AA;

Alignment Scores:  
Pred. No.: 0 Length: 1083  
Score: 5698.00 Matches: 1082  
Percent Similarity: 99.91% Conservative: 0  
Best Local Similarity: 99.91% Mismatches: 1  
Query Match: 93.58% Indels: 0  
DB: 3 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x AAY44778 (1-1083)

QY 1 ATGCCGGCCATGGGGGCTCTCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60  
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Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGCAGCGGGCTGTGCTGCTGCTCTCTCTTATGGGCGACACACAGTGAGTCTCGTCCGC 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGCAAGCCCTGGACGACCAAGGAGTCAAGGCTGAGCTGATCCTGTAC 300  
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QY 301 CGGAAGAGCGGGCTCCCGTCTCTGGTGTCTCTCTGGATGTATACCCATAAAGATGAGAAA 360  
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QY 361 GCGGAGGTGGCTCTCTCTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGCCCCGACAGATGGAAGGAGACAGTGCTGGTGGCGCGCGGATATGGCGGGCAGATCC 480  
Db 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 160  
QY 481 AAAGGCTTCAATGCCAACCGGGCGGAGCCGGCGCTCTACACACCTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAGCAGCCCAAGGGCAAGCAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCTCTGTGCACTGT 660  
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGTTCATCTGCTCGCCACACTCTATGTGGCTGTC 720  
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QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCAGTGCCGCCCGCGGCCCG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCTCATCTCTTGACATTGTGCTGAATTTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTCTGTCCAAGTCGGGCCAGGTGGTGTGTTTGTCCCAAGTCCATTGCTC 900

Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
QY 901 CACTACGTCAACACCTGGTTCCTGCTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA 960  
Db 301 HistyrValThrTrpPheLeuLeuAspValIleAlaAlaLeuPropheAspLeuLeu 320  
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QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGCAATCCGAGCTGCCTGAGATTGGCTGGCTG 1200  
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QY 1201 GAGCTGGCCCGCACTGGAGACTCCCTACTACTGCTGGTGGCGGAGGCCAGCTGGAGGG 1260  
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Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGCAGCCTCACAGCGTGGCTTCGGCAACGTGTCCGCCAAACACGACACCCGAGAAGATC 1440  
Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480  
QY 1441 TTCTCCATCTGCACCATGTCTCATCGCGCCCTGTATGCACGCGGTGGTGTGGGAACGTG 1500  
Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500  
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Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520  
QY 1561 CTGCGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGTCTGGAG 1620  
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QY 1801 GCCTTCTGACGCCGGGAGTACCTCATCCACCAAGCGCATGCCCTGCGAGGCCCTCTAC 1860  
Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
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Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640  
QY 1921 AAGGGCAGCCTGATCGGCTGTGAGTGTGCCCGCGGAGCAGGTGGTAAAGGCCAATGCC 1980



Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660

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Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680

QY 2041 AGCCTTGGCTGTACCCCGAGTTTGGCCCGCGCTTCAGTCTGGCTCCGAGGGGAGCTC 2100

Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700

QY 2101 AGTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGCACACAGCTCCCTGAGCGC 2160

Db 701 SerTyrAsnLeuGlyAlaGlyGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720

QY 2161 GACAATACCTTATGTCCAGCTGGAGGAGGAGGAGACAGATGGGAGCAGGGCCCCACG 2220

Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740

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Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780

QY 2341 GGCAGAGGGAGGCCAGCGAGGGCAGGGGCTTTGAAGCTGAGGCTGGCCCTGTCTCCC 2400

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QY 2401 CCACGGGCCCCAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2460

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QY 2581 GGCCTGCTCACTGTTCCCCATGGGCCAGCGAGGCAAGGAACACACACACTGGACAAG 2640

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QY 2641 CTTCCGAGGGGTGACAGAGCTGTACAGCAGGTGCTGCAGATGGCGGAAGGACTGCAG 2700

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QY 2701 TCACCTGCCAGGCTGTGCAGTTGTCTGCGGCCCGCCACAGGAGGGTCCGTGCCCTCGG 2760

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QY 2761 GCATCGGAGAGGGCCGTGCCACGACACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820

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QY 2881 TGGCCCCACCTCGTCCGGGGCTCTCTCCCTCATGGACCCCTGGCCCTGGGGTCCCCA 2940

Db 961 TrpProHisProAlaProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980

QY 2941 CGGTCTCAGAGTCCCCCTGGCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCA 3000

Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000

QY 3001 GAGCCCCCTGCCTCAGGACCTCTGTCTGTAGCCCCAGACCCCTGCCTCCCTCCTCCT 3060

Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020

QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC 3120

Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040

QY 3121 ACTGAGAGCCCCCACCAGGTCAGGGGCTGGCCCTTGCCCTGGGACCCCCACAGCCTG 3180

Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060

QY 3181 GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGGC 3240

Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080

QY 3241 ACAGGGGTC 3249

Db 1081 ThrGlyVal 1083

RESULT 5

AAAY44779

ID AAY44779 standard; protein; 1083 AA.

XX

AC AAY44779;

XX

DT 04-MAY-2000 (first entry)

XX

DE Human Elk voltage gated potassium channel monomer variant #1.

XX

KW Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;

KW Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;

KW chromosome 12q13; resting potential; cell excitability; seizure; marker;

KW CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;

KW ion flux disorder; reporter molecule; detection; gene therapy;

KW antimigrane; cerebroprotective; neuroprotective; antipsychotic.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 452..710

FT /label= Extended\_P-S6\_region

FT /note= "Extended\_Pore-S6 region with conserved amino

FT acids"

FT Region 452..514

FT /label= P-S6\_region

FT /note= "Pore-S6 region with conserved amino acids"

FT Misc-difference 1065

FT /note= "Wild type Ile substituted with Val; Ile is stated

FT to be located at 1064 in the specification"

XX

PN WO200001819-A1.

XX

PD 13-JAN-2000.

XX

PF 30-JUN-1999; 99WO-US014944.

XX

PR 01-JUL-1998; 98US-0091469P.

PR 21-JAN-1999; 99US-0116621P.

XX

PA (ICAG-) ICAGEN INC.

XX

PI Jegla TJ, Wickenden A;

XX

DR WPI; 2000-182114/16.

XX

PT Novel polynucleotides and polypeptides of human ELK, a voltage-gated

PT potassium channel subunit useful for treating ELK miss-expression and to

PT screen for inhibitors and activators of such channels.

XX

PS Disclosure; Page; 79pp; English.

XX

CC The present sequence is the human ELK (hElk) polypeptide variant #1,

CC comprising an alpha subunit of the voltage-gated potassium channel

CC (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily,

CC Eag (ether a go-go) family and Elk subfamily of potassium channel  
CC monomers. hElk gene is mapped to chromosome 12q13. It is isolated from  
CC brain and maintains the resting potential and controls excitability of  
CC the cell. It has antimigraine, cerebroprotective, antipsychotic,  
CC neuroprotective and anticonvulsant activity. The hElk polypeptide can be  
CC used to screen for modulators of VGPCs, that are useful for treating  
CC abnormal ion flux disorders, CNS disorders such as migraines, hearing and  
CC vision problems, seizures, psychotic disorders and to prevent strokes. It  
CC can be used as a marker for diagnosis of diseases linked to this gene and  
CC also as reporter molecule in detection systems. The polynucleotide is  
CC useful for gene therapy, to rectify ELK expression. Note: The present  
CC sequence is not found in the specification, but is derived from hELK  
CC amino acid sequence found in page 62  
XX  
SQ Sequence 1083 AA;

Alignment Scores:  
Pred. No.: 0 Length: 1083  
Score: 5697.00 Matches: 1081  
Percent Similarity: 99.91% Conservative: 1  
Best Local Similarity: 99.82% Mismatches: 1  
Query Match: 93.56% Indels: 0  
DB: 3 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x AAY44779 (1-1083)  
QY 1 ATGCCGGCCATCGGGGCTCTCTGGCGCTCAGAACACCTTCCTGGACACCATCGTACG 60  
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTCTGGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPhenValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCCGGCTGAGTTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGCAGCGGGGTGCTGCT 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCTGTATC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGAGCGGGCTCCGCTTCTGGTGTCTCTCTGATGTGATACCCATAAAGAAATGAGAAA 360  
Db 101 ArgLysSerGlyLeuProPheThrCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGGAGGTGGCT 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGGCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
Db 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 160  
QY 481 AAGGCTTCAATGCCAACCGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGCCTGAGTACAAAGTAGCCGCGCATCCGGAAGTCGCCCTTCATCTCTGTCAGTGT 660  
Db 201 AsnLeuProGluTyrLysValAlaIleArgLysSerProPheIleLeuLeuHisCys 220  
QY 661 GGGGCACTGAGACCCACTGGGATGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240

QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGACACGGGAGCCAGTCCCGCGCGCCG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
QY 781 CCCAGCGTCTGTGACCTGGCGTGGAGGTCTCTTTCATCTTGCATTTGCTGCTGAATTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTTTGGCCCAAGTCCATTGCTC 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
QY 901 CACTACGTACACCACTGGTTCCTGCTGGATGTCTCGAGCGCTGCCCTTTGACCTGCTA 960  
Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320  
QY 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCTGCTG 1020  
Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340  
QY 1021 CGCTGTCTGCGCTGCTTCCGGCGTGGACCGGTACTCGCAGTACAGCCGCTGGTGGTGG 1080  
Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360  
QY 1081 ACACGTCTCATGGCCGCTGTTCGCCCTGCTGCTGCGCACTGGGTGCGCTCTGTTTAC 1140  
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCGTGAGATTGGCTGGCTGCAG 1200  
Db 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400  
QY 1201 GAGCTGGCCCGCGCTGAGACTCCCTACTACTGCTGGTGGCGGAGGCCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420  
QY 1261 AACAGCTCCGGCCAGAGTGACAACCTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGGCTG 1320  
Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440  
QY 1321 GAGCTGTGGCGCGCTGCTGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCCGACTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAGATC 1440  
Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480  
QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCCTGATGATGACCGGTGGTGTGTTGGGAACGTG 1500  
Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500  
QY 1501 ACGGCCATCATCCAGCGCATGTACCGCCCGCTTCTGTGTACACAGCCGACCGCGGAC 1560  
Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAsp 520  
QY 1561 CTGCGCGACTACATCCGCTATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540  
QY 1621 TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCGAGCTGCTGCAGAGC 1680  
Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560  
QY 1681 CTCCCTGACGAGCTGCGCGCAGCATCGCCATGACCTGACACAGGAGGTCTCTGACGCTG 1740  
Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580  
QY 1741 CCACCTGTTGAGGCGGCCAGCGCGCTGCTGCGGCACTGTCTCTGCGCCCTGCGGCC 1800  
Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600

QY 1801 GCCTTCTGCACGGCGGCGAGTAGCTCATCTCATCCACCAAGCGGATGCCCTGCAGGCCCTCTAC 1860  
Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGTCAAGGGTGGCACCGTGTCTCGCCATCTAGGG 1920  
Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640  
QY 1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAGGCCAATGCC 1980  
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGCTGACGTACTGCGTCCCTGCAGTGTCTGCAGCTGGCTGGCTGCACGAC 2040  
Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680  
QY 2041 AGCCTTGCGCTGTACCCCGAGTTTGCCCGCGCTTCAGTCGTGGCTCCCGAGGGAGCTC 2100  
Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700  
QY 2101 AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAAGCTCCCTGAGCGGC 2160  
Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACAAATACCTTATGTCCACGCTGGAGAGAAGGAGACAGATGGGAGCAGGGCCCCACG 2220  
Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCGAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCTGGCTGCACCTCC 2280  
Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760  
QY 2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAAACAGCACCCCGCCCTCGTCTAGGT 2340  
Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780  
QY 2341 GGCAGAGGAGGCCAGGCAGGCGAGGGCTTTGAAGGCTGAGCTGGCCCTCTGTCTCCC 2400  
Db 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800  
QY 2401 CCACGGCCCTTAGAGGGGCTACGGCTGCCCCCCTATGCCATGGAATGTGCCCCCAGATCTG 2460  
Db 801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTyrAsnValProProAspLeu 820  
QY 2461 AGCCCCAGGGTAGTAGATGGCAATTGAAGACGGCTGTGGCTCGACACCGCCCAAGTTCTCT 2520  
Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840  
QY 2521 TTCGCGTGGCCAGTCTGCCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAC 2580  
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QY 2581 GGCTTGCTCACTGTTCCCCCATGGGCCCGAGCGAGGCAAGGAACACAGACACTGGACAAG 2640  
Db 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880  
QY 2641 CTTCGGCAGGCGGTGACAGAGCTGTACAGACAGGTGTGCAGATCGGGAGGACTGCAG 2700  
Db 881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900  
QY 2701 TCACTTCGCCAGGCTGTGAGCTTGTCTGGCGCCCCACAGGGAGGGTCCGTGCCCTCGG 2760  
Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920  
QY 2761 GCATCGGGAGAGGGCGGTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940  
QY 2821 GACACTGGGGCATCCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTTGAGTGGACT 2880  
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Db 961 TrpProHisProAlaProGlyProProProLeuMetAlaProTyrProTyrGlyProPro 980  
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Db 981 AlaSerGlnSerSerProTyrProArgAlaThrAlaPheTyrThrSerThrSerAspSer 1000  
QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCCAGCACCCCTGCCTCCCTCCTCCT 3060  
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QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCCGAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC 3120  
Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040  
QY 3121 ACTGGAGAGCCCCACCAGGCTCAGGGGGCTGGCCCTTGGCCCTGGGACCCCCACAGCCTG 3180  
Db 1041 ThrGlyGluProProGlySerGlyLeuAlaLeuProTyrAspProHisSerLeu 1060  
QY 3181 GAGATGTGCTTATTGGCTGCCATGGCTGTGGCAGTCCAGTCCAGCCAGGAAGGC 3240  
Db 1061 GluMetValLeuValGlyCysHisGlySerGlyThrValGlnTyrThrGlnGluGly 1080  
QY 3241 ACAGGGGTC 3249  
Db 1081 ThrGlyVal 1083  
RESULT 6  
AAY44780  
ID AAY44780 standard; protein; 1083 AA.  
XX  
AC AAY44780;  
XX  
DT 04-MAY-2000 (first entry)  
XX  
DE Human Elk voltage gated potassium channel monomer variant #2.  
XX  
KW Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;  
KW Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;  
KW chromosome 12q13; resting potential; cell excitability; seizure; marker;  
KW CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;  
KW ion flux disorder; reporter molecule; detection; gene therapy;  
KW antimigrane; cerebroprotective; neuroprotective; antipsychotic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Region 452..710  
FT /label= Extended P-S6 region  
FT /note= "Extended Pore-S6 region with conserved amino  
FT acids"  
FT Region 452..514  
FT /label= P-S6 region  
FT /note= "Pore-S6 region with conserved amino acids"  
FT Misc-difference 1060  
FT /note= "Wild type Leu substituted with Ile"  
XX  
PN WO200001819-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 30-JUN-1999; 99WO-US014944.  
XX  
PR 01-JUL-1998; 98US-0091469P.  
PR 21-JAN-1999; 99US-0116621P.  
XX  
PA (ICAG-) ICAGEN INC.  
XX  
PI Jegla TJ, Wickenden A;  
XX  
DR WPI; 2000-182114/16.  
XX



PT Novel polynucleotides and polypeptides of human ELK, a voltage-gated  
PT potassium channel subunit useful for treating ELK miss-expression and to  
PT screen for inhibitors and activators of such channels.

PS Disclosure; Page; 79pp; English.

The present sequence is the human ELK (hElk) polypeptide variant #2, comprising an alpha subunit of the voltage-gated potassium channel (VGPCs). It is a member of the Kv (Voltage gated potassium) superfamily, Eag (ether a go-go) family and Elk subfamily of potassium channel monomers. hElk gene is mapped to chromosome 12q13. It is isolated from brain and maintains the resting potential and controls excitability of the cell. It has antimigraine, cerebroprotective, antipsychotic, neuroprotective and anticonvulsant activity. The hElk polypeptide can be used to screen for modulators of VGPCs, that are useful for treating abnormal ion flux disorders, CNS disorders such as migraines, hearing and vision problems, seizures, psychotic disorders and to prevent strokes. It can be used as a marker for diagnosis of diseases linked to this gene and also as reporter molecule in detection systems. The polynucleotide is useful for gene therapy, to rectify ELK expression. Note: The present sequence is not found in the specification but derived from hELK amino acid sequence found in page 62

Sequence 1083 AA;

Alignment Scores:			
Pred. No.:	0	Length:	1083
Score:	5696.00	Matches:	1081
Percent Similarity:	99.91%	Conservative:	1
Best Local Similarity:	99.82%	Mismatches:	1
Query Match:	93.55%	Indels:	0
DB:	3	Gaps:	0

US-09-965-830-1 COPY 6 3257 (1-3252) x AAY44780 (1-1083)

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QY	61	CGCTTCGACGGCACGCACAGTAACCTCGTCTGGCAACGCCAGGTGGCGGGCTCTTC	120
Db	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe	40
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC	180
Db	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal	60
QY	181	ATGACGGGGCTGTGCTGCTCCTTCCTTTATGGCCAGACACCACTGAGCTCGTCCGC	240
Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg	80
QY	241	CAACAGATCCGCAAGGCCCTGGACGACACAAGGAGTTCAAGGCTGAGTGATCCTGTAC	300
Db	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr	100
QY	301	CGGAAGACGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAA	360
Db	101	ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys	120
QY	361	GGGAGGTGGCTCTCTCCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG	420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGTGGCCCGCCCGCATATGGCCGGGCACGATCC	480
Db	141	GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer	160
QY	481	AAAGGCTTCAATGCAACCGGGCGGAGCCGGGCGCTGTCTACCACTGTCCGGGCAC	540
Db	161	LysGlyPheAsnAlaAsnArgArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180
QY	541	CTGCAGAAGCAGCCCAAGGGCAAGCACCAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA	600

QY 1681 CTCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCTCTGCAGCTG 1740  
Db |||||  
561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580  
QY 1741 CCACTGTTTGAGGCGGCCAGCGCGGCTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCC 1800  
Db |||||  
581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600  
QY 1801 GCCTTCTGCACGCGCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1860  
Db |||||  
601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTCGCCATCCTAGGG 1920  
Db |||||  
621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640  
QY 1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGCGGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db |||||  
641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGGCTGACGTACTGCGTCTGTGAGTGTCTGAGCTGGCTGGCTGCACGAC 2040  
Db |||||  
661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680  
QY 2041 AGCCTTGCGCTGTAACCCGAGTTTGCCCGCGCTTCAGTCGTGGCCTCCGAGGGAGCTC 2100  
Db |||||  
681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700  
QY 2101 AGCTACAACCTGGTCTGGGGAGGCTCTGCAGAGGTGGACACCAAGTCCCTGAGCGGC 2160  
Db |||||  
701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACAATACCTTATGTCACGCTGGAGGAGAAGAGACAGATGGGGAGCGGCCCCACG 2220  
Db |||||  
721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCGACCCAGCTGATGAGCCCTCCAGCCCTGCTGTCTGCCCTGGCTGCACCTCC 2280  
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Db |||||  
761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780  
QY 2341 GGCAGAGGAGGCCAGGCGAGGCGAGGGCTTTGAAGGCTGAGGTGGCCCTCTGTCTCC 2400  
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781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800  
QY 2401 CCACGGGCCCTAGAGGGGCTACGGTGGCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2460  
Db |||||  
801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTyrAsnValProProAspLeu 820  
QY 2461 AGCCCCAGGCTAGTAGTGGCATGAAGACGGCTGTGGCTCGGACCGCCCAAGTTCTCT 2520  
Db |||||  
821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840  
QY 2521 TTCCGCGTGGCCAGTCTGGCCCGGAATGTAGCAGCGCCCTCCCTGGACCAGAGAGC 2580  
Db |||||  
841 PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860  
QY 2581 GGCCTGCTCACTGTTCCCATGGGCCCGAGCGAGGCAAGAACACACACTGGACAAG 2640  
Db |||||  
861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880  
QY 2641 CTTCCGCGAGGCGGTGACAGAGCTGTACAGAGCAGGTGTGCAGATCGGGAGGACTGCAG 2700  
Db |||||  
881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900  
QY 2701 TCACTTCGCCAGGCTGTGAGCTTGTCTCTGGCGCCACAGGGAGGGTCCGTCGCTCGG 2760  
Db |||||  
901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920

QY 2761 GCATCGGAGAGGGGCGTGTCCCGAGCCAGCACCTCCGGGGCTTCTGCAGCCTCTGTGTGTG 2820  
Db |||||  
921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940  
QY 2821 GACACTGGGGCATCCTCCTACTGCCTGCAGCCCCCAGTGGCTCTGTCTTGTAGTGGACT 2880  
Db |||||  
941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960  
QY 2881 TGGCCCCACCTCGTCCGGGGCTCTCTCCCTCAITGGACACCTGGCCCTGGGGTCCCCCA 2940  
Db |||||  
961 TrpProHisProAlaProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980  
QY 2941 GCGTCTCAGAGCTCCCTCGGCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000  
Db |||||  
981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000  
QY 3001 GAGCCCCCTGCCTCAGAGACCTCTGCTCTGAGCCCGAGCACCCCTGCCCTCCCTCCTCCT 3060  
Db |||||  
1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020  
QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCCGAGAGCCTGTGAGCCAGGCTGAGGCTACGAGC 3120  
Db |||||  
1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040  
QY 3121 ACTGGAGAGCCCCACAGGCTCAGGGGCTGGGGCTGGCCCTTGCCCTGGGACCCACAGCCTG 3180  
Db |||||  
1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerIle 1060  
QY 3181 GAGATGGTGTATTGGCTGCCATGGCTCTGGCAGTCCAGTGGACCCAGGAAGAGGC 3240  
Db |||||  
1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080  
QY 3241 ACAGGGGTC 3249  
Db |||||  
1081 ThrGlyVal 1083

RESULT 7  
AAV44781  
ID AAY44781 standard; protein; 1083 AA.  
XX  
AC AAY44781;  
XX  
DT 04-MAY-2000 (first entry)  
XX  
DE Human Elk voltage gated potassium channel monomer variant #3.  
KW Voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;  
KW Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;  
KW chromosome 12q13; resting potential; cell excitability; seizure; marker;  
KW CNS; migraine; treat; hearing/vision problem; psychotic; anticonvulsant;  
KW ion flux disorder; reporter molecule; detection; gene therapy;  
KW antimigrane; cerebroprotective; neuroprotective; antipsychotic.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Region 452..710  
FT /label= Extended P-S6 region  
FT /note= "Extended\_Pore-S6 region with conserved amino  
FT acids"  
FT Region 452..514  
FT /label= P-S6 region  
FT /note= "Pore-S6 region with conserved amino acids"  
FT Misc-difference 744  
FT /note= "Wild type Ala substituted with Ser"  
XX  
PN WO200001819-A1.  
XX  
PD 13-JAN-2000.  
XX  
PF 30-JUN-1999; 99WO-US014944.  
XX

PR 01-JUL-1998; 98US-0091469P.  
PR 21-JAN-1999; 99US-0116621P.  
XX  
XX  
PA (ICAG-) ICAGEN INC.  
XX  
PI Jegla TJ, Wickenden A;  
XX  
XX  
DR WPI; 2000-182114/16.  
XX  
PT Novel polynucleotides and polypeptides of human ELK, a voltage-gated  
PT potassium channel subunit useful for treating ELK miss-expression and to  
PT screen for inhibitors and activators of such channels.  
XX  
XX  
PS Disclosure; Page; 79pp; English.  
XX  
CC The present sequence is the human ELK (hElk) polypeptide variant #3,  
CC comprising an alpha subunit of the voltage-gated potassium channel  
CC (VGPCs). It is a member of the Kv (voltage gated potassium) superfamily,  
CC Eag (ether a go-go) family and Elk subfamily of potassium channel  
CC monomers. hElk gene is mapped to chromosome 12q13. It is isolated from  
CC brain and maintains the resting potential and controls excitability of  
CC the cell. It has antimigrane, cerebroprotective, antipsychotic,  
CC neuroprotective and anticonvulsant activity. The hElk polypeptide can be  
CC used to screen for modulators of VGPCs, that are useful for treating  
CC abnormal ion flux disorders, CNS disorders such as migraines, hearing and  
CC vision problems, seizures, psychotic disorders and to prevent strokes. It  
CC can be used as a marker for diagnosis of diseases linked to this gene and  
CC also as reporter molecule in detection systems. The polynucleotide is  
CC useful for gene therapy, to rectify ELK expression. Note: The present  
CC sequence is not found in the specification but derived from hElk amino  
CC acid sequence found in page 62  
XX  
SQ Sequence 1083 AA;

Alignment Scores:  
Pred. No.: 0 Length: 1083  
Score: 5695.00 Matches: 1081  
Percent Similarity: 99.91% Conservative: 1  
Best Local Similarity: 99.82% Mismatches: 1  
Query Match: 93.53% Indels: 0  
DB: 3 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x AAY44781 (1-1083)

QY 1 ATGCGGCCATCGGGGCTCTGGCGCTCAGAACACCTCTCTGGACACCATCGGTACG 60  
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
QY 121 CCGTGGTCTACTGCTGTATGGCTTCTGTGACCTCACGGGTTCTCCCGGCTGAGTTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGACGGGGCTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGAGTTCAAGGTGAGCTGATCCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGAGCGGCTCCCGTTCTGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
Db 101 ArgLysSerGlyLeuProPheThrCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGAGGTGGTCT 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGCCCCGACAGATGAAGGAGACAGGTGTTGGCCCGCCGATATGGCCGGGCACGATCC 480

Db 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 160  
QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCCCGGCGCTCTTACACCTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGCTGAGTACAAAGTAGCGCCCATCCGGAAGTCGCCCTTTCATCTGTGCACTGT 660  
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuHisCys 220  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTGCGCACACTCTATGTGGTGT 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTGGCGCCCGGCCCG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
QY 781 CCCAGCGTCTGTGACCTGGCGGTGGAGTCTCTTCATCCTTGACATGTGTGAATTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTCGTGTCCAAGTCGGGCGGAGGTGTTTGGCCCCAAAGTCCATTTCCTC 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
QY 901 CACTACGTACACACCTGGTTCCTGCTGATGTATCGCAGCGCTGCCCTTGACCTGTCTA 960  
Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320  
QY 961 CATGCCCTTCAAGTCAACGTGTACTTCGGGGGCCATCTGCTGAAGACGGTGGCCTGTCTG 1020  
Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340  
QY 1021 GCGCTGTGCGGCTGCTCCGCGGTGGACCGGTACTCGCAGTACAGCGCGGTGGTGTCTG 1080  
Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360  
QY 1081 AACTGTCTCATGGCGCTGTTCCCTGCTGCGGCTGGTGGTGGTGGTGGTGGTGGTGGT 1140  
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
QY 1141 ATTGGCAGCGGGAGATCGAGAGCAGCGAATCCGAGTGCCTGAGATTGGCTGGCTGCAG 1200  
Db 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400  
QY 1201 GAGCTGGCGCGGCTGAGACTCCCTACTACTACTGCTGGCGCGGAGGCCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1320  
Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440  
QY 1321 GAGCTGTGGCGCGGCTGCTGCTGCGCAGCGCTCATCATCCTCCCTCTACTCTGCACTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGCAGCTCACAGCGTGGGCTTCGGCAACCGTGTCCCGCCCAACACGAGCACCCGAGAATC 1440  
Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480  
QY 1441 TTCTCCATCTGCACCATGTCTCATCGGCGCCCTGATGCACGCGGTGTGTGTGGGAACGTG 1500  
Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACACGCGCACGCGCGAC 1560



Db	501	ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp	520
QY	1561	CTGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620
Db	521	LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu	540
QY	1621	TACTTCCAGGCCACTGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGC	1680
Db	541	TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer	560
QY	1681	CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCAAGGAGTCTCTGCAGCTG	1740
Db	561	LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu	580
QY	1741	CCACTGTTTGAGGCGGCAGCCGGCTGCCTGCGGCACTGTCTCTGGCCCTGCGGCC	1800
Db	581	ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro	600
QY	1801	GCCTTCTGCACGCCGCGGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC	1860
Db	601	AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr	620
QY	1861	TTTGTCTGCTCTGGTCCATGGAGGTGCTCAAGGTGGCACCGTGCTCGCCATCCTAGGG	1920
Db	621	PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly	640
QY	1921	AAGGGCGACCTGATCGGCTGTGAGTGCCCGCGGGAGCTCTGAGTGGTAAAGGCCAATGCC	1980
Db	641	LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla	660
QY	1981	GACGTGAAGGGCTGACGTACTCGTCTCGCAGTGTCTGCAGCTGGCTGGCCCTGCACGAC	2040
Db	661	AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp	680
QY	2041	AGCCTTGCGTGTACCCGAGTTTGCCCGCGTTCAGTCGTGGCCCTCCGAGGGAGCTC	2100
Db	681	SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu	700
QY	2101	AGCTACAACCTGGTGTGGGGAGGCTCTGCAGAGGTGGACACAGCTCCCTGAGCGGC	2160
Db	701	SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly	720
QY	2161	GACAATACCTTATGTCCACGCTGGAGGAGAGGAGACAGATGGGAGCAGGCCCCACG	2220
Db	721	AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr	740
QY	2221	GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTGTFCCCTGGCTGCACCTCC	2280
Db	741	ValSerProSerProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer	760
QY	2281	TCATCCTCAGTGCCCAAGCTGCTATCCCCACGTGCAACAGACACCCCGCCTCGTCTAGST	2340
Db	761	SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly	780
QY	2341	GGCAGAGGGAGGCCAGGCAGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCTCTGCTCCC	2400
Db	781	GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro	800
QY	2401	CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG	2460
Db	801	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu	820
QY	2461	AGCCCCAGGGTAGTAGTGCAATTGAAGACGGCTGTGGCTCGGACCAAGTCTCTCT	2520
Db	821	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	840
QY	2521	TTCCCGTGGGCCAGTCTGGCCCCGGAATGTAGCAGACAGCCCTCCCTGGACCAAGAGC	2580
Db	841	PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer	860
QY	2581	GGCCTGCTCACTGTTCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG	2640
Db	861	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	880
QY	2641	CTTCGGCAGGCGGTGACAGAGCTGTGACAGCAGGTGCTGCAGATCGGGGAGGACTGCAG	2700
Db	881	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	900
QY	2701	TCACTTCGCCAGGCTGTGCAGCTTGTCTGGCGCCCCACAGGGAGGTCGCTGCCCTCGG	2760
Db	901	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	920
QY	2761	GCATCGGAGAGGGGCGGTGCCAGCCAGCCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG	2820
Db	921	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal	940
QY	2821	GACACTGGGGCATCCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTTGAFTGGACT	2880
Db	941	AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr	960
QY	2881	TGGCCCCACCTCGTCCGGGGCCTCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA	2940
Db	961	TrpProHisProAlaProGlyProProProLeuMetAlaProTrpProTrpGlyProPro	980
QY	2941	GCGTCTCAGAGTCCCCCTGGCCTCGAGCCACAGCTTCTTGGACCTCCACCTCAGACTCA	3000
Db	981	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	1000
QY	3001	GAGCCCCCTGCTCAGGAGACCTCTGCTCTGAGCCCCAGCACCCCTGCCCTCCCTCCTCT	3060
Db	1001	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1020
QY	3061	TCTGAGGAAGGGCTAGGACTGGGCCCCCAGAGCCCTGTGAGCCAGGCTGAGGCTACCAGC	3120
Db	1021	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1040
QY	3121	ACTGGAGAGCCCCACAGGGTCAAGGGGCGCTGGCCCTGGCCCTGGGACCCCCACAGCCTG	3180
Db	1041	ThrGlyGluProProProGlySerGlyLeuAlaLeuProTrpAspProHisSerLeu	1060
QY	3181	GAGATGCTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGACCCAGGAAGAGC	3240
Db	1061	GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly	1080
QY	3241	ACAGGGGTC 3249	
Db	1081	ThrGlyVal 1083	
RESULT 8			
AAAY84835			
ID	AAAY84835 standard; protein; 1083 AA.		
XX	AC		
XX	AAAY84835;		
DT	08-AUG-2000 (first entry)		
XX	Herg4, a potassium channel protein of the ERG family.		
DE	Human; potassium channel protein; Herg4; human erg related gene 4;		
XX	epilepsy; migraine; cell proliferation disorder; cancer;		
KW	comportemental trouble; neurotransmitter; hormone; ischemia;		
KW	brain disease; cardiac disease; inflammation; pain.		
XX	Homo sapiens.		
OS	WO200022001-A2.		
XX	20-APR-2000.		
PN	13-OCT-1999; 99WO-EP007671.		
XX	13-OCT-1998; 98EP-00402540.		
PR	(SNFI ) SANOFI-SYNTHELABO.		
XX	Renard S, Avenet P;		

XX WPI; 2000-317948/27.  
DR N-PSDB; AAA14893.  
XX  
PT Novel herg4 polypeptide of human erg potassium channel family useful for  
PT treatment of epilepsy, migraine, cell proliferation.  
XX  
PS Claim 11; Page 45-48; 48pp; English.  
XX  
CC The present sequence represents a human potassium channel protein of the  
CC ERG family, which is designated Herg4 (human erg related gene 4). The  
CC Herg4 polypeptides and polynucleotides are useful in the treatment of  
CC epilepsy, migraine, cell proliferation disorders, cancer, comportemental  
CC troubles, and to prevent or alter the effect of endogenous  
CC neurotransmitters and hormones. Antibodies against Herg4 are also useful  
CC for the treatment of cerebral, cardiac and renal ischemias, brain and  
CC cardiac diseases, inflammation, pain, and to mimic or antagonize the  
CC effect of endogenous neurotransmitters and hormones  
XX  
SQ Sequence 1083 AA;

Alignment Scores:  
Pred. No.: 0 Length: 1083  
Score: 5695.00 Matches: 1081  
Percent Similarity: 99.91% Conservative: 1  
Best Local Similarity: 99.82% Mismatches: 1  
Query Match: 0 Indels: 0  
DB: 3 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x AAY84835 (1-1083)

QY 1 ATGCCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCTGGACACCATCGCTACG 60  
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTGTGGGCAACGCCAGGTGGGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
QY 121 CCCGTGGTCTACTGCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGCAGCGGGCTGTGCTGCTCCTCTCTTTATGGGCCAGACACCATGAGTGTGCTCCGC 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCAACAAGAGTTCAAGGCTGAGCTGATCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGAGCGGGTCCCGTTCTGGTGTCTCTGATGTGATACCCATAAAGATGAGAAA 360  
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGGAGGTGGCTCTCTTCTTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGGCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGGATATGGCGGACCGATCC 480  
Db 141 GlyProAspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 160  
QY 481 AAGGCTTCAATGCCAACCGGGCGGAGCCGGCGCGTGTCTTACCATCTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAGCAGCCCAAGGGCAGACACAAGCTCAATAAGGGGTGTTGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCTGTTGCACTGT 660

Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220  
QY 661 GGGGCACTGAGAGCCACTGGGATGGCTTATCTCTGCTCGCCACACTCTATGTGGTGTCT 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTCCGCCCGCGGCCG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTTCATCTTGCATTTGACATTTGTGAATTTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTTCGCCCAAGTCCATTTGCCTC 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
QY 901 CACTACGTCAACACCTGGTTCCTGCTGCTGGATGTATCGAGCGCTGCCCTTTGACCTGCTA 960  
Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320  
QY 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCTGTCTTAC 1020  
Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340  
QY 1021 CGCCTGCTGCGCCTGCTTCCGGCGGTGACCGGTACTCGCAGTACAGCGCCGTGGTGTCTG 1080  
Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360  
QY 1081 ACATGCTCATGGCCGTGTTTCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTGTTTAC 1140  
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGTGCCTGAGATGGCTGGCTGCAG 1200  
Db 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400  
QY 1201 GAGCTGGCCCGCGACTGGAGACTCCCTACTACTGCTGGTGGCGGAGGCCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGGCTG 1320  
Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440  
QY 1321 GAGCTGCTGGCGCGCCGCTCGCTCGCAGCGCTACATCACCTCCCTCTACTTCGCACTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGCAGCCTCACGCGTGGGCTTCGGCAACCTGTCGCCCAACACGACGACACCGAGAAGATC 1440  
Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480  
QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACGCGGTGGTGTGGGAACGTG 1500  
Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPheGlyAsnVal 500  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTATACCAGCCGACCGCCGAC 1560  
Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520  
QY 1561 CTGCGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540  
QY 1621 TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGC 1680  
Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560  
QY 1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCTCTGCAGCTG 1740  
Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580

QY 1741 CCACCTGTTTGAGGGCGGCGAGCCGCGGCTGCCTGCGGCACTGTCTCTGGCCCTCGCGCCC 1800  
Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600  
QY 1801 GCCTTCTGCACGCCGGCGAGTAGCTACCTCATCCACCAAGCGATGCCCTGCAGGCGCTCTAC 1860  
Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTTGGCACCGTGCTCGCCATCCTAGGG 1920  
Db 621 PheValCysSerGlyPheMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640  
QY 1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGCGGGAGCAGGTGGTAAGGCCAATGCC 1980  
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGGCTACGTACTCGTCCCTGAGTGTCTGCAGCTGGCTGGCCTGCACGAC 2040  
Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680  
QY 2041 AGCCTTGCGTGTACCCCGAGTTTGCCCGCGCTTCAGTGTGCGCTCGAGGGAGCTC 2100  
Db 681 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 700  
QY 2101 AGCTACAACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCACTCCTGAGCGGC 2160  
Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACAATACCTTATGTCCACGCTGGAGGAGAAGGACAGATGGGAGCAGGGCCCCACG 2220  
Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCTGGCTGCACCTCC 2280  
Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760  
QY 2281 TCATCTCAGCTGCCAAGCTGCTATCCCCACGTGCAACAGCACCCCGCCTCGTCTAGGT 2340  
Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780  
QY 2341 GGCAGAGGAGGCCAGGCAGGCGAGGGGCTTTGAAGGCTGAGCTGGCCCTCTGCTCCC 2400  
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QY 2401 CCACGGGCCCTAGAGGGGTACGGCTGCCCCCATGCCATGGAATGTGCCCGCCAGATCTG 2460  
Db 801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu 820  
QY 2461 AGCCCCAGGGTAGTAGTGCAATGAAGACGGCTGTGGTCGGACCAAGCCCCAAGTTCTCT 2520  
Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840  
QY 2521 TTCCCGCTGGCCAGTCTGGCCCGGAATGTAGCAGAGCCCTCCCTGGACCAAGAGC 2580  
Db 841 PheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860  
QY 2581 GGCCTGCTCACTGTTCCCATGGGCCCGCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2640  
Db 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880  
QY 2641 CTTCCGGCAGGCGGTACAGAGCTGTTCAGAGCAGGTGTGCAGATCGGGGAGGACTGCAG 2700  
Db 881 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900  
QY 2701 TCACTTCGCCAGGCTGTGCAGCTTGTCTGCTGGCGCCCCACAGGGAGGTCCGTGCCCTCGG 2760  
Db 901 SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg 920  
QY 2761 GCATCGGAGAGGGCGCTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysLeu 940

QY 2821 GACACTGGGGCACTCCTCTACTGCTGCCTGCAGCCCCAGCTGGCTGTCTTGTAGTGGACT 2880  
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QY 2881 TGGCCCCACCCCTCGTCCGGGGCCTCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA 2940  
Db 961 TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980  
QY 2941 GCGTCTCAGAGTCCCCCTGGCCTCGAGCCACAGCTTCTTGACCTCCACCTCAGACTCA 3000  
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QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCACAGCACCCCTGCCCTCCCTCCTCCT 3060  
Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020  
QY 3061 TCTGAGGAAGGGCTAGGACTGGGCTCAGGGGCGCTGGCCTTGCCCTGGAGCCCCACAGCCTG 3120  
Db 1021 SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer 1040  
QY 3121 ACTGGAGAGCCCCACAGGCTCAGGGGCTCAGGGGCGCTGGCCTTGCCCTGGAGCCCCACAGCCTG 3180  
Db 1041 ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060  
QY 3181 GAGATGCTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGC 3240  
Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080  
QY 3241 ACAGGGGTC 3249  
Db 1081 ThrGlyVal 1083  
RESULT 9  
AAY77738  
ID AAY77738 standard; protein; 1080 AA.  
XX  
AC AAY77738;  
XX  
DT 19-MAY-2000 (first entry)  
XX  
DE Human ESK1 (hESK1) protein.  
XX  
KW ESK1; eag similar K+ channel; potassium channel associated disorder;  
KW neurological; Alzheimer's disease; anxiety; panic; autism; hyperactivity;  
KW obsessive-compulsive disorder; schizophrenia; Huntington's disease;  
KW epilepsy; cardiovascular; musculoskeletal; proliferative; cancer;  
KW ESK channel blocker; nootropic; neuroprotective; antidepressant;  
KW tranquilizer; neuroleptic; antiParkinsonian; cardiant; cytostatic;  
KW anticonvulsant.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 212..239  
FT /note= "potential transmembrane domain S1"  
FT Domain 259..277  
FT /note= "potential transmembrane domain S2"  
FT Domain 297..320  
FT /note= "potential transmembrane domain S3"  
FT Domain 329..349  
FT /note= "potential transmembrane domain S4"  
FT Domain 356..378  
FT /note= "potential transmembrane domain S5"  
FT Modified-site 418  
FT /note= "potential N-glycosylation site"  
FT Modified-site 425  
FT /note= "potential N-glycosylation site"  
FT Modified-site 433  
FT /note= "potential N-glycosylation site"  
FT Domain 449..468  
FT /note= "potential pore-forming P domain"  
FT Modified-site 467  
FT /note= "potential N-glycosylation site"



FT Domain 477..501 /note= "potential transmembrane domain S6"  
FT Modified-site 496 /note= "potential N-glycosylation site"  
FT Domain 601..668 /note= "putative cyclic nucleotide binding domain (cNBD)"  
XX WO200009534-A1.  
XX 24-FEB-2000.  
XX 13-AUG-1999; 99WO-US018556.  
XX 14-AUG-1998; 98US-0096570P.  
XX (ELAN-) ELAN PHARM INC.  
XX Forsayeth JR, Zhao BB;  
XX WPI; 2000-224270/19.  
DR N-PSDB; AAZ87712.  
XX Novel eag similar potassium channel polypeptide useful for treating  
PT various neurological, cardiovascular, musculoskeletal and proliferative  
PT disorders.  
XX Claim 3; Fig 1A-E; 52pp; English.  
XX This represents a eag similar K+ channel (ESK) polypeptide (hESK1). The  
CC hESK1 protein can be expressed by standard recombinant methodology. The  
CC ESK polypeptide, polynucleotides and antibodies are useful for treating  
CC and diagnosing various potassium channel associated disorders such as  
CC neurological disorders, e.g. Alzheimer's disease, depression, anxiety,  
CC panic, obsessive-compulsive disorders, attention deficit, epilepsy;  
CC hyperactivity disorders, autism, schizophrenia, Huntington's disease and  
CC Parkinson's disease, cardiovascular disorders, musculoskeletal disorders  
CC and proliferative disorders such as cancer. The ESK polynucleotide is  
CC also useful for synthesis of ESK and gene mapping. The polypeptide can be  
CC used in an assay to identify molecules such as synthetic drugs,  
CC antibodies, peptides or other molecules which have an effect on the  
XX activity of the ESK channel  
SQ Sequence 1080 AA;  
  
Alignment Scores:  
Pred. No.: 0 Length: 1080  
Score: 5688.00 Matches: 1080  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.41% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-965-830-1\_COPY\_6\_3257 (1-3252) x AAY77738 (1-1080)  
  
QY 10 ATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACGGCTTCGAC 69  
Db 1 MetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThrArgPheAsp 20  
  
QY 70 GGCACGCACAGTAACCTTCGTCTGGGCAACGCCAGGTGGCGGGCTCTCCCGTGGTC 129  
Db 21 GlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPheProValVal 40  
  
QY 130 TACTGCTCTGATGGCTTCCTGACCTCAGGGCTTCCTCCGGGCTGAGGTCAATGACCGG 189  
Db 41 TyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluValMetGlnArg 60  
  
QY 190 GGCTGTGCTGCTCCTTCCTTTATGGCCAGACACCATGAGCTCGTCCGCCAACAGATC 249  
Db 61 GlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArgGlnGlnIle 80  
  
QY 250 CGCAAGSCCTGGACGACACAGAGTTCAAGGCTGAGCTGATCCTGTACCGGAAGAGC 309  
Db 81 ArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyrArgLysSer 100

QY 310 GGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAAATGAGAAAGGGAGGTG 369  
Db 101 GlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLysGlyGluVal 120  
  
QY 370 GCTCTCTTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGGGCCCCGAC 429  
Db 121 AlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGlyGlyProAsp 140  
  
QY 430 AGATGGAAGGAGACAGGTGGTGGCCGGCCGCGATATGGCCGGGCACGATCCAAAGGTTTC 489  
Db 141 ArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSerLysGlyPhe 160  
  
QY 490 AATGCCAACCGCGGCGAGCCGGCCGTCTCTACACCTGTCCGGGCACCTGCAGAAAG 549  
Db 161 AsnAlaAsnArgArgArgSerArgAlaValLeuTyrHisLeuSerGlyHisLeuGlnLys 180  
  
QY 550 CAGCCCAAGGCAAGCACAGCTCAATAAGGGGTGTGGGGAGAAACCAAACCTTGCTT 609  
Db 181 GlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysProAsnLeuPro 200  
  
QY 610 GAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTTCATCCTGTGTCACTGTGGGCATG 669  
Db 201 GluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCysGlyAlaLeu 220  
  
QY 670 AGAGCCACCTGGGATGGCTTCATCTCTGCTCGCCACACTCTATGTGGCTGTCACTGTGCC 729  
Db 221 ArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaValThrValPro 240  
  
QY 730 TACAGCGTGTGTGAGCACAGACGGGAGCCAGTGCCGCCGGGGCCCCAGCGCTC 789  
Db 241 TyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyProProSerVal 260  
  
QY 790 TGTGACCTGGCGGTGGAGGTCTCTTCATCTTCATCTTGACATTTGCTGAATTTCCGTACCACA 849  
Db 261 CysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPheArgThrThr 280  
  
QY 850 TTCGTGTCCAAGTCGGGCCAGGTGGTGTGGTTCGCCAAAGTCCATTTGCTTCCACTACGTC 909  
Db 281 PheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeuHisTyrVal 300  
  
QY 910 ACCACCTGTTCTGTGGATGTCTCGAGCGCTGCCCTTTGACCTGTACATGCCTTC 969  
Db 301 ThrThrTrpPheLeuLeuAspValIleAlaLeuProPheAspLeuLeuHisAlaPhe 320  
  
QY 970 AAGGTCAACGTGTACTTCGGGGCCCATCTCTGAAGACGGTGGCTGTGCTGGCTGTG 1029  
Db 321 LysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeuArgLeuLeu 340  
  
QY 1030 CGCCTGCTTCGGCGGTGGACCGGTACTCGAGTACAGCCCGGTGGTGTGACACTGCTC 1089  
Db 341 ArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeuThrLeuLeu 360  
  
QY 1090 ATGGCCGTGTTCCGCTGTCTCGCGCACTGGGTGGCTGTGCTGTGTTTACATTGGCCAG 1149  
Db 361 MetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyrIleGlyGln 380  
  
QY 1150 CGGAGATCGAGAGCAGCAATCCGAGCTCCCTGAGATTGGTGGTGCAGGAGCTGGCC 1209  
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QY 1210 CGCCGACTGGAGACTCCCTACTACCTGGTGGCCGGAGCCAGCTGGAGGGAACAGCTCC 1269  
Db 401 ArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGlyAsnSerSer 420  
  
QY 1270 GGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCACCGGACGGGGCTGGAGCTGCTG 1329  
Db 421 GlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeuGluLeuLeu 440  
  
QY 1330 GGGGGCCCGTGGTGGCGAGCCCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTC 1389  
Db 441 GlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeuSerSerLeu 460

QY	1390	ACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACAGGACACCGAGAAAGATCTTCTCCATC	1449	Db	821	ValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSerPheArgVal	840
Db	461	ThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIlePheSerIle	480	QY	2530	GGCCAGTCTGGCCCGAATGTAGCAGCAGCCCTCCCTGGACCAGAGCGGCTGCTC	2589
QY	1450	TGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGGTGTGGAAACGTGACGGCCATC	1509	Db	841	GlyGlnSerGlyProGluCysSerSerSerProGlyProGlySerGlyLeuLeu	860
Db	481	CysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnValThraIle	500	QY	2590	ACTGTTCCCATGGGCCAGCGAGGCAAGAACACACAGACACACTGGACAAGTTCGGCAG	2649
QY	1510	ATCCAGCGCATGTACGCCCGCTTCTGTACACAGCGCAGCGCGACCTGGCGAC	1569	Db	861	ThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLysLeuArgGln	880
Db	501	IleGlnArgMetTyrAlaArgPheLeuTyrHisSerArgThrArgAspLeuArgAsp	520	QY	2650	GCGGTGACAGAGCTGTACAGCAGGTGCTGCAGATCGCGGAAGGACTGCAGTCACTTCGC	2709
QY	1570	TACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAG	1629	Db	881	AlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGlnSerLeuArg	900
Db	521	TyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGluTyrPheGln	540	QY	2710	CAGGCTGTGCAGCTTGTCTGGCGCCCCACAGGAGGGTCCGTGCCCTCGGGCATCGGA	2769
QY	1630	GCCACCTGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGCCTCCCTGCAC	1689	Db	901	GlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArgAlaSerGly	920
Db	541	AlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSerLeuProAsp	560	QY	2770	GAGGCGCGTGCAGCCAGCCAGCACTCCGGGCTTCTGCAGCCTCTGTGTGGACACTGGG	2829
QY	1690	GAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGTCTGCAGCTGCCACTGTTT	1749	Db	921	GluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysValAspThrGly	940
Db	561	GluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeuProLeuPhe	580	QY	2830	GCATCCTCTACTGCTGCAGCCCGCAGCTCCGGGCTTCTGTAGTGGGACTTGGCCCCAC	2889
QY	1750	GAGGCGCAGCGCGGTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCGCCCTTCTGC	1809	Db	941	AlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThrTrpProHis	960
Db	581	GluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgProAlaPheCys	600	QY	2890	CCTCGTCCGGGCGCTCCTCCCTCATGGCACCCCTGGCCCTGGGTCGCCCTCTGAGGTCAG	2949
QY	1810	ACGCCGGGAGTACCTCATCCACCAAGCGCATGCCCTGCAGGCGCTCTACTTGTCTGC	1869	Db	961	ProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProProAlaSerGln	980
Db	601	ThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyrPheValCys	620	QY	2950	AGTCCCCCTGGCCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCAGAGCCCCCT	3009
QY	1870	TCTGGTCCATGAGGTGCTCAAGGTGGCACCGTGTCCCATCTCTAGGGAAGGCGGAC	1929	Db	981	SerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSerGluProPro	1000
Db	621	SerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGlyLysGlyAsp	640	QY	3010	GCCTCAGGAGACCTCTGCTCTGAGCCAGCCAGCCCTGCCCTGCCCTCCTCTCTGAGGAA	3069
QY	1930	CTGATCGGCTGTAGCTGCCCGCGGGGAGGAGTGTAAGGCCAATGCCGACCTGAAG	1989	Db	1001	AlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProSerGluGlu	1020
Db	641	LeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAlaAspValLys	660	QY	3070	GGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGCCAGCTACCCAGCAGGAG	3129
QY	1990	GGGCTGACGTACTGCGTCTCTCAGTGTCTGAGCTGGCTGGCTGCACGACAGCCTGCG	2049	Db	1021	GlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSerThrGlyGlu	1040
Db	661	GlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAspSerLeuAla	680	QY	3130	CCCCCACCAGGTTCAGGGGCGCTGGCCCTGCCCTGGGACCCCGCCAGCCTGGAGTGTG	3189
QY	2050	CTGTACCCCGAGTTTGGCCCGCGCTTCTCAGTCTGCTGGCTCCGAGGGGAGCTCAGTAC	2109	Db	1041	ProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeuGluMetVal	1060
Db	681	LeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeuSerTyrAsn	700	QY	3190	CTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAAGGACAGGGGTC	3249
QY	2110	CTGGTGTGGGGAGGCTCTGCAGAGGTGGACACAGCTCCCTGAGCGGCGACAATACC	2169	Db	1061	LeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGlyThrGlyVal	1080
Db	701	LeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGlyAspAsnThr	720	RESULT 10			
QY	2170	CTTATGTCCACGCTGGAGGAGAGGAGACAGATGGGAGCAGGCGCCACCGTCTCCCA	2229	AA44904			
Db	721	LeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThrValSerPro	740	ID	AA44904	standard; protein; 1083 AA.	
QY	2230	GCCCCAGCTGATGAGCCCTCCAGCCCTGCTGTCTGCTGGCTGCACCTCTCATCTCA	2289	XX			
Db	741	AlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSerSerSer	760	XX	AC	AA44904;	
QY	2290	GCTGCCAAGCTGTATCCCCACGTCGAACAGCACCCCGGCTCTGCTAGTGGCAGAGGG	2349	DT	XX	18-MAY-2000 (first entry)	
Db	761	AlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGlyGlyArgGly	780	DE	DE	Monkey potassium channel molecule ERG-LP1.	
QY	2350	AGGCCAGGCAGGGCGGGCTTTGAAGCTGAGGCTGGCGCCCTCTGCTCCCGCAGGGCC	2409	XX	XX	Monkey; potassium channel molecule; ERG-like protein 1; ERG-LP1;	
Db	781	ArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaProProArgAla	800	KW	KW	neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;	
QY	2410	CTAGAGGGGTACGGTGCCTCCCATGCAATGCAATGCAATGCAATGCAATGCAATGCA	2469	KW	KW	neuroleptic; nootropic; treatment; CNS disorder; central nervous system;	
Db	801	LeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeuSerProArg	820	KW	KW	potassium channel mediated disorder; epilepsy; Alzheimer's disease;	
QY	2470	GTAGTAGATGGCATTGAAGACGGGTGTGGCTCGGACCGCCCAAGTTCTCTTCCGCGTG	2529	XX	XX	Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia.	
				OS	OS	Primates.	
				XX	XX	Key	Location/Qualifiers
				FT	FT	Modified-site	13. .16
				FT	FT	/note= "Casein kinase II phosphorylation site"	
				FT	FT	Modified-site	20. .23





Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGCAGCGGGCTGTGCTGCTCCTTATGGGCCAGACACAGTGAGCTCGTCCGC 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGAAGGCCCTGGACGAGCACAAAGAGTTCAAGCTGAGCTGATCCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATFACCCATAAAGAAATGAGAA 360  
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGAGGTGGCTCTCTTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGCCCGACAGATGGAAGGACAGGTGGTGGCGCGCGGATATGGCGGCGCATCC 480  
Db 141 GlyProAspArgTrpLysGluThrGlySerGlyArgArgTyrGlyArgAlaArgSer 160  
QY 481 AAAGGTTCAATGCCAAACCGCGCGGAGCGGGCGTGTCTACCACTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAAGCAGCCCAAGGGCAAGCAAGCTCAATAAGGGGTGTTGGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCTTATCCTGTTGCACTGT 660  
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220  
QY 661 GGGGCACTGAGACCCACTGGGATGGCTTCATCTGCTGCCACACTCTATGTGGTGTC 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGGAGCCAGTGCCTGCGCGCGCGCG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
QY 781 CCCAGCGTCTGTGACTGGCGCGTGGAGGTCTCTTCTATCCTTGACATTGTGTAATTTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTCTGTGTCCAAGTCGGGCCAGGTGGTGTGTTGCCCAAGTCCATTTGCCCTC 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValPheAlaProLysSerIleCysLeu 300  
QY 901 CACTACGTCACCACCTGTTCTGCTGATGTATCGCAGCGCTGCCCTTTGACCTGCTA 960  
Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320  
QY 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCTGTGCTG 1020  
Db 321 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 340  
QY 1021 CGCCTGTGCGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCCGCTGGTGTGCTG 1080  
Db 341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360  
QY 1081 ACACCTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTTTAC 1140  
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGTGCCTGAGATTGGCTGGTGCAG 1200  
Db 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400  
QY 1201 GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGCGGAGGCCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420

QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGGCAACGGGACGGGGCTG 1320  
Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440  
QY 1321 GAGCTGTGGCGGGCCGTCGCTGCGCAGCGCCTACATCACCTCCTCTACTTCGCACCTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGCAGCCTCACAGCGGTGGCTTCGGCAACGTGTCCGCCAACACGACACCGAGAGATC 1440  
Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480  
QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCGCTGATGACGCGGTGGTGTGGGAAACGTG 1500  
Db 481 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 500  
QY 1501 ACGGCGCATCATCCAGCGCATGTACGCCCGCTATCCCCAAGCCCCCTCAAGCAGCGCATG 1560  
Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520  
QY 1561 CTGCGCGACTACATCCCGCATCCACCGTATCCCCAAGCCCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540  
QY 1621 TACTTCCAGGCCACTGGGGGTGAACAATGGCATCGACACCCACCGAGCTGCTGCAGAGC 1680  
Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 560  
QY 1681 CTCCTTGACGAGCTGCGCGCAGACATCGCCCATGCACCTGCACAAGAGGTCTGCAGCTG 1740  
Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580  
QY 1741 CCACTGTTGAGSGCGCAGCCGCGGTGCTCGGGGCACTGTCTCTGGCCCTGCGGCC 1800  
Db 581 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 600  
QY 1801 GCCTTCTGCACGCGGGGAGTACCTCATCCACCAAGGCGATGCCCTGAGGCCCTCTAC 1860  
Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCCGCATCCTAGGG 1920  
Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640  
QY 1921 AAGGGGCACTGATCGGCTGTGAGCTGCCCCGCGGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGGTGACGTACTGCTGCTCCTGAGTGTCTGCAGCTGGCTGGCCTGCACGAC 2040  
Db 661 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 680  
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QY 2101 AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGACACAGATGGGAGCAGGCCCCACG 2160  
Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACAATACCTTATGTCCACGCTGGAGGAGAGACAGATGGGAGCAGGCCGCCACG 2220  
Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCCAGCCCCAGTGTATGAGCCCTCCAGCCCCCTGTCTCCCCCTGGCTGCACCTCC 2280  
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QY 2281 TCATCTCAGCTGCCAAGCTGTCTATCCCCACGTGCAACAGACCCCCGGCCTCGTCTAGGT 2340  
Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780



QY 181 ATGACGGGGCTGTGCCTGCTCCTTCCTTTATGGCCAGACACCAAGTGAAGTCTGTCCTCCG 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGACACAAGGATTCAAGGCTGAGCTGATCCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGACGGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360  
Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGAGGTGGCTCTCTTCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
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QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCGATATGGCCGGGCACGATCC 480  
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QY 481 AAAGGCTTCAATGCCAACCGGGCGGAGCGGGCGCTGCTCTACACCTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGCAGAACGAGCCCAAGGCAAGCACACAGCTCAATAAGGGGGTGTTTGGGAGAAACCA 600  
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QY 601 AACTTGCTGAGTACAAAGTAGCGGCCATCCGGAAGTGGCCCTTCATCCTGTGTGCACTGT 660  
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC 720  
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QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCCGAGTGGCCGCCCGCCCG 780  
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QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTTCATCCTTGACATTGTGTAATTTC 840  
Db 261 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 280  
QY 841 CGTACCACATTCTGTGTCCAAGTCGGGCCAGGTGGTGTGGCCCCAAAGTCCATTGCTC 900  
Db 281 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 300  
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Db 301 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 320  
QY 961 CATGCCCTCAAGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCCTGCTG 1020  
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QY 1021 CGCCTGCTGCGCCTGCTTCGCGGCTGGACCGGTACTCGCAGTACAGCGCGTGGTGTGCTG 1080  
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QY 1081 ACACCTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGTTCGCTGCTGCTGTTTAC 1140  
Db 361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 380  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG 1200  
Db 381 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 400  
QY 1201 GAGCTGGCCCGCGACTGAGAGACTCCCTACTACTTGGTGGGCCGGAGCCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420  
QY 1261 AACAGCTCCGGCCAGAGTGACAACCTGCAGCAGCAGCAGGCGCAACCGGACGGGGCTG 1320

Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440  
QY 1321 GAGCTGTGGGGCGCCGCTCGCTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACCTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGACGCTCACGAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGACACCGAGAAGATC 1440  
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QY 1441 TTCTCCATCTGCACCATGTCTATCGCGCCCTGATGCACGCGTGGTGTTTGGGAACGTG 1500  
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QY 1561 CTGCGCGACTACATCCGCGCATCCCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
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QY 1621 TACTTCCAGGCCACCTGGGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGC 1680  
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QY 1681 CTCCTGACGAGCTGCGCGCAGACATCGCCATCGACCTGCACAGGAGGTCTCTGCAGCTG 1740  
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QY 1741 CCACCTGTTGAGCGGCCAGCCGCGCTGCCTGCGGCACTGTCTCTGGCCCTGCGGCC 1800  
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Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGTCTCAAGGGTGGCACCGTGTCTGCCCATCTAGG 1920  
Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640  
QY 1921 AAGGGCGACCTGATCGGCTGTGAGTGGCCCGCGGAGCAGGTGTGTAAGGCCAATGCC 1980  
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGCTGACGTACTGCGTCTCTGACGTGTCTGACGTGGCTGGCTGCACGAC 2040  
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Db 701 SerTyrAsnLeuGlyAlaGlyGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACAATACCTTATGTCCACGCTGGAGGAGAGGAGACAGATGGGGAGCAGSGCCCCACG 2220  
Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTGTCCCCCTGGCTGCACCTCC 2280  
Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760  
QY 2281 TCATCCTCAGTGCACAAGCTGCTATCCCCACGTGCAACAGCACCCCGGCTCGTCTAGGT 2340  
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QY 2341 GGCAGAGGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCTCTGTCTCCC 2400



Db 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800  
QY 2401 CCACGGGCCCTAGAGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2460  
Db 801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu 820  
QY 2461 AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCCAAGTTCTCT 2520  
Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer 840  
QY 2521 TTCGGCTGGGCCAGTCTGGCCCCGGAATGTAGACAGCCCTCCCTCGGACAGAGAGC 2580  
Db 841 PheArgMetGlyGlnSerGlyProGluCysSerSerSerProSerProGlyProGluSer 860  
QY 2581 GGCCTGCTCACTGTTCCTCCATGGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2640  
Db 861 GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys 880  
QY 2641 CTTCCGCGAGGGTGACAGAGCTGTGCAGAGCAGGTGCTGCAGATCGGGGAAGACTGCAG 2700  
Db 881 LeuArgGlnAlaValMetGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln 900  
QY 2701 TCACCTCGCCAGGCTGTGCAGCTTGTCTCTGGCCCCCACAGGAGGCTCCGTGCCCTCGG 2760  
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QY 2761 GCATCGGGAGAGGGCCGTCGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
Db 921 AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal 940  
QY 2821 GACACTGGGGCATCCTCCTACTGCTGCAGCTGAGCCCCCAGCTGGCTCTGTGTGAGTGGACT 2880  
Db 941 AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr 960  
QY 2881 TGGCCCCACCTCGTCCGGGGCTCTCCCTCATGGCACCCCTGGCCCTGGGTCCCCCA 2940  
Db 961 TrpProHisProArgProGlyProProProLeuMetAlaProTrpProTrpGlyProPro 980  
QY 2941 GCGTCTCAGAGTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000  
Db 981 AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer 1000  
QY 3001 GAGCCCCCTGCTCAGGAGACCTCTGCTGTGAGCCACGACCCCTGCTCCCTCCTCCT 3060  
Db 1001 GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro 1020  
QY 3061 TCTGAGGAAGGGCTAGGACTGGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC 3120  
Db 1021 SerGluGluGlyAlaArgThrGlyProProGluProValSerGlnAlaGluAlaThrSer 1040  
QY 3121 ACTGGAGAGCCCCACAGGTCAGGGGCTGGCCTTGCCCTGGGACCCCCACAGCCTG 3180  
Db 1041 ThrGlyGluProProProValSerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu 1060  
QY 3181 GAGATGGTCTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGC 3240  
Db 1061 GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly 1080  
QY 3241 ACAGGGGTC 3249  
Db 1081 ThrGlyVal 1083

RESULT 12

ADB66795  
ID ADB66795 standard; protein; 1083 AA.  
XX  
XX  
AC ADB66795;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Monkey ERG-like protein 1 (ERG-LP1).  
XX  
KW Monkey; ERG potassium channel like protein; ERG-LP1; tumour; cytostatic.

XX  
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Macaca sp.  
US2003104429-A1.  
05-JUN-2003.  
27-JUN-2002; 2002US-00185867.  
21-JUL-1998; 98US-00119855.  
21-JUL-1999; 99US-00358383.  
(CURT/) CURTIS R A J.  
Curtis RAJ;  
WPI; 2003-687835/65.  
N-PSDB; ADB66794.  
New isolated nucleic acid, useful for producing a polypeptide and preparing a composition for diagnosing or treating diseases e.g., a tumor.

Claim 8; Fig 1; 122pp; English.

The present invention relates to novel ERG potassium channel like proteins, designated ERG-LPs, and the polynucleotide sequences encoding them. Also disclosed are: a host cell containing the polynucleotide, an antibody that selectively binds to the polypeptide, a method for producing the polypeptide, a method for detecting the presence of the polypeptide or the nucleic acid in a sample, a method for identifying a compound that binds to the polypeptide, a method for modulating the activity of the polypeptide, a method for identifying a compound that modulates the activity of the polypeptide, and a kit. The polynucleotide sequences are useful for producing the ERG-LP polypeptides. The ERG-LP polynucleotide and polypeptide sequences are useful for preparing a composition for diagnosing or treating diseases e.g. tumours. The present sequence represents monkey ERG-LP1.

Sequence 1083 AA;

Alignment Scores:

Pred. No.: 0 Length: 1083  
Score: 5675.00 Matches: 1078  
Percent Similarity: 99.63% Conservative: 1  
Best Local Similarity: 99.54% Mismatches: 4  
Query Match: 93.20% Indels: 0  
DB: 7 Gaps: 0

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x ADB66795 (1-1083)

QY 1 ATCCCGCCATCGGGGCTCTGCGCCCTCAGAACACCTTCTGGACACCATCGTACG 60  
Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCACGACAGTAACCTTCGTGCTGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGTC 180  
Db 41 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60  
QY 181 ATGCAGCGGGCTGTGCCTGCTCCTTCTCTTATGGGCCACAGACACCATCGTCCGC 240  
Db 61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAGGAGTTCAGGCTGAGCTGATCCTGTAC 300  
Db 81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGATGAGAAA 360

Db 101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 120  
QY 361 GGGAGGTGGCTCTTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 121 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 140  
QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCGATATGGCCGGCACGATCC 480  
Db 141 GlyProAspArgTrpLysGluThrGlySerGlyArgArgArgTyrGlyArgAlaArgSer 160  
QY 481 AAAGGCTTCAATGCCAACCGCGGCGGAGCCGGCCGTGCTCTACCACTGTCCGGGCAC 540  
Db 161 LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180  
QY 541 CTGAGAGAGAGCCCAAGGGCAAGCAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600  
Db 181 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 200  
QY 601 AACTTGGCTGAGTACAAAGTAGCCGGCATCCGGAAGTCGCGCTTCATCCTGTTGCACGTG 660  
Db 201 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 220  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC 720  
Db 221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCGAGTCGCGCCCGGCCCG 780  
Db 241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260  
QY 781 CCCAGGTCGTGACCTGGCCGTGGAGTCCTCTTCATCCTTGACATTGTCTGAATTC 840  
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QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG 1200  
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QY 1201 GAGCTGGCCCCGCGACTGGAGACTCCCTACTPACCTGGTGGCGCGGAGCGCAGCTGGAGGG 1260  
Db 401 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 420  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGCTG 1320  
Db 421 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 440  
QY 1321 GAGCTGCTGGGGCCCGCTCGCTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC 1380  
Db 441 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyriIleThrSerLeuTyrPheAlaLeu 460  
QY 1381 AGCAGCCTCACAGCGTGGGCTTCGGCAACGFTGTCCGCCAACACGACCGACCGAGAATC 1440  
Db 461 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 480

QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACCGGTGGTGTTTGGGAACGTG 1500  
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Db 501 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 520  
QY 1561 CTGCGCACTACATCCGCATCCACCGTATCCCCAAGCCCCCTCAAGCAGCGCATGTGGAG 1620  
Db 521 LeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 540  
QY 1621 TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGC 1680  
Db 541 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuGlnSer 560  
QY 1681 CTCCTTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCTCTGCAGCTG 1740  
Db 561 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 580  
QY 1741 CCACTGTTTGGGGCGCCAGCCCGGCTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCC 1800  
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QY 1801 GCCTTCTGCACGCCGGCGAGTACTCTCATCCACCAAGGGGATGCCCTGCAGGCCCTCTAC 1860  
Db 601 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 620  
QY 1861 TTTGTCTGCTCTGGTCCATGGAGTGCTCAAGGGTGGCACCGTGTCTGCCATCTTAGGG 1920  
Db 621 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 640  
QY 1921 AAGGGCAGCTGATCGGCTGTAGCTGCCCGCGGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 641 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 660  
QY 1981 GACGTGAAGGGCTGACGTACTGCTCTCTGCAGTGTCTGCAGCTGCTGGCTGCACGAC 2040  
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QY 2041 AGCCTTGGCTGTACCCCGAGTTTGCCTCCGCGCTTCAGTCGTGGCTCCGAGGGGAGCTC 2100  
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QY 2101 AGCTACAACCTGGGTCTGGGGAGGCTCTGCAGAGTGGACACAGCTCCCTGAGCGGC 2160  
Db 701 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 720  
QY 2161 GACAATACCTTATGTCCACGCTGGAGGAGAAGGAGACAGATGGGAGCAGGGCCCCACG 2220  
Db 721 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 740  
QY 2221 GTCTCCCGACGCCAGCTGATGAGCCCTCCAGCCCCCTGTCTCCCTGGCTGCACCTCC 2280  
Db 741 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 760  
QY 2281 TCATCCTCAGCTGCCAAGCTGTATCCCCACGTTCGAACAGCACCCCGGCCCTCGTCTAGGT 2340  
Db 761 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 780  
QY 2341 GGCAGAGGAGGCCAGGCAGGGCAGGGCTTTGAAGGCTGAGGCTGGCCCCCTCTGCTCCC 2400  
Db 781 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 800  
QY 2401 CCACGGCCCTAGAGGGCTACGGCTGCCCCCCCATGCCATGGAATGTGCCCCAGATCTG 2460  
Db 801 ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu 820  
QY 2461 AGCCCCAGGGTAGTAGTGGCATTGAAGACGGCTGTGGCTCGGACCGACCCCAAGTTCTCT 2520  
Db 821 SerProArgValValAspGlyIleGluAspGlyCysGlySeraspGlnProLysPheSer 840





Db 60 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 79  
QY 241 CAACAGATCCGCAAGGCCCTGGACGACACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 80 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 99  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360  
Db 100 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys 119  
QY 361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 120 GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly 139  
QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCGATATGCGCGGCACGATCC 480  
Db 140 GlyProaspArgTrpLysGluThrGlyGlyArgArgArgTyrGlyArgAlaArgSer 159  
QY 481 AAAGGCTTCAATGCCAACCGCGCGCGGAGCCGGCGCTCTACCACTGTCCGGGCAC 540  
Db 160 LysGlyPheAsnAlaasnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 179  
QY 541 CTGCAGAAGCAGCCCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTGGGGAGAAACCA 600  
Db 180 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro 199  
QY 601 AACTTGCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCGCTTCATCCTGTTGCACGTG 660  
Db 200 AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys 219  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGC 720  
Db 220 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 239  
QY 721 ACTGTGCCTACAGCGTGTGTGTGAGCACAGCAGGAGCCAGTCGCGCCCGCGGCCCG 780  
Db 240 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 259  
QY 781 CCCAGCGTGTGACCTGGCCGTGGAGGTCCTCTTCATCCTTGACATTGTGCTGAATTC 840  
Db 260 ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe 279  
QY 841 CGTACCAATTGCGTGTCCAAGTCGGGCCAGGTGGTGTTCGCCCAAAGTCCATTTGCCTC 900  
Db 280 ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu 299  
QY 901 CACTACGTACACCACCTGGTTCCTGTGCGATGTATCGCAGCGCTGCCTTTGACCTGCTA 960  
Db 300 HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu 319  
QY 961 CATGCCTTCAAGGTCAACGTGACTTCGGGGCCCATCTGCTGAAGACGGTGCCTGCTG 1020  
Db 320 HisAlaPheLysValAsnValTyrPheGlyAlaHisLeuLeuLysThrValArgLeuLeu 339  
QY 1021 CGCCTGCTGCGCCTGCTTCGCGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGCTG 1080  
Db 340 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 359  
QY 1081 ACACTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGTGCCTGCGTCTGTTTTAC 1140  
Db 360 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr 379  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATFGGCTGGCTGCAG 1200  
Db 380 IleGlyGlnArgGluIleGluSerSerGluSerGluLeuProGluIleGlyTrpLeuGln 399  
QY 1201 GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGCCGAGCCAGCTGGAGGG 1260  
Db 400 GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValGlyArgArgProAlaGlyGly 419  
QY 1261 AACAGCTCCGSCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAACCGGACGGGGCTG 1320

Db 420 AsnSerSerGlyGlnSerAspAsnCysSerSerSerGluAlaAsnGlyThrGlyLeu 439  
QY 1321 GAGCTGCTGGCGGCGCGTCCGTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC 1380  
Db 440 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyrPheAlaLeu 459  
QY 1381 AGCAGCCTCACAGCGTGGGCTTCGCAACGCTGTCCGCCAACACAGCAGCACCGAGAATC 1440  
Db 460 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 479  
QY 1441 TTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGGTGTGGAAACGTG 1500  
Db 480 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPheGlyAsnVal 499  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTTCTGTATCCACAGCCGACGCGAC 1560  
Db 500 ThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArgThrArgAsp 519  
QY 1561 CTGCGGCACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 520 GlnArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArgMetLeuGlu 539  
QY 1621 TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGC 1680  
Db 540 TyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeuLeuGlnSer 559  
QY 1681 CTCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAGGAGTCTTCGACGCTG 1740  
Db 560 LeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluValLeuGlnLeu 579  
QY 1741 CCCTGTTGAGCGGCCAGCCGCGCTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCC 1800  
Db 580 ProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAlaLeuArgPro 599  
QY 1801 GCCTTCTGCACGCCGGCGAGTACCTCATCCACCAAGCGATGCGCTGCAGGCCCTCTAC 1860  
Db 600 AlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGlnAlaLeuTyr 619  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTCGCCATCCTAGGG 1920  
Db 620 PheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAlaIleLeuGly 639  
QY 1921 AAGGGCACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 640 LysGlyAspLeuIleGlyCysGluLeuProArgArgGluGlnValValLysAlaAsnAla 659  
QY 1981 GACGTGAAGGGCTGACGTACTGCTCTGCTGCACTGTCTGCAGTGGCTGGCTGCACGAC 2040  
Db 660 AspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp 679  
QY 2041 AGCCTTCCGCTGTACCCCGAGTTTGCCTCCCGCTTCAGTCTGGCTCCGAGGGGAGCTC 2100  
Db 680 SerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArgGlyGluLeu 699  
QY 2101 AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACAGCTCCCTGAGCGGC 2160  
Db 700 SerTyrAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly 719  
QY 2161 GACATATACCTTATGTCCACGCTGGAGGAGAGGAGACAGATGGGAGCAGGGCCCCCAGC 2220  
Db 720 AspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGlnGlyProThr 739  
QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCTCCCTGGTGCACCTCC 2280  
Db 740 ValSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGlyCysThrSer 759  
QY 2281 TCATCTCAGCTGCCAAGCTGTATCCCCACGTTCGAACAGACCCCGGCTCGTCTAGGT 2340  
Db 760 SerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgProArgLeuGly 779  
QY 2341 GGCAGAGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCTCTGCTCCC 2400  
Db 780 GlyArgGlyArgProGlyArgAlaGlyAlaLeuLysAlaGluAlaGlyProSerAlaPro 799

QY	2401	CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGCCAATGTGCCCCCAGATCTG	2460
Db	800	ProArgAlaLeuGluGlyLeuArgLeuProProMetProTrpAsnValProProAspLeu	819
QY	2461	AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCCCAAGTTCTCT	2520
Db	820	SerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnProLysPheSer	839
QY	2521	TTCCGCGTGGGCCAGTCTGGCCCCGGAATGTAGCAGCAGCCCCCTCCCTGGACCCAGAGAGC	2580
Db	840	PheArgValGlyGlnSerGlyProGluCysSerSerProSerProGlyProGluSer	859
QY	2581	GGCCTGCTCACTGTTCCCCATGGGCCCCAGCGAGGCAAGAACACAGACACACTGGACAAG	2640
Db	860	GlyLeuLeuThrValProHisGlyProSerGluAlaArgAsnThrAspThrLeuAspLys	879
QY	2641	CTTCGGCAGGCGGTGACAGAGCTGTACAGACAGGTGCTGCAGATCGGGGAAGGACTGCAG	2700
Db	880	LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln	899
QY	2701	TCACTTCGCCAGGCTGTGCAGCTTGTCTCTGGGCCCCACAGGGAGGGTCCGTGCCCTCGG	2760
Db	900	SerLeuArgGlnAlaValGlnLeuValLeuAlaProHisArgGluGlyProCysProArg	919
QY	2761	GCATCGGAGAGGGGCCGTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG	2820
Db	920	AlaSerGlyGluGlyProCysProAlaSerThrSerGlyLeuLeuGlnProLeuCysVal	939
QY	2821	GACACTGGGCGATCTCTCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTTGTAGTGGACT	2880
Db	940	AspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeuSerGlyThr	959
QY	2881	TGGCCCCACCCCTCGTCCGGGGCCTCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA	2940
Db	960	TrpProHisProArgProGlyProProProLeuMetAlaProArgProTrpGlyProPro	979
QY	2941	CGGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA	3000
Db	980	AlaSerGlnSerSerProTrpProArgAlaThrAlaPheTrpThrSerThrSerAspSer	999
QY	3001	GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCCAGCACCCCTGCCTCCCTCCTCCT	3060
Db	1000	GluProProAlaSerGlyAspLeuCysSerGluProSerThrProAlaSerProProPro	1019
QY	3061	TCTGAGGAAGGGGCTAGGACTGGGCCCCGAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC	3120
Db	1020	SerGluGluGlyAlaArgThrGlyProAlaGluProValSerGlnAlaGluAlaThrSer	1039
QY	3121	ACTGGAGAGCCCCACAGGGTCAAGGGGCGCTGGCCTTGCCCTGGGACCCCCACAGCCTG	3180
Db	1040	ThrGlyGluProProProGlySerGlyGlyLeuAlaLeuProTrpAspProHisSerLeu	1059
QY	3181	GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAAGGC	3240
Db	1060	GluMetValLeuIleGlyCysHisGlySerGlyThrValGlnTrpThrGlnGluGly	1079
QY	3241	ACAGGGGTC	3249
Db	1080	ThrGlyVal	1082

## RESULT 14

AD55602

ID ADE55602 standard; protein; 1087 AA.

AC ADE55602;

XX DT 29-JAN-2004 (first entry)

XX  
DE Rat Protein CAA07586, SEQ ID NO 1421.

XX  
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS XX PN XX PD XX PF XX PR PR PR XX PA PA XX PI XX DR DR

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1: Page: 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp.wipo.int/pub/published/pct](http://ftp.wipo.int/pub/published/pct) sequences.

Sequence 1087 AA;

Alignment Scores:

Pred. No.:	0	Length:	1087
Score:	5428.00	Matches:	1039
Percent Similarity:	96.60%	Conservative:	11
Best Local Similarity:	95.58%	Mismatches:	33
Query Match:	89.14%	Indels:	4
DB:	7	Gaps:	2

US-09-965-830-1 COPY 6 3257 (1-3252) x ADE55602 (1-1087)

QY 1 ATGCCGGCCATGCGGGGCTCCTGGGCGCTCAGAACACCTTCCCTGGACACCATCGTACG 60

Qy	61	CGCTTCGACGGCACGACAGTAAC	TTCGTCTGGGCAACGCCAGGTGGGGGCTCTTC	1200
Db	21	ArgpHeAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe		40

QY	121	CCC	TGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC	180
Db	41	ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal	60	
QY	181	ATG	CAGCGGGGCTGTGCCTGCTCCTTCTCTTATGGCCAGACACCAAGTCAAGGCTGAGCTCGTCCGC	240
Db	61	MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg	80	
QY	241	CAA	CAGATCCGCAAGGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC	300
Db	81	GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr	100	
QY	301	CGA	AGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATATAAGAATGAGAAA	360
Db	101	ArgLysSerGlyLeuProPheTrpCysLeuLeuAspValIleProIleLysAsnGluLys	120	
QY	361	GGG	GAGTGGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGGAGG	420
Db	121	GlyGluValAlaLeuPheLeuValSerHisLysAspIleSerGluThrLysAsnArgGly	140	
QY	421	GGC	CCGACAGATGGAAGGAGACAGTGGTGGCCGGCCCGATATGGCCGGGCACGATCC	480
Db	141	GlyProAspAsnTrpLysGluArgGlyGlyGlyArgArgArgTyrGlyArgAlaGlySer	160	
QY	481	AAAG	GCTTCAATGCCAACCCGGCGGCGAGCGGGCCGTGCTCTACCACTGTCCGGGCAC	540
Db	161	LysGlyPheAsnAlaAsnArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis	180	
QY	541	CTG	CAGAAGCAGCCCAAGGCAAGCAACAAGCTCAATAAGGGGTGTTGGGAGAAACCA	600
Db	181	LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValPheGlyGluLysPro	200	
QY	601	AACT	TGCCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTCATCTGTGCACTGT	660
Db	201	AsnLeuProGluTyrLysValAlaAlaIleArgLysSerProPheIleLeuLeuHisCys	220	
QY	661	GGG	CACTGAGAGCCACCTGGGATGGCTTCATCTCTGCTCGCCACACTCTATGTGGCTGTC	720
Db	221	GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal	240	
QY	721	ACT	TGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCAGTGCCCGCCCGCGGCCCG	780
Db	241	ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro	260	
QY	781	CCC	AGCTGTGTGACCTGGCCGTGGAGGTCTCTTTCATCCTTGACATTGCTGAATTC	840
Db	261	ProSerValCysAspLeuAlaValGluValLeuPheIleLeuAspIleValLeuAsnPhe	280	
QY	841	CGT	ACCACATTCGTGCCAAGTCGGGCCAGGTGGTGTGTTGCCCAAAAGTCCATTTGCCTC	900
Db	281	ArgThrThrPheValSerLysSerGlyGlnValValPheAlaProLysSerIleCysLeu	300	
QY	901	CAC	TACGTCACCACTGGTTCTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGCTA	960
Db	301	HisTyrValThrThrTrpPheLeuLeuAspValIleAlaAlaLeuProPheAspLeuLeu	320	
QY	961	CAT	GCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGTCTGAAGACGGTGCGCCTGCTG	1020
Db	321	HisAlaPheLysValAsnValTyrValGlyAlaHisLeuLeuLysThrValArgLeuLeu	340	
QY	1021	CGC	TGTGCGCTGTTCCGCGGTGGACCGGTACTCGAGTACAGCGCCGTGGTGCTG	1080
Db	341	ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu	360	
QY	1081	ACA	TGCTCATGGCCGCTGTTCCGCCCTGCTCGCGCACTGGGTCCGCTCGCTGTTTAC	1140
Db	361	ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValTrpPheTyr	380	
QY	1141	ATT	GCCAGCGGGAGATCGACAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG	1200
Db	381	IleGlyGlnGlnGluIleGluAsnSerGluSerGluLeuProGluIleGlyTrpLeuGln	400	

QY	1201	GAGCTGGCCCGCCGACTGGAGACTCCCTACTACTCTGGTGGCCGAGGCCAGCTGGAGGG	1261
Db	401	GluLeuAlaArgArgLeuGluThrProTyrTyrLeuValSerArgSerProAspGlyGly	420
QY	1261	AACAGCTCCGGCCAGCTGACAACTGCAGCAGCAGC-----AGCGAGGCCAACGGG	1311
Db	421	AsnSerSerGlyGlnSerGluAsnCysSerSerSerGlyGlyGlySerGluAlaAsnGly	440
QY	1312	ACGGGGCTGGAGCTGCTGGCGGGCCCGTCGCTGCAGCGCCTACATCACCTCCCTCTAC	1371
Db	441	ThrGlyLeuGluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyr	460
QY	1372	TTGCGACTCAGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACC	1431
Db	461	PheAlaLeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThr	480
QY	1432	GAGAAAGATCTTCTCCATCTGCACCATGTCTATCGGCGCCCTGATGCACGCGTGGTGT	1491
Db	481	GluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValValPhe	500
QY	1492	GGGAAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACACAGCCGC	1551
Db	501	GlyAsnValThrAlaIleIleGlnArgMetTyrAlaArgArgPheLeuTyrHisSerArg	520
QY	1552	ACGCGCGACCTGCGGCACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGC	1611
Db	521	ThrArgAspLeuArgAspTyrIleArgIleHisArgIleProLysProLeuLysGlnArg	540
QY	1612	ATGCTGGAGTACTTCCAGGCCACCTGGCGCGTGAACAATGGCATCGACACACCAGCTG	1671
Db	541	MetLeuGluTyrPheGlnAlaThrTrpAlaValAsnAsnGlyIleAspThrThrGluLeu	560
QY	1672	CTGCAGAGCCTCCCTACGAGCTGGCGCGCAGACATCGCCATGCACCTGCACAAAGGAGTC	1731
Db	561	LeuGlnSerLeuProAspGluLeuArgAlaAspIleAlaMetHisLeuHisLysGluVal	580
QY	1732	CTGCAGCTGCCACTGTTTGAGCGGCCAGCGCGCTGCCTGCGGGCACTGTCTCTGGCC	1791
Db	581	LeuGlnLeuProLeuPheGluAlaAlaSerArgGlyCysLeuArgAlaLeuSerLeuAla	600
QY	1792	CTGCGGCCCGCCTTCTGCACGCCGGCGAGTACCTCATCCACCAGGCGATGCCCTGCAG	1851
Db	601	LeuArgProAlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGln	620
QY	1852	GCCCTCTACTTTGTCTGCTCTGGCTCCATGAGAGGTGCTCAAGGTGGCACCGTGCTCGCC	1911
Db	621	AlaLeuTyrPheValCysSerGlySerMetGluValLeuLysGlyGlyThrValLeuAla	640
QY	1912	ATCTAGGGAAGGCGACCTGATCGGCTGTGAGCTGCCCCCGGGGAGCAGGTGGTAAAG	1971
Db	641	IleLeuGlyLysGlyAspLeuIleGlyCysGluLeuProGlnArgGluGlnValValLys	660
QY	1972	GCCAAATGCCGAGTGAAGGGGCTGACGTACTGCGTCTCTGCAGTGTCTGCAGCTGGCTGC	2031
Db	661	AlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGly	680
QY	2032	CTGCACGACAGCCTTGCGTGTATCCCGAGTTGCCCCCGCTTCAGTCTGGCCTCCGA	2091
Db	681	LeuHisGluSerLeuAlaLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArg	700
QY	2092	GGGGAGCTCAGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCACTCC	2151
Db	701	GlyGluLeuSerTyrAsnLeuGlyAlaGlyGlyValSerAlaGluValAspThrSerSer	720
QY	2152	CTGAGCGGGCACAATACCTTATGTCCACGCTGGAGGAGAGGACAGATGGGAGCAG	2211
Db	721	LeuSerGlyAspAsnThrLeuMetSerThrLeuGluGluLysGluThrAspGlyGluGln	740
QY	2212	GGCCCCACGGTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTCTCCCTGGC	2271
Db	741	GlyHisThrIleSerProAlaProAlaAspGluProSerSerProLeuLeuSerProGly	760
QY	2272	TGCACCTCTCATCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCT	2331



Db 761 CysThrSerSerSerAlaAlaLysLeuLeuSerProArgArgThrAlaProArgPro 780  
QY 2332 CGTCTAGGTGGCAGGAGGAGCCAGGCAGGGGGCTTTGAAGGCTGAGGCTGGCCCC 2391  
Db 781 ArgLeuGlyGlyArgGlyArgProSerArgAlaGlyValLeuLysProGluAlaGlyPro 800  
QY 2392 TCTGCTCCCCCGGCCCCCTAGAGGGGCTACGGCTGCCCCCCCATGCCATGCCAATGTGCC 2451  
Db 801 SerAlaHisProArgThrLeuAspGlyLeuGlnLeuProProMetProTrpAsnValPro 820  
QY 2452 CCAGATCTGAGCCCCAGGGTAGTAGATGGCAATTGAAGACGGCTGTGGCTCGGACCCAGCCC 2511  
Db 821 ProAspLeuSerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnHis 840  
QY 2512 AAGTTCTCTTTCCGCTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTCGGA 2571  
Db 841 LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGly 860  
QY 2572 CCAGAGAGCGGCTGCTCACTGTTCCCATGGGCCAGCGAGGCAAGGAACACAGACACA 2631  
Db 861 ThrGluSerGlyLeuLeuThrValProLeuValProSerGluAlaAlaArgAsnThrAspThr 880  
QY 2632 CTGGACAAGCTTCGGCAGGCGGTGACAGAGTGTCTCAGAGCAGGTGTGCGATCGCGGAA 2691  
Db 881 LeuAspLysLeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGlu 900  
QY 2692 GGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTGGGCCCCACAGGAGGAGGTCCG 2751  
Db 901 GlyLeuGlnSerLeuArgGlnAlaValGlnLeuLeuValProGlnGlyGluGln 920  
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RESULT 15  
AAY44907  
ID AAY44907 standard; protein; 1107 AA.  
XX  
AC AAY44907;  
XX

DT 18-MAY-2000 (first entry)  
XX Human potassium channel molecule ERG-LP2 full-length protein.  
XX Human; potassium channel molecule; ERG-like protein 2; ERG-LP2;  
KW neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;  
KW neuroleptic; nootropic; treatment; CNS disorder; central nervous system;  
KW potassium channel mediated disorder; epilepsy; Alzheimer's disease;  
KW Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia;  
KW chromosome 3p21.3-24.3.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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PN W0200005346-A1.

XX 03-FEB-2000.

PF 21-JUL-1999; 99WO-US016752.

PR 21-JUL-1998; 98US-00119855.

PA (MILL-) MILLENNIUM PHARM INC.

PI Curtis RAJ;

DR WPI; 2000-182682/16.  
DR N-PSDB; AAZ50455.

XX Novel gene encoding potassium channel molecule useful in treating central nervous system disorders such as Alzheimer's disease, multiple sclerosis, and schizophrenia.

PS Example 1; Fig 8; 144pp; English.

XX The present sequence is a full-length ERG-like protein 2 (ERG-LP2) which is a member of ERG potassium channel family. This sequence is a result of additional sequencing of clone jlhbaa042h05 which was obtained from human brain library. ERG-LP2 gene is mapped to human chromosome 3p21.3-24.3, between markers WI-4218 and RP-L15\_1. It is predominantly expressed in the brain. The protein functions as a potassium channel modulator and has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant, neuroleptic and nootropic activities. The present sequence is useful for treating several potassium channel mediated disorders (CNS disorders) such as Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy, depression, schizophrenic disorders and amnesia

XX Sequence 1107 AA;

Alignment Scores:

Pred. No.: 8.44e-154 Length: 1107

Score: 2529.50 Matches: 559  
Percent Similarity: 60.24% Conservative: 150  
Best Local Similarity: 47.49% Mismatches: 267  
Query Match: 41.54% Indels: 201  
DB: 3 Gaps: 27

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x AAY44907 (1-1107)

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QY 61 CGTTTCGACGGCACGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGTATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60  
QY 181 ATGCAGCGGGCTGTGCCTGCTCCTTCTCTTATGGGCCAGACACCAGTGAGTCTGTCCTGC 240  
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QY 481 ---AAAGGCTTCAATGCCAACCGCGCGGGAGCGCGCGTCTCTACACCTGTCCGGG 537  
Db 157 GlyThrHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176  
QY 538 CACCTGCAGAAGAGCCCCAAGGGCAAGCACAGCTCAATAAGGGGTGTTGGGGAGAAA 597  
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QY 718 GTCACCTGCGCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCGCCCGCGGC 777  
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QY	2965	CGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTC	3024
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Search completed: September 1, 2004, 16:05:29  
Job time : 474.5 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 14:38:36 ; Search time 161 Seconds  
(without alignments)  
11209.319 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3245.8	99.8	3249	4	US-09-343-494-2 Sequence 2, Appli
3	3218	99.0	3857	4	US-09-336-643A-19 Sequence 19, Appli
4	3156	97.0	3355	4	US-09-358-383C-1 Sequence 1, Appli
5	3153	97.0	3249	4	US-09-358-383C-3 Sequence 3, Appli
6	2664.8	81.9	3715	4	US-09-600-776-9 Sequence 9, Appli
7	884.8	27.2	3064	4	US-09-600-776-5 Sequence 5, Appli
8	869.8	26.7	3736	4	US-09-600-776-10 Sequence 10, Appli
9	844.4	26.0	870	4	US-09-358-383C-9 Sequence 9, Appli
10	844.4	26.0	1132	4	US-09-358-383C-7 Sequence 7, Appli
11	761.2	23.4	3321	4	US-09-358-383C-17 Sequence 17, Appli
12	761.2	23.4	5107	4	US-09-358-383C-15 Sequence 15, Appli
13	572.8	17.6	1626	4	US-09-358-383C-6 Sequence 6, Appli
14	572.8	17.6	2694	4	US-09-358-383C-4 Sequence 4, Appli
15	572.8	17.6	5955	4	US-09-358-383C-14 Sequence 14, Appli
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19	342.8	10.5	3950	3	US-09-226-012-3 Sequence 3, Appli
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23	281.2	8.6	3083	4	US-09-694-777A-2 Sequence 2, Appli
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ALIGNMENTS

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; Sequence 1, Application US/09600776  
; Patent No. 6326168  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/600,776  
; CURRENT FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-011434  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
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US-09-600-776-1

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QY 1621 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCCGAGCTGTGCAGAGC 1680  
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QY 2461 AGCCCCAGGGTAGTAGTGGCATTTGAAGACGGCTGTGGCTCGGACCGGCCAAGTTCTCT 2520  
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QY	2581	GGCCTGCTCACTGTTCCCCATGGGCCACGCGAGGCAAGGAACACAGACACACTGGACAAG	2640
Db	2586	GGCCTGCTCACTGTTCCCCATGGGCCACGCGAGGCAAGGAACACAGACACACTGGACAAG	2645
QY	2641	CTTCGGCAGGCGGTGACAGAGCTGTCAAGACAGGTGCTGCAGATGCGGGAAGGACTGCAG	2700
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QY	3241	ACAGGGTCTGA	3252
Db	3246	ACAGGGTCTGA	3257

RESULT 2  
US-09-343-494-2  
; Sequence 2, Application US/09343494  
; Patent No. 6413741  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy J.  
; APPLICANT: Wickenden, Alan  
; APPLICANT: ICAgen, Incorporated  
; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit  
; FILE REFERENCE: 018512-001320US  
; CURRENT APPLICATION NUMBER: US/09/343,494  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: US 60/091,469  
; EARLIER FILING DATE: 1998-07-01  
; EARLIER APPLICATION NUMBER: US 60/116,621  
; EARLIER FILING DATE: 1999-01-21  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 2

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; LENGTH: 3249
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3249)
; OTHER INFORMATION: hElk
US-09-343-494-2

Query Match      99.8%; Score 3245.8; DB 4; Length 3249;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGCTGAGGTC 180
Db 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGCTGAGGTC 180

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RESULT 3

US-09-336-643A-19

; Sequence 19, Application US/09336643A

; Patent No. 6399761

; GENERAL INFORMATION:

; APPLICANT: Miller, Andrew P.

; APPLICANT: Curran, Mark Edward

; APPLICANT: Hu, Ping

; APPLICANT: Rutter, Marc

; APPLICANT: Wang, Jian-Wang

; TITLE OF INVENTION: No. 6399761el Human Potassium Channels

; FILE REFERENCE: SEQ-15P

; CURRENT APPLICATION NUMBER: US/09/336,643A

; CURRENT FILING DATE: 1999-06-18

; PRIOR APPLICATION NUMBER: 60/076,687

; PRIOR FILING DATE: 1998-08-07

; PRIOR APPLICATION NUMBER: 60/116,448

; PRIOR FILING DATE: 1999-01-19

; PRIOR APPLICATION NUMBER: PCT/US99/03826

; PRIOR FILING DATE: 1999-02-22

; NUMBER OF SEQ ID NOS: 87

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 3857

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (249)...(3495)

; OTHER INFORMATION: K+Hnov14

US-09-336-643A-19

Query Match 99.0%; Score 3218; DB 4; Length 3857;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3244; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

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QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180

Db 366 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 425

QY 181 ATGCAGCGGGGCTGTGCCCTGCTCCTTTATGGGCAGACACCAAGTGTGAGCTGATCCTGTAC 240

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Db 1146 CACTACGTCAACACCTGGTTCTGCTGGATGTCTATCGCAGCGTGCCTTTTGACCTGCTA 1205

QY 961 CATGCCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCTGCTG 1020

Db 1206 CATGCCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCTGCTG 1265

QY 1021 CGCTGTGCTGCGCTGCTTCGGCGGTGGACCGGTACTCGCAGTACAGCGCCGTGGTGTG 1080

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QY 1081 AACTGTCTATGGCGGTGTTCGCCCTGCTCGCGACTGGGTGCGCTGCGTCTGGTTTAC 1140

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Db 1386 ATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGGCTGCAG 1445

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Db 1986 CCACCTGTTGAGCGGCCAGCCCGCGCTGCTGCGGGCACTGCTGTCGCCCTGCGGCC 2045  
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QY 2041 AGCCTTGCGCTGTACCCCGAGTTTGGCCCGCGCTTTCAGTCTGTCGCTCCGAGGGGAGCTC 2100  
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Db 2766 TTCCGCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGC 2825  
QY 2581 GGCCTGCTCACTGTTCCCATGGGCCAGGAGGAGGAACACAGACACACTGGACAAG 2640  
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QY 2641 CTTCGGCAGGCGGTGACAGAGCTGTGAGCAGAGTGTGTCAGATGCGGGAGGACTGCGAG 2700  
Db 2886 CTTCGGCAGGCGGTGACAGAGCTGTGAGCAGAGTGTGTCAGATGCGGGAGGACTGCGAG 2945  
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Db 3066 GACACTGGGGCATCCTCCTACTGCTGTCAGCCCCCAGCTGGCTGTCTTGTAGTGGGACT 3125  
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QY 3001 GAGCCCTCTCAGAGACTCCCCCTGGCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCA 3060  
Db 3246 GAGCCCTCTCAGAGACTCCCCCTGGCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCA 3305  
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QY 3121 ACTGAGAGCCCCCACCAGGGTCAAGGGGCTGGCCCTTGGCCCTGGGACCCCCACAGCCTG 3180  
Db 3366 ACTGAGAGCCCCCACCAGGGTCAAGGGGCTGGCCCTTGGCCCTGGGACCCCCACAGCCTG 3425  
QY 3181 GAGATGCTGCTTATTGGCTGCCATGGCTGTGGCAGCTGCGACAGTCCAGTGGAGGAGGAGGC 3240  
Db 3426 GAGATGCTGCTTATTGGCTGCCATGGCTGTGGCAGCTGCGACAGTCCAGTGGAGGAGGAGGC 3485  
QY 3241 ACAGGGGTCTGA 3252  
Db 3486 ACAGGGGTCTGA 3497

RESULT 4

US-09-358-383C-1  
; Sequence 1, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358,383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3355  
; TYPE: DNA  
; ORGANISM: Macaca sp.  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: (104)..(3352)									
US-09-358-383C-1									
Query Match 97.0%; Score 3156; DB 4; Length 3355;									
Best Local Similarity 98.2%; Pred. No. 0;									
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;									
QY	1	ATGCCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCTCGACACCATCGCTACG	60						
Db	104	ATGCCGGCCATGCGGGCCCTCCTGGCGCCGAGAACACCTTCTCGACACCATCGCTACG	163						
QY	61	CGTTTCAGCGGCACGCACAGTAACTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC	120						
Db	164	CGTTTCAGCGGCACGCACAGTAACTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC	223						
QY	121	CCCCTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC	180						
Db	224	CCCCTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC	283						
QY	181	ATGCAGCGGGCTGTGCCCTGCTCCTTCTCTTTATGGGCCAGACACCACTCGTCCGC	240						
Db	284	ATGCAGCGGGCTGTGCCCTGCTCCTTCTCTTTATGGGCCAGACACCACTCGTCCGC	343						
QY	241	CAACAGATCCGCAAGCCCTGGACGAGCAACAAGAGTTCAAGGCTGAGCTGATCCTGTAC	300						
Db	344	CAACAGATCCGCAAGCCCTGGACGAGCAACAAGAGTTCAAGGCTGAGCTGATCCTGTAC	403						
QY	301	CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTATACCCATAAAGAATGAGAA	360						
Db	404	CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTATACCCATAAAGAATGAGAA	463						
QY	361	GGGAGGTGGCTCTCTTCTTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG	420						
Db	464	GGGAGGTGGCTCTCTTCTTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG	523						
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGCGATATGGCCGGCACGATCC	480						
Db	524	GGCCCTGACAGATGGAAGGAGACAGGTAGTGGCCGCGCGGATATGGCCGGCACGATCC	583						
QY	481	AAAGGCTTCAATGCCAACCGCGCGGAGCCGGCCGTGCTTACCACCTGTCCGGGCAC	540						
Db	584	AAAGGCTTCAATGCCAACCGCGCGGAGCCGGGCTGIGCTTACCACCTGTCCGGGCAC	643						
QY	541	CTGCAGAAAGCAGCCCAAGGCAAGCAAGCTCAATAAGGGGTGTTTGGGAGAAACCA	600						
Db	644	CTGCAGAAAGCAGCCCAAGGCAAGCAAGCTCAATAAGGGGTGTTTGGGAGAAACCA	703						
QY	601	AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCCCTCATCCTGTGCACTGT	660						
Db	704	AACTTGCCTGAGTACAAAGTAGCTGCCATCCGGAAGTCGCCCCCTCATCCTGTGCACTGT	763						
QY	661	GGGGCACTGAGAGCCACTGGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC	720						
Db	764	GGGGCGCTGAGGGCCACCTGGGATGGCTTCATCCTGCTCGCCACGCTCTATGTGGCTGTC	823						
QY	721	ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCAGTGCCGCCCGCGGCCCG	780						
Db	824	ACCGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCAGTGCCGCCCGCGGCCCA	883						
QY	781	CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCACTCCTTGACATTGTGCTGAATTC	840						
Db	884	CCCAGCGTCTGTGACCTGGCTGTGGAGGTCTCTTCACTCCTTGACATTGTGCTGAATTC	943						
QY	841	CGTACCACATTGCTGTCCAAAGTCGGGCCAGGTGGTGTGCTGCTGACATTGTGCTGAATTC	900						
Db	944	CGTACCACATTGCTGTCCAAAGTCGGGCCAGGTGGTGTGCTGCTGACATTGTGCTGAATTC	1003						
QY	901	CACTACGTCAACCACCTGGTCTCTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA	960						
Db	1004	CAC'TACGTCAACCACCTGGTCTCTGTGATGTATCGCAGCGCTGCCCTTTGACCTGCTG	1063						
QY	961	CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGTGAAGACGGTGCCTGCTG	1020						
Db	2144	AGCCTTGGCTCTACCCCCGAGTTTGGCCCCGCGCTTCAGCCGTGGCCTCCGAGGGGAGCTC	2203						
Db	1064	CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCACCTGTCTGAAGACGGTGCCTGCTG	1123						
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QY	1081	ACACTGCTCATGGCCGTGTTCCGCTGCTGCGCACCTGGTGCCTGCTGCTGTTTAC	1140						
Db	1184	ACACTGCTCATGGCCGTGTTTGCCTGCTTGGCACCTGGTTCGCTGCTGCTGTTTAC	1243						
QY	1141	ATTGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCCTGAGATTGGCTGCAG	1200						
Db	1244	ATTGCTCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCCTGAGATTGGCTGCAG	1303						
QY	1201	GAGTGGCCCGCCGACTGGAGACTCCCTACTACTACCTGGTGGCGGAGCCAGCTGGAGG	1260						
Db	1304	GAGTGGCCCGCCGACTGGAGACCCCTACTACTTGGTGGSCCGAGACCAGCCGAGGG	1363						
QY	1261	AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTG	1320						
Db	1364	AACAGCTCTGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTG	1423						
QY	1321	GAGTGTGGGGCGGCGCTCGTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC	1380						
Db	1424	GAGTGTAGGGCGGCGGCTCGTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC	1483						
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Db	1484	AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGGACACTGAGAAGATC	1543						
QY	1441	TTCTCCATCTGCACCATGTCTCATCGGCGCCCTGTATGCAAGCGGTGGTGTGGGAACGTG	1500						
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Db	1604	ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCCGACCGCGGAC	1663						
QY	1561	CTGGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1620						
Db	1664	CTGGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG	1723						
QY	1621	TACTTCCAGGCCACCTGGCGGTGAACATGGCATCGACACCAACCGAGTGTGCAAGAC	1680						
Db	1724	TACTTCCAGGCCACCTGGCGGTGAACATGGCATCGACACCAACCGAGTGTGCAAGAC	1783						
QY	1681	CTCCCTGACGAGCTGCGCGAGACATCGCCATGCACTGCAACAAGGAGGTCTGCAAGCTG	1740						
Db	1784	CTCCCTGACGAGCTGCGCGAGACATCGCCATGCACTGCAACAAGGAGGTCTGCAAGCTG	1843						
QY	1741	CCACTGTTTGAAGCGCGCAGCCCGGCTGCTGCGGCACTGTCTCTGGCCCTGCGGCC	1800						
Db	1844	CCGCTGTTTGAAGCAGCAGCCCGGCTGCTGCGGCACTGTCTCTGGCCCTGCGGCC	1903						
QY	1801	GCCTTCTGCACCGCGCGAGTACCTCATCCCAAGGCGATGCCCTGCAGGCCCTCTAC	1860						
Db	1904	GCCTTCTGCACCGCGCGAGTACCTCATCCCAAGGCGATGCCCTGCAGGCCCTCTAC	1963						
QY	1861	TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTTGGCACCGTGTCCCATCTAGGG	1920						
Db	1964	TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTTGGCACCGTGTCCCATCTAGGG	2023						
QY	1921	AAGGGCAGCCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTGAAGCCCAATGCC	1980						
Db	2024	AAGGGTGAACCTGATCGGCTGTGAGCTGCCCGGAGGAGCAGGTGGTGAAGGCCCAACGCC	2083						
QY	1981	GACGTGAAGGGGTGACGTACTGCGTCTGCAGTGTCTGCAGTGGTGGCTGCACGAC	2040						
Db	2084	GATGTGAAGGGGTGACGTACTGCGTCTCTGAGTGTCTGCAGTGGTGGCTGCACGAC	2143						
QY	2041	AGCCTTGGCTGTACCCCGAGTTTGGCCCGCGCTTCAGTGTGGCTCCGAGGGGAGCTC	2100						
Db	2144	AGCCTTGGCTGTACCCCGAGTTTGGCCCGCGCTTCAGCCGTGGCCTCCGAGGGGAGCTC	2203						



QY 2101 AGCTACAACTGGTGTGGGGAGGCTCTGCAGAGGTGGACACACAGCTCCCTGAGCGC 2160  
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QY 2161 GACAATACCTTATGTCCACGCTGGAGGAGAGGAGACAGATGGGAGCAGGCCCCACG 2220  
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QY 2281 TCATCTCAGCTGCCAAGCTGTATCCCCACGTCGAAACAGACACCCCGGCTCTGTAGGT 2340  
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QY 2384 TCATCTCGCTGCCAAGCTGTATCCCCACGTCGAAACAGACACCCCGGCTCTGTAGGT 2443  
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QY 2341 GGCAGAGGAGGCCAGGCGAGGCGGGCTTTGAAGGCTGAGGCTGGCCCTCTGTCTCC 2400  
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QY 2444 GGCAGAGGAGACCAGGCGAGGCGGGCTTTGAAGGCTGAGGCTGGCCCTCTGTCTCC 2503  
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QY 2401 CCACGGGCCCTAGAGGGCTACGGCTGCCCCCCCATGCTGCAATGTGCCCCAGATCTG 2460  
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QY 2624 TTCCGATGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAAGAGT 2683  
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QY 2684 GGCCTGTCACTGTTCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2743  
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RESULT 5

US-09-358-383C-3  
; Sequence 3, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358,383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 3249  
; TYPE: DNA  
; ORGANISM: Macaca sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3249)  
US-09-358-383C-3

Query Match 97.0%; Score 3153; DB 4; Length 3249;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 3189; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGCGGGCCATGCGGGGCTCTCTGGCGCTCAGAACACCTTCTGACACCATCGCTACG 60  
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QY 1 ATGCGGGCCATGCGGGGCTCTCTGGCGCTCAGAACACCTTCTGACACCATCGCTACG 60  
Db |||||  
QY 61 CGTTTCGACGGCACGCACAGTAATCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db |||||  
QY 61 CGTTTCGACGGCACGCACAGTAATCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db |||||  
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCAGGGGCTTCTCCGGGCTGAGGTC 180  
Db |||||  
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCAGGGGCTTCTCCGGGCTGAGGTC 180  
Db |||||  
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QY 181 ATGACGGGGCTGTGCTGCTCTCTCTTTATGGCCAGACACAGTGTGCTCGC 240  
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RESULT 6

US-09-600-776-9

; Sequence 9, Application US/09600776

; Patent No. 6326168

; GENERAL INFORMATION:

; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: A novel potassium channel protein

; FILE REFERENCE: Y9903-PCT

; CURRENT APPLICATION NUMBER: US/09/600,776

; CURRENT FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: JP P1998-011434

; PRIOR FILING DATE: 1998-01-23

; PRIOR APPLICATION NUMBER: JP P1998-346198

; PRIOR FILING DATE: 1998-12-04

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9

; LENGTH: 3715

; TYPE: DNA

; ORGANISM: Rattus sp.

US-09-600-776-9

Query Match 81.9%; Score 2664.8; DB 4; Length 3715;  
Best Local Similarity 89.0%; Pred. No. 0;  
Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;

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QY 61 CGCTTCGACGGCACGCACAGTAACCTTCGTGCTGGGCAACGCCCAGGTGGCGGGCTCTC 120  
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QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGGCTTCTCCCGGGCTGAGGTC 180  
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RESULT 7  
US-09-600-776-5  
; Sequence 5, Application US/09600776  
; Patent No. 6326168  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein

; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/600,776
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: JP P1998-011434
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 3064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(3057)
US-09-600-776-5

Query Match 27.2%; Score 884.8; DB 4; Length 3064;
Best Local Similarity 65.5%; Pred. No. 3.1e-177;
Matches 1408; Conservative 0; Mismatches 622; Indels 120; Gaps 3;

QY 1 ATGCCGGCCATCGGGCCCTCCTGGCGCCTCAGAACACCTTCTCTGGACACCATCGCTACG 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CGCTTCGACGGCACAGTAACCTTCGTGCTGGGCAAGCCAGGTGGGGGCTCTTC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 64 CGTTTTCGCGAACGACAGCAACTTCTGCTGGCCCAACGACAGGGCACAGGGGCTTT 123
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTACTCACGGGCTTCTCCGGGCTGAGTTC 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124 CCCATCGTCTACTGCTCCGACGGCTTCTGCGAGCTCACAGGCTACGGTCGACCGAGTTC 183
QY 181 ATGCAGCGGGGCTGTGCTCTCTCTCTTTATGGCCAGACACCACTGAGTCTGTCGCG 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 184 ATGCAGAAAGACCTGCAGCTGCCGTTTCTCTACGGCCAGAGACCACTGAGCCAGCCCTG 243
QY 241 CAACAGATCCGCAAGCCCTGGACGAGCAACAGGATTCAGGCTGAGCTGATCTGTAC 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 244 CAGCGTCTGCACAAAGCCCTGGAGGGCCACAGAGACACCGGCTGAAATCTGCTTCTAC 303
QY 301 CGGAAGAGCGGGTCCCGTCTCTAGTCTCTCACAGACATC-----AGCGAAACCAAGAAC 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 304 CGCAAGGATGGCTCAGCCCTTTGGTGCCTCTCGACATGATGCCCATCAAGAAATGAGATG 363
QY 361 GGGGAGGTGGTCTCTCTCTAGTCTCTCACAGACATC-----AGCGAAACCAAGAAC 414
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 364 GGGGAGGTGCTGCTCTCTCTTTTCAAGGATATCACTCAGAGTGAAGCCAGGA 423
QY 415 CGAGGGGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGGCGGTGCTCTACCACTGTCC 474
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 CTTGGCCCCCAAGGAGCGCGGGGACAGTAATCACGAAACTCCCTTGTGTAGAAAGGGA 483
QY 475 CGATCCAAAGGCTTCAATGCCAACCGGCGGCGAGCCGGCGGTGCTCTACCACTGTCC 534
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 484 GCCACCTGGAAATTTCCGCTCTGCCAGAAGACGGAGCCGTAATGCTCTACCGACTGACC 543
QY 535 GGGCACCTGCAGAGCAGCCCCAAGGCAAGCAAGCTCAATAAGGGGGTGTGTTGGGAG 594
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 544 GGCCACTTTGGCCCCGGGGCCAGGGAGGATGAAGGCCAATAATAACGTGTTGAGCCA 603
QY 595 AAACCAAACCTTGCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCCTTCATCTCTGTTG 654
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 604 AAGCCATCAGTGCCGAGTACAAGGTGGCCTCCGTGGGGGGTCTCGCTGCTCTCTCCTC 663
QY 655 CACTGTGGGGCACTGAGAGCCACCTGGGATGGCTTCTATCTCTGCGCCACTCTATGTG 714
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 664 CACTACAGCGTCTCAAGGCCCATCTGGGACGGCCTTATCTCTCTGCGCCACTTCTACGTT 723
QY 715 GCTGTCACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCACTGCGCCCGC 774
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 724 GCGGTACCCGTCCTACAATGTCTGTTTCTCGGTGACGATGACACCCCATCACTTCG 783
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 775 GGCCCCGCCAGCGTCTGTGACCTGGCCGTGAGGTCTCTTTCATCTTACATTTGACATTTGCTG 834
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 835 AATTTCCGTACCAATTCGTGTCCAAGTCGGGCCAGGTGGTGTGTTTGGCCCCAAAGTCCATT 894
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 844 AACTTCCGCACACACCTATGTGTCCAGTCCGGCCAGGTAATCTCTGCTCCTCGTTCATT 903
QY 895 TGCCTCCACTACGTACCACTGTTTCCGTGCTGATGTATCGAGCGCTGCGCTTTTGAC 954
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 904 GGCCTCCACTACCTGGCCACCTGGTTCTTTCATCGACCTTATTTGCTCTGCTCTGCTTTGAC 963
QY 955 CTGCTACATGCTTCAAGGTCAACGTGTACTTTCGGGGCCCACTCTGCTGAAGACGGTGGCG 1014
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 964 CTGCTTTTACATCTTCAACATCACCGTGACCTGCTGGTGGTGCACCTACTGAAGACAGTGGCG 1023
QY 1015 CTGCTGCGCTGCTGCGCTGCTTCCGGGCTGGACCGGTACTCGCAGTACAGCGCCGCTG 1074
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1075 GTGCTGACACTGCTCATGGCGGTGTTCCGCCCTGCTCGGCACCTGGTTCGCTGCTGCTG 1134
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1135 TTTTACATTTGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGG 1194
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1144 TATGTATCGGGCGCGGAGATGGAGGCCAATGACCCGCTGCTCTGGGACATTTGGCTGG 1203
QY 1195 CTGCAGGAGCTGGCCCGCGACTGGAGACTTCCCTACTACTGTTGGGCGGAGGCCAGCT 1254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1204 TTGCATGAGTTGGCAAGCGTCTGGAGGTGCGCTATGTCAATGGCTC----- 1250
QY 1255 GGAGGGAAAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGGCAACGGGACG 1314
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1315 GGGCTGAGCTGCTGGGGCGCCGCTGCTGGCAGCGCCTACATCACCTCCCTCTACTTC 1374
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1375 GCACTCAGCAGCCTCACAGCGTGGGCTTCGGCAACGTTCCGCCAACACCGGACACCGGAG 1434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1390 ACTTAAGCAGCCTCACAGTGTGGGCTTTGGCAACGTTGTGTGCCAACACCGGAG 1359
QY 1435 AAGATCTTCTCCATCTGCACCATGCTCATCGCGCCCTGATGCACCGCGGTGTTTGGG 1494
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1495 AACGTGACGGCCATCATCCAGCGATGTACGCCCGCGCTTTCTGTACACAGCGCGACG 1554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1555 CGCGACCTGGCGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATG 1614
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1615 CTGGAGTACTTCCAGGCCACCTGGGGGTGAACAATGGCATCGACACCAACCGAGCTGCTG 1674
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1675 CAGAGCCTCCCTGACGAGCTGGCGCAGACATCGCCATGCACCTGCACAAAGGAGGTCTCTG 1734
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1735 CAGCTGCCACTGTTTGGGGCGCCAGCCCGGCTGCTGCGGGCACTGTCTTGGCCCTG 1794
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1795 CGGCCCCGCTTCTGCACGCCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCC 1854
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1720 AAGACCTCGTTCGGCTCCGGGCGAGTACCTGTTGCGCCGTGGGATGCCCTGCAGGCA 1779
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||





QY	1492	GGGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCAAGCCGC	1551
Db	1552	GGGAATGTCACAGCCATCATCCAGCGCATGTACTCCGACGCTCGCTCTACCAAGCCGC	1611
QY	1552	ACGCGGACCTGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGC	1611
Db	1612	ATGAAGGATCTCAAGGACTTCATCCGAGTGCATGCTGCCCGCCCACTCAAGCAGCGC	1671
QY	1612	ATGCTGGAGTACTTCCAGGCCACCTGGCGGTGAACAAATGGCATCGACACCACCGAGCTG	1671
Db	1672	ATGCTGAGTACTTCCAGACTACATGGGCCGTCAACAGCGGCATCGATGCCAACGAGTTA	1731
QY	1672	CTGCAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGTCT	1731
Db	1732	CTGCGTGACTTCCCGATGAGCTGCGAGCTGACATCGCCATGCACCTGAATCGGGAGATC	1791
QY	1732	CTGAGCTGCCACTGTTTGAGCGGCCAGCCGGGCTGCCTGCGGGCACTGCTCTGTGGCC	1791
Db	1792	CTGAGCTGCCCTTGTGTTGGAGCAGCAAGCAGGGGCTGCCTTCGTGCCCTCTCCCTGCAC	1851
QY	1792	CTGCGGCCCGCCTTCTGCACGCCGGGCGAGTACCTCATCCACCAAGCGATGCCCTGCAG	1851
Db	1852	ATCAAGACCTCATTTGTGTCTCTGGGGAGTTCCTGTACTAGCCGTGGGGATGCCCTGCAG	1911
QY	1852	GCCCTCTACTTTGTGTCTCTGGCTCCATGGAGTGTCTCAAGGTGGCACCGTGTCTGCC	1911
Db	1912	GCACACTACTATGTGTCTCTGGCTCTCTTTGAGTGTCTCCGAGACAAACCGTGTCTGCC	1971
QY	1912	ATCCTAGGGAAGSGCAGCCTGATCGGCTGTGAGCTGCCCGCGCGGAGCAG-----	1962
Db	1972	ATCCTTGGAAAGGGGACTTGATTGGGGCAGACATCCCTGAGTTGGGGCAGGAGCCCTGGG	2031
QY	1963	-----GTGGTAAAGGCCAATGCCGACGTGAAGGGGTGACGTACTGCGTC	2007
Db	2032	GCAGGGCAGGCTCGCTGTGAAGACCAAGCGCTGATGTGAAGCACTGACTTACTGCGGC	2091
QY	2008	CTGCAGTGTCTGCAGCTGGCTGGCCTGCACGACAGCCTTTCGCTGTACCCCGAGTTTGCC	2067
Db	2092	CTGCAGCAGCTGAGCAGCCGAGGGCTGGCCGAGGTCTTCGGTTGTATCCGGAATATGTG	2151
QY	2068	CCGCGCTTCAGTCGTGGCCCTCCGAGGGGAGCTCAGCTACAACCTGGG	2114
Db	2152	GCTGCCCTTCAGGGCTGGCCTACCCCGGACCTTAACCTTCAACCTGCG	2198

## RESULT 9

US-09-358-383C-9  
; Sequence 9, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358,383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn ver. 2.0

```
Query Match      26.0%; Score 844.4; DB 4; Length 870;
Best Local Similarity 99.9%;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY	1	ATGCCGGCCATGCGGGGCTCTCTGGCGCCTCAGAAACACCTTCTCTGGACACCATCGCTACG	60
Db	1	ATGCCGGCCATGCGGGGCTCTCTGGCGCCGAGAACACCTTCTCTGGACACCATCGCTACG	60
QY	61	CGCTTCGACGGCACGCACAGTAACTTCGTCTGGGCAACGCCAGGTGGCGGGCTCTTC	120
Db	61	CGCTTCGACGGCACGCACAGTAACTTCGTCTGGGCAACGCCAGGTGGCGGGCTCTTC	120
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC	180
Db	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC	180
QY	181	ATGCAGCGGGCTGIGCCTGCTCCTTCTCTTTATGGGCCAGACACCAAGTGAGCTCGTCCGC	240
Db	181	ATGCAGCGGGCTGTGCCCTGCTCTCTTCTTTATGGGCCAGACACCAAGTGAGCTCGTCCGC	240
QY	241	CAACAGATCCGCAAGGCTTGACGAGCACAAAGGATTCAAGCTGAGCTGATCCTGTATC	300
Db	241	CAACAGATCCGCAAGGCTTGACGAGCACAAAGGATTCAAGCTGAGCTGATCCTGTATC	300
QY	301	CGGAAGAGCGGGCTCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAAATGAGAAA	360
Db	301	CGGAAGAGCGGGCTCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAAATGAGAAA	360
QY	361	GGGGAGGTGGCTCTTCTCTAGTCTCTCAAAAGGACATCAGCGAAACCAAGAACCGAGGG	420
Db	361	GGGGAGGTGGCTCTTCTCTAGTCTCTCAAAAGGACATCAGCGAAACCAAGAACCGAGGG	420
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGCATATGGCCGGGCACGATCC	480
Db	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGCATATGGCCGGGCACGATCC	480
QY	481	AAAGGCTTCAATGCCAACCGGCGGGAGCCGGCCGCTGCTCTACCACTGTCCGGGCAC	540
Db	481	AAAGGCTTCAATGCCAACCGGCGGGAGCCGGCCGCTGCTCTACCACTGTCCGGGCAC	540
QY	541	CTGCAGAAGCAGCCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA	600
Db	541	CTGCAGAAGCAGCCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA	600
QY	601	AACCTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTGGCCCTTCATCTGTGTGCACTGT	660
Db	601	AACCTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTGGCCCTTCATCTGTGTGCACTGT	660
QY	661	GGGGCACTGAGAGCCACCTGGGATGGCTTCATCTCTGCTCGCCACACTCTATGTGGCTGTC	720
Db	661	GGGGCACTGAGAGCCACCTGGGATGGCTTCATCTCTGCTCGCCACACTCTATGTGGCTGTC	720
QY	721	ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTGCCGCCCGGCCCG	780
Db	721	ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTGCCGCCCGGCCCG	780
QY	781	CCCAGCGTCTGTGACCTTGGCCGTGGAGGTCTCTTCTATCTCTTGACATTTGCTGAATTC	840
Db	781	CCCAGCGTCTGTGACCTTGGCCGTGGAGGTCTCTTCTATCTCTTGACATTTGCTGAATTC	840
QY	841	CGTACC	846
Db	841	CGTACC	846

## RESULT 10

US-09-358-383C-7  
; Sequence 7, Application US/09358383C  
; Patent No. 6518398  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/09/358,383C  
; CURRENT FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-09-358-383C-7

Query Match 26.0%; Score 844.4; DB 4; Length 1132;
Best Local Similarity 99.9%; Pred. No. 7.6e-169;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCTGGACACCATCGCTACG 60
Db |||||||
QY 263 ATGCGGCCATGCGGGCCCTCCTGGCGCGCAGAACACCTTCTGGACACCATCGCTACG 322
Db |||||||
QY 61 CGCTTCGACGGCAGCCACAGTAACCTTCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120
Db |||||||
QY 323 CGCTTCGACGGCAGCCACAGTAACCTTCTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 382
Db |||||||
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180
Db |||||||
QY 383 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 442
Db |||||||
QY 181 ATGACGGGGCTGTGCTCTCTCTCTCTCTTATGGCCAGACACCACTGAGCTCGTCCGC 240
Db |||||||
QY 443 ATGACGGGGCTGTGCTCTCTCTCTCTTATGGCCAGACACCACTGAGCTCGTCCGC 502
Db |||||||
QY 241 CAACAGATCCGAAGGCCCTGGACGACACAAGGATTCAAGGTGAGCTGATCCTGTAC 300
Db |||||||
QY 503 CAACAGATCCGAAGGCCCTGGACGACACAAGGATTCAAGGTGAGCTGATCCTGTAC 562
Db |||||||
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTCTCTCTGGATGTGATACCCATAAAGATGAGAA 360
Db |||||||
QY 563 CGGAAGAGCGGGCTCCCGTTCTGGTCTCTCTGGATGTGATACCCATAAAGATGAGAA 622
Db |||||||
QY 361 GGGAGGTGGCTCTTCTCCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 420
Db |||||||
QY 623 GGGAGGTGGCTCTTCTCCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 682
Db |||||||
QY 421 GGCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGCGATGGCCGGGCACGATCC 480
Db |||||||
QY 683 GGCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGCGATGGCCGGGCACGATCC 742
Db |||||||
QY 481 AAAGGTTCAATGCCAACCGGCGGAGCGCGCGTGTCTTACCACTGTCCGGGCAC 540
Db |||||||
QY 743 AAAGGTTCAATGCCAACCGGCGGAGCGCGCGTGTCTTACCACTGTCCGGGCAC 802
Db |||||||
QY 541 CTGCAGAAGCAGCCCAAGGCAAGCAAGCTCAATAAGGGGTGTTGGGAGAAACCA 600
Db |||||||
QY 803 CTGCAGAAGCAGCCCAAGGCAAGCAAGCTCAATAAGGGGTGTTGGGAGAAACCA 862
Db |||||||
QY 601 AACTTGCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCTATCCTGTTGCACTGT 660
Db |||||||
QY 863 AACTTGCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCTATCCTGTTGCACTGT 922
Db |||||||
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCTATCCTGCGCCACACTCTATGTGGCTGTC 720
Db |||||||
QY 923 GGGGCACTGAGAGCCACCTGGGATGGCTTCTATCCTGCGCCACACTCTATGTGGCTGTC 982
Db |||||||
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCACTGCGCCCGCGGCCG 780
Db |||||||
QY 983 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCACTGCGCCCGCGGCCG 1042
Db |||||||
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGTCTCTTCTATCCTTTGACATTGTCTGAATTC 840
Db |||||||
QY 1043 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCTATCCTTGTGACATTGTCTGAATTC 1102
Db |||||||
QY 841 CGTACC 846
Db |||||||

Db 1103 CGTACC 1108

RESULT 11
US-09-358-383C-17
; Sequence 17, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3321)
US-09-358-383C-17

Query Match 23.4%; Score 761.2; DB 4; Length 3321;
Best Local Similarity 62.2%; Pred. No. 3.4e-151;
Matches 1319; Conservative 0; Mismatches 708; Indels 93; Gaps 4;

QY 1 ATGCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCTTGGACACCATCGCTACG 60
Db |||||||
QY 1 ATGCGGGTTATGAAAGGATTACTGGCGCCGCAAAACACCTTCTTGGACACCATCGCCACC 60
Db |||||||
QY 61 CGTTTCGACGGCACGACAGTAACCTTCTGTCTGGCAACGCCAGGTGGCGGGCTCTTC 120
Db |||||||
QY 61 CGTTTTCGCGAACACATAGCAACTTCATCCTTGCCAATGCCAGGTGGCTAAGGGTTTC 120
Db |||||||
QY 121 CCCGTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180
Db |||||||
QY 121 CCCATAGTCTACTGTTCCGATGGCTTCTCGAGCTTGTGGATTGCCCCGAACCTGAAGTC 180
Db |||||||
QY 181 ATGACGGGGCTGTGCTCTCTCTTCTTATGGCCAGACACCACTGAGCTCGTCCGC 240
Db |||||||
QY 181 ATGAGAAGAGTTGTAGCTGCAAGTCTTATTTGGGTTGAACCAATGAGCAACTGATG 240
Db |||||||
QY 241 CAACAGATCCGCAAGGCCCTTGACGAGCACAAAGGATTCAGGCTGAGCTGATCCTGTAC 300
Db |||||||
QY 241 CTTCAAAATAGAAAAGTCACTGGAGGAGAAAACAGAATTCAAAGGAGAAATTATGTTCTAC 300
Db |||||||
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTATACCCATAAAGAAATGAGAAA 360
Db |||||||
QY 301 AAGAAAAACGGGTCTCCATTTTGGTGCCTACTGGATAATTGTTCCCATAAAGAAATGAAAA 360
Db |||||||
QY 361 GGGAGGTGGCTCTCTTCTTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420
Db |||||||
QY 361 GGAGATGTAGTACTTTTCTGSCCTCGTTCAAAGATATAACAGATA-CAAAAAGTGAAGAT 419
Db |||||||
QY 421 GGCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGGATATGGCCGGGCACGATCC 480
Db |||||||
QY 420 TACTCCAGAAGATAAAAAGAGACAAAGTCAAAGGAAGATCAAGAGCAGGACCCCA--- 476
Db |||||||
QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCTGTCTTACCACCTGTCCGGGCAC 540
Db |||||||
QY 477 -----CTTTGACTCAGCCCGGAGACGGAGTCGAGCAGTCTTATCACATCTCTGGGCAC 531
Db |||||||
QY 541 CTGCAGAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600
Db |||||||
QY 532 CTGCAAGAAGAGAGAAAAGAACAAATTGAAAATAAATAACAATGTTTTTTGTAGATAAACCA 591
Db |||||||
QY 601 AACTTGCCTGAGTACAAAGTAGCGGCCCATCCGGAAGTCGCCCTTCTATCCTGTTGCACTGT 660
Db |||||||
QY 592 GCATTTCCGGAGTATAAAGTTTCTGATGCAAAAAGTCCAAAATTCATACTTCTGCAATTT 651
Db |||||||





Db 376 ATGCAGAAAGATTGTAGCTGCAAGTTCCTTAATTGGGGTTGAAACCAATGAGCAACTGATG 435

QY 241 CAACAGATCCGCAAGGCCCTGGACGACAAAGGAGTTC AAGGCTGAGCTGATCCTGTAC 300

Db 436 CTTCAATAGAAAAAGTCAC TGGAGGAGAAAAACAGAAATTC AAGGAGAAATATGTTCTAC 495

QY 301 CGGAAGAGCGGGCTCCCGTTC TGGTGTCTCTCGATGTGATACCCATAAAGAAATGAGAAA 360

Db 496 AAGAAAAACGGGTCTCCATTTTGGTGCCTACTGGATATTGTTCCCATAAAGAAATGAAAA 555

QY 361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCA CAAGGACATCAGCGAAACCAAGAACCGAGGG 420

Db 556 GGAGATGTAGTACTTTTCTGGCCTCGTTCAAAGATATAACAGATA -CAAAAGTGAAGAT 614

QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGTGTGGCCCGGCCCGATATGCGCGGGCACGATCC 480

Db 615 TACTCCAGAAATAAAAAAGAGACAAAGTCAAAGGAAGATCAAGAGCAGGGACCCA --- 671

QY 481 AAAGGCTTCAATGCCAAACCGCGCGGAGCGGGCCCGTCTCTACCACTGTCCGGGCAC 540

Db 672 -----CTTTGACTCAGCCCGGAGACGGAGTCGAGCAGTCCTTTATCACATCTCTGGGCAC 726

QY 541 CTGCAGAAAGCAGCCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTGGGGAGAAACCA 600

Db 727 CTGCAAAAGAGAGAAAAAGAACAAATTGAAAATAAATAACAATGTTTTTGTAGATAAACCA 786

QY 601 AACTTGCCTAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTGTGCACGTG 660

Db 787 GCATTTCCGGAGTATAAAGTTTCTGATGCAAAAAAGTCCAAATTCATACTTCTGCATTTT 846

QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC 720

Db 847 AGCACTTTTAAAGCTGGCTGGGACTGGCTTATTTTGTGGCAACGTTTTATGTGTCTGTG 906

QY 721 ACTGTGCCCTFACAGCGTGTGTGTGAGCACAGCAGGGAGCCCCAGTGCCGCCCGCGGCCG 780

Db 907 ACTGTACCTTACAAAGTTTGCTTTATTGGCAATGACGACCTGTCCACAACCTCGGAGC --- 963

QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCATCCTTGACATGTGCTGAATTTC 840

Db 964 ACAACCGTCAGTGACATTCAGTGGAGATCTTTTATTATAGATATTATTAAATTC 1023

QY 841 CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTGCCCCCAAGTCCATTTGCCCTC 900

Db 1024 CGAACAACTTATGTACAGCAAGTCTGGCCCAAGTATCTTTGAAGCAAGATCAATTTGCATC 1083

QY 901 CACTACGTCAACACCTGGTTCCTGCTGGATGTTCATCGCAGCGCTGCCCTTTGACCTGCTA 960

Db 1084 CACTATGTCAACACCTGGTTCATCATTTGATTTAATCGCTGCCCTGCTTGTGATCTTCTG 1143

QY 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCGCCCTGCTG 1020

Db 1144 TATGCTTTCAACGTACAGTGGTGTCTCTCGTGCATCTTCTAAAGACAGTGCGCCCTCTTG 1203

QY 1021 CGCCTGCTGCGCTGCTTCCGCGCTGGACGGTACTCGCAGTACAGCGCGTGGTCTG 1080

Db 1204 CGTCTTTTGGCTGCTGCAGAAAGTTAGACCGCTATTCCCAACACAGTACTATCGTCTCTG 1263

QY 1081 ACAC TGTCTATGGCGGTGTTGCGCCCTGCTCGCGCACTGGGTGCGCTCGTCTGGTTTTAC 1140

Db 1264 ACTCTGCTCATGTCCATGTTTGCACTCTCTGCACTGGATGGCGTGTATCTGGTACGTC 1323

QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCCTGAGATTGGTGGCTGCAG 1200

Db 1324 ATTGGAAAAATGGAGAGGGAAGACAAACAGCCTTCTGAAAGTGGGAAGTTGGTGGCTTCAT 1383

QY 1201 GAGCTGGCCCCGCACTGGAGACTCCCTACTACTGCTGGTGGCCGGAGGCCAGCTGGAGGG 1260

Db 1384 GAGTTGGAAAGAGACTGGAATCTCCATACTAT ----- 1416

QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCGAGCAGCAGCAGGGCCAAACGGGACGGGGCTG 1320

Db 1417 -----GGCAAC 1422

QY 1321 GAGCTGCTGGGCGGCCCGTGGCTGGCAGCGCCCTACATCACCTCCCTCTACTTGCACCTC 1380

Db 1423 AATACCTTGGGGGGCCCGTCGATCCGAAAGTGCCTATATTGCCGCTCTGTACTTCACGCTG 1482

QY 1381 AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGACACCGAGAAAGATC 1440

Db 1483 AGCAGCCTCACAGCGTGGGTTTGGGAACGTCTCTGCTAATACAGATGCAGAAAAAGATC 1542

QY 1441 TTCTCCATCTGCACCAATGCTCATCGCGGCCCTGATGCACGCGGTGTGTTTGGAAACGTG 1500

Db 1543 TTCTCCATCTGCACCAATGCTGATTGGTGGCTTGATGCACGCTTGGTGTGTTGGAAACGTG 1602

QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTTCTGTACCAACAGCCGACGCGCGAC 1560

Db 1603 ACAGCAATCATACAGAGGATGTACTCCAGATGGTCCCTCTATCACACTAGAACTAAGGAT 1662

QY 1561 CTGCGCGACTACATCCGCTATCCACCGGTATCCCCAAGCCCCCTCAAGCAGCGCATGCTGGAG 1620

Db 1663 CTGAAAGATTTCATCCGTGTCCATCATCTTGCCTCCCAACAACTCAAGCAGAGGATGCTCGAA 1722

QY 1621 TACTTCCAGCCACCTGGGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGC 1680

Db 1723 TATTTTCAAAACCTGGTCAGTCAACAATGGAATAGATTCAAATGAGCTTTTGAAGAC 1782

QY 1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGACCTGCAACAGGAGGTCTCTGCAGCTG 1740

Db 1783 TTTCCAGATGAATGCGTTCTGACATCACTATGCACTTGAACAAGGAGATCTTACAGTTG 1842

QY 1741 CCAC TGTGTGAGGCGCCAGCCGCGTGCCTGCGGCACTGTCTGTGSCCTCGGCCCC 1800

Db 1843 TCCCCTTTTGAATGTGCCAGCCGGGCTGCCTCAGGTCTCTGTCTCTACACATCAAAACC 1902

QY 1801 GCCTTCTGCACGCCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1860

Db 1903 TCTTTCTGTGCTCCGGGGAGTATCTGCTGCGTCAAGGGATGCTTTGCAGGCCATCTAC 1962

QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTGCTGCCATCCTAGGG 1920

Db 1963 TTTGTATGCTCGGGCTCCATGGAAGTCTTAAAGACAGCATGGTGTGGCTATTTCTTGGG 2022

QY 1921 AAGGGCAGCTGATCGGCTGTGAGCTGCCCCCGGGAGCAGGTGGTAAAGGCCAATGCC 1980

Db 2023 AAAGGGGATTTAATTGGAGCAAATCTATCAATTAAGGACCAAGTGATCAAGACCAATGCA 2082

QY 1981 GACGTGAAGGGCTGACGTACTGCTGCTGCTGCAAGTGTCTGCAGTGGCTGGCTGCACGAC 2040

Db 2083 GATGTAAAGGCTTTAACTTACTGTGATCTCCAGTGTATCATCCTCAAAGGACTCTTTGAA 2142

QY 2041 AGCCTTGGCTGTACCCCGAGTTTGCCTCCGCGCTTCAGTCTGTGSCCTCCGAGGGGAGCTC 2100

Db 2143 GTGCTAGACCTTTACCCAGAATATGCTCACAAATTCGTGGAAGACATTGAGCATGACCTC 2202

QY 2101 AGCTACAACCTGGGTGCTGG 2120

Db 2203 ACATACAACCTCCGAGAAG 2222

RESULT 13

US-09-358-383C-6

; Sequence 6, Application US/09358383C

; Patent No. 6518398

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

; FILE REFERENCE: MNI-055CP

; CURRENT APPLICATION NUMBER: US/09/358,383C

; CURRENT FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: USSN 09/119,855

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

```

; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1626)
US-09-358-383C-6

Query Match      17.6%; Score 572.8; DB 4; Length 1626;
Best Local Similarity 61.8%; Pred. No. 1.3e-111;
Matches 1034; Conservative 0; Mismatches 547; Indels 93; Gaps 4;

QY 1 ATGCCGGCCATGCGGGCCCTCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
Db 1 ATGCCGGTTATGAAGGATTACTGGCGCCGCAAAACACCTTCCTGGACACCATCGCCACC 60

QY 61 CGCTTCGACGGCAGCGCACAGTAACCTTCGTGCTGGGCAACGCCAGGTGCGGGCTCTTC 120
Db 61 CGTTTTCACGGAAACACATAGCAACTTCATCCTTGCCAAATGCCAGGTGGCTAAGGTTTC 120

QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGTC 180
Db 121 CCCATAGTCTACTGTTCCGATGGCTTCTGCGAGCTTCTGCTGGATTTCGCCGAACCTGAAGTC 180

QY 181 ATGCAGCGGGCTGTGCTGCTCTCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGTC 240
Db 181 ATGCAGAAAGATTGTAGCTGCAAGTTCTTAATTGGGGTTGAAACCAATGAGCAACTGATG 240

QY 241 CAACAGATCCGCAAGGCCCTTGACGAGCAGCAAGAGATTCAAGGCTGAGCTGATCCTGTAC 300
Db 241 CTTCAATAGAAAGTCACTGGAGGAGAAACAGAAATTCAAAGGAGAAATATGTTCTTAC 300

QY 301 CGGAAGAGCGGCTCCCGTTCTGTTGCTCTCTGATGTGATACCCATAAAGAAATGAGAAA 360
Db 301 AAGAAAAACGGTCTCCATTTTGGTGCCTACTGTGATATGTTCCCATAAAGAAATGAAAA 360

QY 361 GGGAGGTGGCTCTCTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420
Db 361 GGAGATGTAGTACTTTTCTGGCTCTGTTCAAGATATAACAGATA-CAAAAGTGAAGAT 419

QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCCGATATGGCGGGCACGATCC 480
Db 420 TACTCCAGAGATAAAAGAAAGACAAAGTCAAAGGAAGATCAAGAGCAGGACCCCA--- 476

QY 481 AAAGGTTCAATGCCAAACCGCGGGCGGAGCCGGCCCGTGTCTTACCACCTGTCCGGGCAC 540
Db 477 -----CTTTGACTCAGCCCGGAGACGGAGTCCAGCAGTCTTTATCACATCTCTGGGCAC 531

QY 541 CTGCAGAAAGCAGCCCAAGGCAAGCACAAGTCAATAAGGGGTGTTGGGGAGAAACCA 600
Db 532 CTGCAAGAGAGAAAGAAACAAATTGAAATAAATAAACAATGTTTTGTAGATAAAACCA 591

QY 601 AACTTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTTCATCTGTGCACTGT 660
Db 592 GCATTTCCGGAGTATAAAGTTTCTGATGCAAAAAAGTCCAAATTCATACTTCTGCAATTT 651

QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCTGCTCGCCACACTCTATGTGGCTGTC 720
Db 652 AGCACTTTTAAAGCTGGCTGGGACTGGCTTATTTTGTGGCAACGTTTATGTGCTGTG 711

QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGGGAGCCCCAGTCCCGCCCGGCCCG 780
Db 712 ACTGTACCTTACAAAGCTTTGCTTTATTTGGCAATGACGACCTGTCCACAACTCGGAGC--- 768

QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTTCATCCTTGACATTGTGCTGAATTC 840
Db 769 ACAACCGTCACTGACATTGCACTGGAGATTCTTTTATATAGATATATTTAAATTC 828

QY 841 CGTACCACATTGCTGTCCAAAGTCGGGCCAGGTGTTGTTGCCCAAGTCCATTTGCCTC 900
Db 829 CGAACAACATTATGTGAGCAAGTCTGGCCAAAGTTATCTTTGAAGCAAGATCAATTTGCATC 888

QY 901 CACTACGTCAACCACCTGGTTCTGTGATGTGATCGCAGCGCTGCCCTTTGACCTGCTA 960
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Db 889 CACTATGTCAAAACCTGGTTTCATCAITGATTAATCGTCGCCCTTTTGATCTTCTG 948
QY 961 CATGCCCTTCAAGGTCAACGTGTACTTCGGGGGCCCATCTGCTGAAGACGGTGCCTGCTG 1020
Db 949 TATGCTTTTCAACGTCAACAGTGGTGTCTCTCGTGCACTTCTTAAAGACAGTGGCCTCTTG 1008
QY 1021 CGCCTGCTGCGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCGTGTGCTG 1080
Db 1009 CGTCTTTTGGCTGTCTGTCAGAAAGTTAGACCGCTATTCCCAACACAGTACTATCGTCTG 1068
QY 1081 AACTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCGCCTGCTGCTGTTTAC 1140
Db 1069 ACTCTGCTCATGTCCATGTTTGCACTCCITGACACTGGATGGCGTGTATCTGTTGACGTC 1128
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG 1200
Db 1129 ATTGGAATAATGGAGAGGGAAGACAAACAGCCTTCTGAAGTGGGAAGTTGGTTGGCTTCAT 1188
QY 1201 GAGCTGGCCCGCACTGGAGACTCCCTACTACTACTGCTGGTGGCCGAGGCGAGCTGGAGGG 1260
Db 1189 GAGTTGGAAAGAGACTGGAATCTCCATACTA----- 1220
QY 1261 AACAGCTCCGGCCAGAGTGAACAACCTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGCTG 1320
Db 1221 -----TGGCAAC 1227
QY 1321 GAGCTGCTGGCGGCCCGCTCGCTCGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACCTC 1380
Db 1228 AATACCTTGGGGGCCCGCTCGATCCGAAGTGCCTATATTGCCGCTCTGTACTTCACTGCTG 1287
QY 1381 AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGGACACCGAGAAAGATC 1440
Db 1288 AGCAGCCTCACAGCGTGGGTTTGGGAACGTCTCTGCTAATACAGATGCAGAAAGATC 1347
QY 1441 TTCTCCATCTGCACCATGCTCATCGGCGCCTGATGCACGCGGTGTTGTTGGGAACGTG 1500
Db 1348 TTTCTCCATCTGCACCATGCTGATTGGTGCTGATGCACGCTTGGTGTGTTGGAACGTG 1407
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCGCACGCGCGAC 1560
Db 1408 ACAGCAATCATACAGAGGATGTACTCCAGATGGTCCCTCTATCACACTAGAACTAAGGAT 1467
QY 1561 CTGGCGCACTACATCCGCACTCCACCGGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620
Db 1468 CTGAAAGATTTCATCCGTGTCCATCACTTGTCCCAACAACACTCAAGCAGAGGATGCTCGAA 1527
QY 1621 TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCCAGCTGCTG 1674
Db 1528 TATTTTCAAAACAACCTGGTCAGTCAACAATGGAATAGATTCAAATGAGGTAATG 1581
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RESULT 14

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US-09-358-383C-4
; Sequence 4, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(1840)
```

US-09-358-383C-4

Query Match		17.6%;	Score 572.8;	DB 4;	Length 2694;
Best Local Similarity		61.8%;	Pred. No. 1.5e-111;		
Matches 1034;		Conservative	0;	Mismatches 547;	Indels 93; Gaps 4;
QY	1	ATGCCGGCCATGCGGGCCTCCTGGCGCTCAGAACACCTTCCTGGACACCATCGCTACG	60		
Db	215	ATGCCGGTTATGAAGGATTACTGGCGCGCAAAACACCTTCCTGGACACCATCGCCACC	274		
QY	61	CGCTTCGACGGCAGCCACAGTAACTTCGTCTGGGCAACGCCAGTGGCGGGGCTCTTC	120		
Db	275	CGTTTTGACGGAACACATAGCAACTTCATCCTTGCCAAATGCCAGGTGGCTAAGGTTTC	334		
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCGTGACCTCACGGGCTTCGCCGGGCTGAGGTC	180		
Db	335	CCCATAGTCTACTGTTCCGATGGCTTCGCGAGCTTGCTGGATTGGCCCGAACTGAAGTC	394		
QY	181	ATGCAGCGGGGTGTCCTGCTCCTTCCTTTATGGGCCAGACACCAAGTGAAGTCTGTCGC	240		
Db	395	ATGCAGAAAGATTGTAGCTGCAAGTTCTTATTTGGGTTGAAACCAATGAGCAACTGATG	454		
QY	241	CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC	300		
Db	455	CTTCAATAGAAAAGTCACTGGAGGAGAAAACAGAAATTCAAAGGAGAAATATGTTCTAC	514		
QY	301	CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAGAAATCAGAAA	360		
Db	515	AAGAAAACGGGTCTCCATTTTGGTGCCCTACTGGATATTGTTCCCATAAAGAAATGAAAA	574		
QY	361	GGGAGGTGGTCTCTTCCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG	420		
Db	575	GGAGATGTAGTACTTTTTCTGGCCTCGTTCAAAGATATAACAGATA-CAAAAGTGAAGAT	633		
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCCGGCCGATATGGCCGGCACGATCC	480		
Db	634	TACTCCAGAAGATAAAAAAAGAAAGACAAAGTCAAAGGAAGATCAAGAGCAGGGACCCA---	690		
QY	481	AAAGGTTCAATGCCAACCGGCGGAGCGGGCCGCTGCTCTACCACTGTCCGGGCAC	540		
Db	691	-----CTTTGACTCAGCCCGGAGACGGAGTCGAGCAGTCTTTATCACAATCTCTGGGCAC	745		
QY	541	CTGCAGAAGCAGCCCCAAGGGCAAGCACAGCTCAATAAGGGGTGTTGGGGAGAAACCA	600		
Db	746	CTGCAAGAGAGAGAAAGAACAAATTGAAATAAATAACAATGTTTTTGTAGATAAACCA	805		
QY	601	AAC TTGCCTGAGTACAAAGTAGCGGCCATCCGGAAGTCGCCCTTCATCCTGTGTGCACTGT	660		
Db	806	GCA TTTCCGGAGTATAAAGTTTCTGATGCAAAAAGTCCAATTCATCTCTGCATTTT	865		
QY	661	GGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC	720		
Db	866	AGCACTTTTAAAGCTGGCTGGACTGGCTTA TTTGTTGGCAACGTTTTATGTTGCTGTG	925		
QY	721	ACTGTGCCCTPACAGCGTGTGTGAGCACAGCAGGGAGCCCAAGTCCGCCCGCGGCCCG	780		
Db	926	ACTGTACCTTACAACAGTTTGCTTTATTGGCAATGACGACCTGTCCACAACCTCGGAGC---	982		
QY	781	CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCATCCTTGACATTGTGCTGAATTC	840		
Db	983	ACAACCGTCACTGACATTGCAGTGGAGATTCTTTTATTATAGATATTATTAAATTC	1042		
QY	841	CGTACCACATTCGTCTCCAAAGTCGGGCCAGGTGGTGTGTTGCCCCAAAGTCCATTTGCCTC	900		
Db	1043	CGAACAACTTATGTGACGAAGTCTGGCCCAAGTTATCTTTGAAGCAAGATCAATTTGCATC	1102		
QY	901	CACTACGTCAACCTGGTTCCCTGCTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA	960		
Db	1103	CACTATGTCACAACCTGGTTCACTATGATTTAATCGCTGCCCTTTCCTTTTGATCTTCTG	1162		
QY	961	CATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCGCTGCTG	1020		
Db	1163	TATGCTTTCAACGTCACAGTGGTGTCTCTCGTGCATCTTCTAAAGACAGTGGCGCTCTTG	1222		

QY	1021	CGCCTGCTGCGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCCCGTGGTGTG	1080
Db	1223	CGTCTTTTGGGTCTGCTGCAGAAAGTTAGACCGCTATTCCCAACACAGTACTATCGTCTG	1282
QY	1081	ACACTGCTCATGGCCGTGTTCCGCCCTGCTCGGCACACTGGGTGCGCTGCGTCTGTTTAC	1140
Db	1283	ACTCTGCTCATGTCATGTTTGCATCTCCTTGCACACTGGATGGCGTGTATCTGGTACGTC	1342
QY	1141	ATTGGCCAGCGGAGATCGAGAGAGCGCAATCCGAGTCCCTGAGATTGGCTGGCTGCAG	1200
Db	1343	ATTGGAATAATGGAGAGGGAAGACAAACAGCCTTCTGAAGTGGAAAGTTGGTTGGCTTCAT	1402
QY	1201	GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTTACCTGGTGGCCGAGGCCAGCTGGAGGG	1260
Db	1403	GAGTTGGGAAAGAGACTGGAATCTCCATACTA-----	1434
QY	1261	AACAGCTCCGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTG	1320
Db	1435	-----TGGCAAC	1441
QY	1321	GAGCTGCTGGGCGGCCCGTGGCTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACCTC	1380
Db	1442	AATACCTTGGGGGGCCCGTCGATCCGAAGTGCCTATATTGCCGCTCTGTACTTCACGCTG	1501
QY	1381	AGCAGCCTCACAGCGTGGGCTTCGGCAACGTTCCGCCAACACCGACACCGAGAAGATC	1440
Db	1502	AGCAGCCTCACAGCGTGGGTTTTTGGGAACGTCTCTGCTAATACAGATGCAGAAAAGATC	1561
QY	1441	TTCTCCATCTGCACCATGCTCATCGCGGCCCTGATGCACGCGGTGGTGTGGGAACGTG	1500
Db	1562	TTCTCCATCTGCACCATGCTGATTGGTGCCTTGTATGCACGCTTGGTGTGGTGTGGAAACGTG	1621
QY	1501	ACGGCCATCATCCAGCGCATGTACGCCCGCGCGCTTCTGTACCAACAGCCGACCGCGGAC	1560
Db	1622	ACAGCAATCATACAGAGGATGTACTCCAGATGGTCCCTCTATCACACTAGAACTAAGGAT	1681
QY	1561	CTGCGCGACTACATCCGCATCCACCGGTATCCCCAAGCCCCCTCAAGCAGCGCATGCTGGAG	1620
Db	1682	CTGAAAGATTTCATCCGTGTCCATCATCTTGCCCCCAACTCAAGCAGAGGATGCTCGAA	1741
QY	1621	TACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTG	1674
Db	1742	TATTTTCAAAACACCTGGTCAGTCAACAATGGAATAGATTCAAATGAGGTAATG	1795

RESULT 15

US-09-358-383C-14

; Sequence 14, Application US/09358383C

; Patent No. 6518398

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

; FILE REFERENCE: MNI-055CP

; CURRENT APPLICATION NUMBER: US/09/358,383C

; CURRENT FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: USSN 09/119,855

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 5955

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: exon

; LOCATION: (196)..(1770)

; NAME/KEY: intron

; LOCATION: (1771)..(2618)

; NAME/KEY: exon

; LOCATION: (2619)..(4364)

; OTHER INFORMATION: At position 5625, n=any nucleic acid

US-09-358-383C-14



Query Match		17.6%;	Score 572.8;	DB 4;	Length 5955;
Best Local Similarity		61.8%;	Pred. No. 1.9e-111;		
Matches 1034;		Conservative 0;	Mismatches 547;	Indels 93;	Gaps 4;
QY	1	ATGCCGGCCATCGCGGCCTCCTGGCGCCTCAGAACACCTTCTCTGGACACCATCGCTACG	60		
Db	196	ATGCCGGTTATGAAAGGATTACTGGCGCCGCAAAACACCTTCTCTGGACACCATCGCCACC	255		
QY	61	CGCTTCGACGGCACCACAGTAACTTCGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC	120		
Db	256	CGTTTTGACGGAAACACATAGCAACTTCATCCTTGCCAAATGCCAGGTGGCTAAGGGTTTC	315		
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC	180		
Db	316	CCCATAGTCTACTGTTCCGATGGCTTCTGCGAGCTTGCTGGAATTTGCCCGAACTGAAGTC	375		
QY	181	ATGCAGCGGGGTGTGCCCTGCTCCTTCCTTTATGGGCCAGACACCAAGTGAAGTCTGCCG	240		
Db	376	ATGCAGAAAGATTGTAGCTGCAAGTTCTTAFTTGGGGTTGAAACCAATGAGCAACTGATG	435		
QY	241	CAACAGATCCGCAAGGCCCTGGACGAGCAACAAGAGTTCAAGGCTGAGCTGATCCTGTAC	300		
Db	436	CTTCAAATAGAAAAGTCACTGGAGGAGAAAACAGAAATTCAAAGGAGAAATATGTTCTAC	495		
QY	301	CGGAAGAGCGGGTCCCGTCTCTGGTGTCTCTCGATGTGATACCCATAAAGAATGAGAAA	360		
Db	496	AAGAAAAACGGGTCTCCATTTTGGTGCCTACTGGATATTGTTCCCATAAAGATGAAAA	555		
QY	361	GGGAGGTGGCTCTCTCCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGGG	420		
Db	556	GGAGATGTAGTACTTTTCTGGCCTCGTTCAAAGATATAACAGATA-CAAAAGTGAAGAT	614		
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGTGGCCGCGCGGATATGGCCGGCACGATCC	480		
Db	615	TACTCCAGAAAGATAAAAAGAAAGACAAAGTCAAAGGAAGATCAAGAGCAGGACCCCA---	671		
QY	481	AAAGGTTTCAATGCCAAACCGCGCGGAGCCGGGCCGTGCTCTACCACTGTCCGGGCAC	540		
Db	672	-----CTTTGACTCAGCCCGGAGACGGAGTCCAGCAGTCCCTTATCACATCTCTGGGCAC	726		
QY	541	CTGCAGAAAGCAGCCCAAGGGCAAGCACAAAGTCAATAAGGGGTGTTTGGGGAGAAACCA	600		
Db	727	CTGCAAGAGAGAGAAAAGAACAAATTGAAATAAATAACAATGTTTTTTGTAGATAAACCA	786		
QY	601	AACCTTGCTGACTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTGTGCACTGT	660		
Db	787	GCATTTCCGGAGTATAAAGTTTCTGATGCAAAAAGTCCAAATTCATACTCTTGCAATTTT	846		
QY	661	GGGGCACTGAGACCCACCTGGGATGGCTTCATCTGCTGCCACACTCTATGTGGCTGTC	720		
Db	847	AGCACTTTTAAAGCTGGCTGGGACTGGCTTAATTTGTTGGCAACGTTTTATGTTGCTGTG	906		
QY	721	ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGGGAGCCCAGTGCCTGCCGCGGCCG	780		
Db	907	ACTGTACCTTACAAACGTTTGTCTTTATTGGCAATGACGACCTGTCCACAACTCGGAGC---	963		
QY	781	CCCAGGCTCTGTGACCTGGCCGTGGAGGTCTCTTTCATCTTGACATTTGCTGAATTC	840		
Db	964	ACAAACCGTCAGTGACATTCAGTGGAGATTCTTTTATTATAGATATTATTTTAAATTC	1023		
QY	841	CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTGTTGCCCAAAGTCATTTGCCTC	900		
Db	1024	CGAACAACTTATGTACAGCAAGTCTGGCCCAAGTTATCTTTGAAGCAAGATCAATTTGCATC	1083		
QY	901	CACTACGTCACCACTGGTTCTCTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGCTA	960		
Db	1084	CACATGTGCACACCTGGTTTCATCATTTGATTTAATCGTGCCTTGCCTTTTGATCTTCTG	1143		
QY	961	CATGCCTTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGGTGGCCCTGCTG	1020		
Db	1144	TATGCTTTCAACGTCACAGTGGTGTCTCTCGTGCATCTTCTAAAGACAGTGGCCCTCTTG	1203		

QY	1021	CGCCTGCTGCGCTGCTTCCGGGGCTGGACCGGTACTCGCAGTACAGCGCGTGGTGTCTG	1080
Db	1204	CGTCTTTTGGCTGTGTCAGAAAGTTAGACCGCTATTCCCAACACAGTACTATCGTCTG	1263
QY	1081	ACACTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCGCTGCTGCTGTTTAC	1140
Db	1264	ACTCTGCTCATGTCCATGTTTGCACTCCTTGCACACTGGATGGCGTGTATCTGGTACGTC	1323
QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG	1200
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Search completed: September 1, 2004, 18:41:43  
Job time : 177 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 14:38:36 ; Search time 8225 Seconds  
(without alignments)  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_htg.\*  
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11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
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16: em\_fun.\*  
17: em\_hum.\*  
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20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
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31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
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35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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5	3244	99.8	3252	6	AX027893	AX027893 Sequence
6	3218	99.0	3857	6	AR212361	AR212361 Sequence
7	3156	97.0	3355	6	AR281263	AR281263 Sequence
8	3153	97.0	3249	6	AR281264	AR281264 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6326168.  
ACCESSION AR179189  
VERSION AR179189.1 GI:20220744  
KEYWORDS  
SOURCE .  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 3323)  
AUTHORS Miyake,A., Mochizuki,S. and Yokoi,H.  
TITLE Brain specific potassium channel protein  
JOURNAL Patent: US 6326168-A 1 04-DEC-2001;  
FEATURES Location/Qualifiers





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ACCESSION AB022696  
VERSION AB022696.1 GI:5804783  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.  
TITLE New ether-a-go-go K(+) channel family members localized in human telencephalon  
JOURNAL J. Biol. Chem. 274 (35), 25018-25025 (1999)  
MEDLINE 99386988  
PUBMED 10455180  
REFERENCE 2 (bases 1 to 3610)  
AUTHORS Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.  
TITLE Direct Submission  
JOURNAL Submitted (21-JAN-1999) Akira Miyake, Yamanouchi Pharmaceutical Co.,Ltd., Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan (E-mail:miyake@yamanouchi.co.jp, Tel:81-298-52-5111(ex.3324), Fax:81-298-52-5444)  
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source  
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AB033108.1 GI:6331347  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (sites)  
Nagase,T., Ishikawa,K., Kikuno,R., Hirose,M., Nomura,N. and  
Ohara,O.  
Prediction of the coding sequences of unidentified human genes. XV.  
The complete sequences of 100 new cDNA clones from brain which code  
for large proteins in vitro  
DNA Res. 6 (5), 337-345 (1999)  
20039619  
10574462  
2 (bases 1 to 3853)  
Ohara,O., Nagase,T. and Kikuno,R.  
Direct Submission  
Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,  
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba  
292-0812, Japan (E-mail:cdmainfo@kazusa.or.jp,  
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,  
Fax:+81-438-52-3914)  
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Matches 3251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	ATGCCGGCATGCGGGGCTCTCTGGCGCTCAGAACACCTTCTTGACACCATCGCTACG	60						
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QY	181	ATGCAGCGGGCTGTGCTGCTCTCTTCTTATGGCCAGACACCAAGTGAAGCTCGTCCGC	240						
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QY	241	CAACAGATCCGCAAGGCCCTGGACGAGCAACAAGGATTCAAGGCTGAGTGCCTGTAC	300						
Db	501	CAACAGATCCGCAAGGCCCTGGACGAGCAACAAGGATTCAAGGCTGAGTGCCTGTAC	560						
QY	301	CGGAAGAGCGGGTCCCCTCTGGTGTCTCTGATGTGATACCCATAAAGATGAGAA	360						
Db	561	CGGAAGAGCGGGTCCCCTCTGGTGTCTCTGATGTGATACCCATAAAGATGAGAA	620						
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QY	481	AAAGGCTTCAATGCCAACCGCGGGGAGCGCGGCTGTCTACCAACCTGTCCGGGCAC	540						
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QY	541	CTGCAGAGCAGCCCAAGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA	600						
Db	801	CTGCAGAGCAGCCCAAGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA	860						
QY	601	AACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTTGTGCACTGT	660						
Db	861	AACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTTGTGCACTGT	920						
QY	661	GGGGCACTGAGAGCCACCTGGGATGGCTTCACTGCTCGCCACACTCTATGTGGCTGTC	720						
Db	921	GGGGCACTGAGAGCCACCTGGGATGGCTTCACTGCTCGCCACACTCTATGTGGCTGTC	980						
QY	721	ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGGAGCCCAAGTGCCGCCGCGGCCCG	780						
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QY	841	CGTACCACATTCTGTCTCAAGTCGGGCCAGGTGGTGTTCGCCCAAGTCCATTGCGCTC	900						
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AR217183

LOCUS AR217183 3249 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 2 from patent US 6413741.  
ACCESSION AR217183  
VERSION AR217183.1 GI:23316610  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3249)  
AUTHORS Jegla,T.J. and Wickenden,A.  
TITLE Human elk a voltage-gated potassium channel subunit  
JOURNAL Patent: US 6413741-A 2 02-JUL-2002;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 99.8%; Score 3245.8; DB 6; Length 3249;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 CGCTTCGACGGCACGCACAGTAATTCGTGCTGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 61 CGCTTCGACGGCACGCACAGTAATTCGTGCTGGCAACGCCAGGTGGCGGCTCTTC 120  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180  
Db 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180  
QY 181 ATGCAGCGGGGCTGTGCCCTGCTCTTCTTTATGGGCCAGACACAGTGAGCTCGTCCGC 240  
Db 181 ATGCAGCGGGGCTGTGCCCTGCTCTTCTTTATGGGCCAGACACAGTGAGCTCGTCCGC 240  
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Db 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTATACCCATAAAGAATGAGAAA 360  
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QY 421 GSCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGCGGATATGGCCGACGATCC 480  
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VERSION AX027893.1 GI:10188725  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Avenet, P. and Renard, S.  
TITLE A potassium channel member of the erg family  
JOURNAL Patent: EP 1002863-A 1 24-MAY-2000;  
SANOFI SYNTHELABO (FR)  
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DEFINITION Sequence 19 from patent US 6399761.

ACCESSION AR212361

VERSION AR212361.1 GI:21515915

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3857)

AUTHORS Miller,A.P., Hu,P., Curran,M,Edward., Rutter,M. and Jiang-Yang,W.

TITLE Nucleic acid encoding human potassium channel K+ nov1 protein

JOURNAL Patent: US 6399761-A 19 04-JUN-2002;

FEATURES location/Qualifiers

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QY 2341 GGCAGAGGGAGGCCAGGGCAGGGGCTTTGAAGGTGAGGCTGGCCCTCTGCTCCC 2400

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Db	2504	CCACGGGCTTAGAGGGGCTACGGGTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG	2563
QY	2461	AGCCCCAGGFPAGTAGATGGCAATTGAACGGCTGTGGCTCGGACGAGCCCAAAGTTCTCT	2520
Db	2564	AGCCCCAGGFPAGTAGATGGCAATTGAACGGCTGTGGCTCGGACGAGCCCAAAGTTCTCT	2623
QY	2521	TTCCGCGTGGCCAGTCTGGCCCGGAATGAGCAGGCTGAGCAGCCCTCCCTCGACGAGAGC	2580
Db	2624	TTCCGCGTGGCCAGTCTGGCCCGGAATGAGCAGGCTGAGCAGCCCTCCCTCGACGAGAGT	2683
QY	2581	GGCCTGCTCACTGTTCCCCCATGGGCCCCAGGAGGCAAGGAACACAGACACACTGGACAAG	2640
Db	2684	GGCCTGCTCACTGTTCCCCCATGGGCCCCAGGAGGCAAGGAACACAGACACACTGGACAAG	2743
QY	2641	CTTCGGCAGGCGGTGACAGAGCTGTGAGCAGGCTGTGAGAGTGGGAGGAGTGCAG	2700
Db	2744	CTTCGGCAGGCGGTGATGGAGCTGTGAGAACAGGTGTGAGATGCGGGAAGGACTACAG	2803
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Db	3104	GAGCCCCCTGCCTCAGGAGACCTCTGCTGTAGCCCCAGCACCCCTGCCCTCCTCCT	3163
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Db	3224	ACTGGAGAGCCCCCGCCAGTGTGAGGGGCTTGCGCTTGCCCTGGGACCCCCACAGCCCTG	3283
QY	3181	GAGATGGTGTATTGCTGCCATGGCTCTGSCACAGTCCAGTGGACCCAGGAAGGC	3240
Db	3284	GAGATGGTGTATTGCTGCCATGGCTCTGSCACAGTCCAGTGGACCCAGGAAGGC	3343
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Db	3344	ACAGGGGTCTGA	3355

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AR281264 LOCUS AR281264 3249 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 3 from patent US 6518398.  
ACCESSION AR281264  
VERSION AR281264.1 GI:29716864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE	1	(bases 1 to 3249)
AUTHORS	Curtis,R.A.J.	
TITLE	ERG potassium channel	
JOURNAL	Patent: US 6518398-A 3 11-FEB-2003;	
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	Best local Similarity	98.2%; Pred. No. 0;
	Matches 3189; Conservative	0; Mismatches 60; Indels 0; Gaps 0;
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QY	61	CGCTTCGACGGCACGACAGTAACTTCGTGTGGGCAACGCCAGGTGGCGGGCTCTTC 120
Db	61	CGCTTCGACGGCACGACAGTAACTTCGTGTGGGCAACGCCAGGTGGCGGGCTCTTC 120
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
Db	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
QY	181	ATGACGGGGCTGTGCCTGCTCTCTTATGGGCCAGACACCACTGAGTCTCGTCCGC 240
Db	181	ATGACGGGGCTGTGCCTGCTCTCTTATGGGCCAGACACCACTGAGTCTCGTCCGC 240
QY	241	CAACAGATCCGCAAGGCCCTGGACGACACAAGGAGTTCAAGGCTGATCCTGTATC 300
Db	241	CAACAGATCCGCAAGGCCCTGGACGACACAAGGAGTTCAAGGCTGATCCTGTATC 300
QY	301	CGGAAGAGCGGGCTCCCGTTCTGTGTCTCTCTGGATGTGATACCCATAAAGAATGAGAAA 360
Db	301	CGGAAGAGCGGGCTCCCGTTCTGTGTCTCTCTGGATGTGATACCCATAAAGAATGAGAAA 360
QY	361	GGGAGGTGGTCTCTTCTTAGTCTCTCACAAAGACATCAGCGAAACCAAGAACCGAGGG 420
Db	361	GGGAGGTGGTCTCTTCTTAGTCTCTCACAAAGACATCAGTGAACCAAGAACCGAGGG 420
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGTGGCCGGCGCGATATGGCCGGGCACGATCC 480
Db	421	GGCCCTGACAGATGGAAGGAGACAGGTAGTGGCCGGCGCGATATGGCCGGGCACGATCC 480
QY	481	AAAGGCTTCAATGCCAACCGCGCGGAGCCGGCCGTGCTCTACCACTGTCCGGGCAC 540
Db	481	AAAGGCTTCAATGCCAACCGCGCGGAGCCGGGCTGTGCTCTACCACTGTCCGGGCAC 540
QY	541	CTGCAGAAGCAGCCCAAGGGCAAGCACAAAGTCAATAAGGGGGTGTGGGAGAAACCA 600
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QY	601	AACCTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCCCTTTCATCTGTGCACTGT 660
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QY	661	GGGGCAGTGAAGCCACCTGGGATGGCTTTCATCTGCTCGCCACACTCTATGTGGCTGTC 720
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QY	841	CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTTCGCCCAAAAGTCCATTTGCCCTC 900
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QY	901	CACTACGTACACCACTGGTTCCCTGCTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA	960
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QY	1021	CGCCTGCTGCGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCTGCTG	1080
Db	1021		
QY	1081	ACACTGCTCATGGCCGTGTTTGCCCTGCTTGCGCACTGGGTTGCCCTGCGTCTGTTTAC	1140
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QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCCTGAGATTGGCTGGCGAG	1200
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QY	1201	GAGTGGCCCGCCGACTGGAGACTCCCTACTACTACCTGGTGGGCCGGAGGCCAGCTGGAGGG	1260
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QY	1261	AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGGCTG	1320
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QY	1501	ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTTCTGTATCCACAGCCCGCACGCGGAC	1560
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QY	1561	CTGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCCCTCAAGCAGCGCATGCTGGAG	1620
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QY	2161	GACAAATACCTTATGTCCACGCTGGAGAGAAGGAGACAGATGGGAGCAGGGCCCCACG	2220
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QY	2281	TCATCTCAGCTGCCAAGCTGCTATCCCCACGTTCGAACAGCACCCCGGCTCGTCTAGGT	2340
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RESULT 9  
RNO7627  
LOCUS RNO7627 3595 bp mRNA linear ROD 05-OCT-1998  
DEFINITION Rattus norvegicus mRNA for ELK channel 2.  
ACCESSION AJ007627  
VERSION AJ007627.1 GI:3702613  
KEYWORDS elk2 gene; potassium channel.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

1  
REFERENCE 1  
AUTHORS Engeland,B., Neu,A., Ludwig,J., Roeper,J. and Pongs,O.  
TITLE Identification of three rat potassium channel genes homologous to  
D. melanogaster elk  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3595)  
AUTHORS Engeland,B.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUL-1998) Engeland B., Zentrum fuer Molekulare  
Neurobiologie Hamburg, Institut fuer Neurale Signalverarbeitung,  
Martinistrasse, D-20246 Hamburg, GERMANY  
Location/Qualifiers

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DEFINITION Sequence 9 from patent US 6326168.  
ACCESSION AR179195  
VERSION AR179195.1 GI:20220750  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3715)  
AUTHORS Miyake,A., Mochizuki,S. and Yokoi,H.  
TITLE Brain specific potassium channel protein  
JOURNAL Patent: US 6326168-A 9 04-DEC-2001;  
FEATURES Location/Qualifiers  
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ORIGIN

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AB022697

LOCUS AB022697 3715 bp mRNA linear ROD 31-AUG-1999  
DEFINITION Rattus norvegicus mRNA for BEC1, complete cds.

ACCESSION AB022697

VERSION AB022697.1 GI:5804785

KEYWORDS BEC1.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (sites)

AUTHORS Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.

TITLE New ether-a-go-go K(+) channel family members localized in human

JOURNAL telencephalon

MEDLINE J. Biol. Chem. 274 (35), 25018-25025 (1999)

PUBMED 99386988

10455180

REFERENCE 2 (bases 1 to 3715)

AUTHORS Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-1999) Akira Miyake, Yamanouchi Pharmaceutical

Co.,Ltd., Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba,

Ibaraki 305-8585, Japan (E-mail:miyake@yamanouchi.co.jp,

Tel:81-298-52-5111(ex.3324), Fax:81-298-52-5444)

FEATURES Location/Qualifiers

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1 (bases 1 to 3615)  
Trudeau,M.C., Titus,S.A., Branchaw,J.L., Ganetzky,B. and  
Robertson,G.A.  
Functional analysis of a mouse brain Elk-type K+ channel  
J. Neurosci. 19 (8), 2906-2918 (1999)  
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Titus,S.A., Ganetzky,B.S., Robertson,G.A., Trudeau,M.C. and  
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AUTHORS Jegla, T., Lee, V. and Huynh, T.  
TITLE Coding sequence of the mouse potassium channel Kcnh3  
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REFERENCE 2 (bases 1 to 3285)  
AUTHORS Jegla, T., Lee, V. and Huynh, T.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2003) Neurobiology, Genomics Institute of the  
Novartis Research Foundation, 10675 John Jay Hopkins Dr., San  
Diego, CA 92121, USA

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QY	1735	C	A	G	T	G	C	C	A	C	T	G	T	T	G	A	
Db	1660	C	A	G	T	G	C	C	G	T	T	C	G	G	G	C	
QY	1795	C	G	G	C	C	G	C	T	T	C	T	G	A	C	A	
Db	1720	A	A	G	A	C	C	T	C	G	T	C	C	G	G	C	
QY	1855	C	T	C	T	A	C	T	T	T	G	T	C	T	G	C	
Db	1780	C	A	T	T	A	C	T	A	T	G	T	C	C	G	C	
QY	1915	C	T	A	G	G	A	A	G	G	C	C	T	G	A	T	
Db	1840	C	T	G	G	G	A	A	G	G	G	A	C	C	T	G	
QY	1963																
Db	1900	G	A	G	C	A	G	A	C	C	C	A	A	C	T	G	
QY	2005	G	T	C	T	G	C	A	G	T	G	G	C	T	G	C	
Db	1960	G	G	C	T	G	C	A	G	C	A	G	C	C	G	A	
QY	2065	G	C	C	C	G	C	T	T	C	A	G	T	C	G	C	
Db	2020	G	G	G	C	T	G	C	C	T	C	C	G	G	C	T	

Search completed: September 1, 2004, 17:10:17  
Job time : 8237 secs



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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 14:38:36 ; Search time 823 Seconds  
(without alignments)  
16786.319 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257  
Perfect score: 3252  
Sequence: 1 atcgccggccatgcggggcct.....aagaaggcacaggggtctga 3252

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3252	100.0	3252	9	ADC47039 BEC1 pota
2	3252	100.0	3323	2	AAX84910 Human bra
3	3250.4	100.0	3829	3	AAX87712 Human ESK
4	3245.8	99.8	3249	3	AAX50119 Human Elk
5	3244	99.8	3252	3	AAA14893 DNA encod
6	3218	99.0	3857	2	AAZ11906 Human pot
7	3156	97.0	3355	3	AAZ50452 Monkey po
8	3156	97.0	3355	7	ACA61728 Monkey ER
9	3156	97.0	3355	9	ADB66794 cDNA enco
10	3153	97.0	3249	7	ACA61729 Monkey ER
11	2664.8	81.9	3715	2	AAX84919 Rat brain
12	2664.8	81.9	3715	9	ADB58253 Toxicity-
13	884.8	27.2	3064	2	AAX84911 Human bra
14	869.8	26.7	3736	2	AAX84918 Rat brain
15	869.8	26.7	3736	9	ADB53481 Primary r
16	844.4	26.0	870	7	ACA61733 Human ERG
17	844.4	26.0	1132	3	AAZ50454 Human pot
18	844.4	26.0	1132	7	ACA61732 Human ERG
19	844.4	26.0	1132	9	ADB66798 Partial c
20	794.4	24.4	3742	3	AAZ93334 Rat elk1
21	761.2	23.4	3321	7	ACA61736 Human ERG
22	761.2	23.4	5107	3	AAZ50455 Human pot
23	761.2	23.4	5107	7	ACA61735 Human ERG

24	761.2	23.4	5107	9	ADB66803	cdNA enco
25	601	18.5	10579	4	AAK70045	Human imm
26	601	18.5	10579	5	ABA20014	Human ner
27	601	18.5	28995	4	AAK70046	Human imm
c	601	18.5	28995	4	AAK79967	Human imm
c	601	18.5	28995	4	AAK85213	Human imm
30	601	18.5	28995	5	ABA20015	Human ner
31	572.8	17.6	1626	7	ACA61731	Human ERG
32	572.8	17.6	2694	9	ADB66796	Partial c
33	572.8	17.6	5955	7	ACA61734	Human ERG
34	572.8	17.6	5955	9	ADB66802	Human ERG
35	572.4	17.6	2694	3	AAZ50453	Human pot
36	571.2	17.6	2694	7	ACA61730	Human ERG
37	561.2	17.3	20974	5	AAZ92595	DNA encod
38	384	11.8	464	3	AAZ93335	Rat elk2
39	365.6	11.2	2877	8	ADB68013	Human 529
40	365.6	11.2	3164	7	ABZ58129	Human pot
41	365.6	11.2	3164	8	ADB68011	Human 529
42	364.2	11.2	4112	4	ABL08835	Drosophil
43	364	11.2	3135	7	ABX12009	Transport
44	362.4	11.1	2746	6	ABK88234	Human erg
45	362.4	11.1	2877	6	AAL44675	Human tra

ALIGNMENTS

RESULT 1  
ADC47039  
ID ADC47039 standard; DNA; 3252 BP.  
XX  
AC ADC47039;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE BEC1 potassium channel inhibitor encoding DNA #SEQ ID 1.  
XX  
KW BEC1 potassium channel inhibitor; nootropic; neuroprotective;  
KW brain-specific eag-like channel 1; dementia; learning disability;  
KW inhibitor; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..3252  
FT /\*tag= a  
FT /product= "BEC1 potassium channel inhibitor"  
XX  
PN WO2003066099-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 03-FEB-2003; 2003WO-JP001065.  
XX  
PR 05-FEB-2002; 2002JP-00028844.  
XX  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
XX  
PI Kubota H, Suzuki T, Miura M, Nakai E, Yahiro K, Miyake A;  
PI Mochizuki S, Nakatou K;  
XX  
DR WPI; 2003-697418/66.  
DR P-PSDB; ADC47040.  
XX  
PT Antidementia agents comprise new and known brain-specific eag-like  
PT channel 1 (BEC1) potassium channel inhibitors.  
XX  
PS Disclosure; Page 75-83; 95pp; Japanese.  
XX  
CC The invention relates to an antidementia agent that comprises a brain-  
CC specific eag-like channel 1 (BEC1) potassium channel inhibitor. Agents of  
CC the invention are used as BEC1 potassium channel inhibitors for treating  
CC and preventing dementia and learning disabilities. The current sequence





Db 2041 AGCCTTGGCTGTACCCGAGTTTGCCCCCGGCTTCAAGTCGTGGCCTCCGAGGGGAGCTC 2100

QY 2101 AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGTGGAACACCAGCTCCCTGAGCGGC 2160

Db 2101 AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGTGGAACACCAGCTCCCTGAGCGGC 2160

QY 2161 GACAATACCCCTTATGTCCACGCTGGAGGAGAAGGAGACAGATGGGAGCAGGCCCCACG 2220

Db 2161 GACAATACCCCTTATGTCCACGCTGGAGGAGAAGGAGACAGATGGGAGCAGGCCCCACG 2220

QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCCCTCCAGCCCCCTGCTGTCCCCCTGGCTGCACCTCC 2280

Db 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCCCTCCAGCCCCCTGCTGTCCCCCTGGCTGCACCTCC 2280

QY 2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGACACCCCGGCTCGTCTAGGT 2340

Db 2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGACACCCCGGCTCGTCTAGGT 2340

QY 2341 GGCAGAGGGAGGCCAGGCAGGGCAGGGGCTTTGAAGCTGAGGCTGGCCCCCTGCTGCC 2400

Db 2341 GGCAGAGGGAGGCCAGGCAGGGCAGGGGCTTTGAAGCTGAGGCTGGCCCCCTGCTGCC 2400

QY 2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCAGATCTG 2460

Db 2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCAGATCTG 2460

QY 2461 AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCCCAAGTTCTCT 2520

Db 2461 AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCCCAAGTTCTCT 2520

QY 2521 TTCCGCGTGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCCCTCCCTGGACCAGAGAGC 2580

Db 2521 TTCCGCGTGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCCCTCCCTGGACCAGAGAGC 2580

QY 2581 GGCCTGCTCACTGTTCCTCCATGGGCCCCAGCGAGGCAAGGAACACAGACACTGGACAAG 2640

Db 2581 GGCCTGCTCACTGTTCCTCCATGGGCCCCAGCGAGGCAAGGAACACAGACACTGGACAAG 2640

QY 2641 CTTCCGCGAGCGGTGACAGAGCTGTCAAGCAGAGGTGTGCAGATGCGGGAAGGACTGCAG 2700

Db 2641 CTTCCGCGAGCGGTGACAGAGCTGTCAAGCAGAGGTGTGCAGATGCGGGAAGGACTGCAG 2700

QY 2701 TCACCTTCGCCAGGTGTGCAGCTTGTCTGGCGCCCCACAGGGAGGTCGCTGCCCTCGG 2760

Db 2701 TCACCTTCGCCAGGTGTGCAGCTTGTCTGGCGCCCCACAGGGAGGTCGCTGCCCTCGG 2760

QY 2761 GCATCGGGAGAGGGCCGTGCCAGCCACTCCGGGCTTCTGCAGCTCTGTGTGTG 2820

Db 2761 GCATCGGGAGAGGGCCGTGCCAGCCACTCCGGGCTTCTGCAGCTCTGTGTGTG 2820

QY 2821 GACACTGGGGCATCCTCTACTGCCTGCAGCCCCCAGCTGGCTCTGTGAGTGGGACT 2880

Db 2821 GACACTGGGGCATCCTCTACTGCCTGCAGCCCCCAGCTGGCTCTGTGAGTGGGACT 2880

QY 2881 TGGCCCCACCTCGTCCGGGGCCTCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA 2940

Db 2881 TGGCCCCACCTCGTCCGGGGCCTCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA 2940

QY 2941 GCGTCTCAGAGTCCCCCTGGCCTCGAGCCAGCTTTCTGGACCTCCACCTCAGACTCA 3000

Db 2941 GCGTCTCAGAGTCCCCCTGGCCTCGAGCCAGCTTTCTGGACCTCCACCTCAGACTCA 3000

QY 3001 GAGCCCCCTGCTCAGGAGACCTCTGTCTGAGCCCCAGCACCCCTGCTCCCTCCTCCT 3060

Db 3001 GAGCCCCCTGCTCAGGAGACCTCTGTCTGAGCCCCAGCACCCCTGCTCCCTCCTCCT 3060

QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGGAGAGCCCTGTGAGCCAGGCTGAGGCTACCAAGC 3120

Db 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGGAGAGCCCTGTGAGCCAGGCTGAGGCTACCAAGC 3120

QY 3121 ACTGGAGAGCCCCCACCAGGGTCAGGGGCGCTGGCCCTTGCCCTGGGACCCCCACAGCCTG 3180

Db 3121 ACTGGAGAGCCCCCACCAGGGTCAGGGGCGCTGGCCCTTGCCCTGGGACCCCCACAGCCTG 3180

QY 3181 GAGATGGTGTCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGC 3240

Db 3181 GAGATGGTGTCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGC 3240

QY 3241 ACAGGGGTCTGA 3252

Db 3241 ACAGGGGTCTGA 3252

RESULT 2

AAX84910  
ID AAX84910 standard; DNA; 3323 BP.

XX AAX84910;

DT 28-SEP-1999 (first entry)

XX Human brain specific potassium channel protein coding sequence.

DE Brain specific potassium channel; human; central nervous system disorder;  
XX dementia; cerebral ischaemic sclerosis; therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 6..3257  
FT /\*tag= a

XX WO9937677-A1.

XX 29-JUL-1999.

XX 20-JAN-1999; 99WO-JP000190.

XX 23-JAN-1998; 98JP-00011434.

XX 04-DEC-1998; 98JP-00346198.

XX (YAMA ) YAMANOUCHI PHARM CO LTD.

XX Miyake A, Mochizuki S, Yokoi H;

XX WPI; 1999-458683/38.

XX P-PSDB; AAY22426.

XX Potassium channel protein expressed specifically in brain tissue and  
method for its production.

XX Claim 6; Page 33-39; 63pp; English.

XX This sequence encodes the potassium channel protein of the invention,  
that is expressed specifically in brain tissue. The protein is used to  
treat and investigate disorders of the central nervous system such as  
dementia and cerebral ischaemic sclerosis

SQ Sequence 3323 BP; 577 A; 1121 C; 1018 G; 607 T; 0 U; 0 Other;

Query Match 100.0%; Score 3252; DB 2; Length 3323;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCGGCCATCGGGGCGCTCCTGGCGCCTCAGAACACCTTCTTGGACACCATCGCTACG 60

Db 6 ATGCCGGCCATCGGGGCGCTCCTGGCGCCTCAGAACACCTTCTTGGACACCATCGCTACG 65

QY 61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC 120

Db 66 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC 125

QY 121 CCCGTGGTCTACTGCTCTGATGGTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180

Db 126 CCCGTGGTCTACTGCTCTGATGGTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 185

QY 181 ATGACGGGGCTGTGCCTGCTCCTTCCTTTATGGCCAGACACAGTGAGCTCGTCCGC 240  
Db 186 ATGACGGGGCTGTGCCTGCTCCTTCCTTTATGGCCAGACACAGTGAGCTCGTCCGC 245  
QY 241 CAACAGATCCGAAGGCCCTGGACGAGCAAGGAGTTCAAGGCTGAGTGATCCTGTAC 300  
Db 246 CAACAGATCCGAAGGCCCTGGACGAGCAAGGAGTTCAAGGCTGAGTGATCCTGTAC 305  
QY 301 CGGAAGAGCGGCTCCCGTTCTGGTGTCTCCTGGATGTATACCCATAAAGAATGAGAA 360  
Db 306 CGGAAGAGCGGCTCCCGTTCTGGTGTCTCCTGGATGTATACCCATAAAGAATGAGAA 365  
QY 361 GGGAGGTGGCTCTCTCCTAGTCTCTCAACAGACATCAGCGAAACCCAAAGACCGAGG 420  
Db 366 GGGAGGTGGCTCTCTCCTAGTCTCTCAACAGACATCAGCGAAACCCAAAGACCGAGG 425  
QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCCGATATGGCCGGCACGATCC 480  
Db 426 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCCGATATGGCCGGCACGATCC 485  
QY 481 AAAGGCTTCAATGCCAAACCGCGGAGCCGGCCCGTGTCTACCACTGTCCGGGCAC 540  
Db 486 AAAGGCTTCAATGCCAAACCGCGGAGCCGGCCCGTGTCTACCACTGTCCGGGCAC 545  
QY 541 CTGCAGAAAGCAGCCCAAGGCAAGCAAAAGTCAATAAGGGGTGTTTGGGAGAAACCA 600  
Db 546 CTGCAGAAAGCAGCCCAAGGCAAGCAAAAGTCAATAAGGGGTGTTTGGGAGAAACCA 605  
QY 601 AACTTGCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCTTTCATCCTGTGTGCACTGT 660  
Db 606 AACTTGCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCTTTCATCCTGTGTGCACTGT 665  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGTGCGCCACACTCTATGTGCTGTC 720  
Db 666 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGTGCGCCACACTCTATGTGCTGTC 725  
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCAAGTCCCGCCCGGCCCCG 780  
Db 726 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCAAGTCCCGCCCGGCCCCG 785  
QY 781 CCCAGCGTGTGACCTGGCCGTGGAGGTCTCTTCATCCTTGACATTTGCTGAATTC 840  
Db 786 CCCAGCGTGTGACCTGGCCGTGGAGGTCTCTTCATCCTTGACATTTGCTGAATTC 845  
QY 841 CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTCCTTCAATCCTTGACATTTGCTG 900  
Db 846 CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTCCTTCAATCCTTGACATTTGCTG 905  
QY 901 CACTACGTCAACCACTGGTTCTCTGTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA 960  
Db 906 CACTACGTCAACCACTGGTTCTCTGTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA 965  
QY 961 CATGCCCTTCAAGGTCAAAGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCCCTGCTG 1020  
Db 966 CATGCCCTTCAAGGTCAAAGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCCCTGCTG 1025  
QY 1021 CGCTGCTGCGCCTGCTTCCGCGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGTGCTG 1080  
Db 1026 CGCTGCTGCGCCTGCTTCCGCGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGTGCTG 1085  
QY 1081 ACCTGCTCATGGCCGTTTCCGCTGCTCGCCACTGGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
Db 1086 ACCTGCTCATGGCCGTTTCCGCTGCTCGCCACTGGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1145  
QY 1141 ATTGGCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTTGGCTGGCTGCGAG 1200  
Db 1146 ATTGGCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTTGGCTGGCTGCGAG 1205  
QY 1201 GAGCTGGCCCGGACTGGAGACTCCCTACTACCTGTGGTGGCCGAGGCGCAGCTGGAGGG 1260  
Db 1206 GAGCTGGCCCGGACTGGAGACTCCCTACTACCTGTGGTGGCCGAGGCGCAGCTGGAGGG 1265  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGACAGCAGCAGCGAGGCGCAACGGGAGCGGGCTG 1320

Db 1266 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTG 1325  
QY 1321 GAGCTGTGGGCGGCCGTGCTGCTGGCAGCGCCTATACATCACTCCTCTACTTCGCACTC 1380  
Db 1326 GAGCTGTGGGCGGCCGTGCTGCTGGCAGCGCCTATACATCACTCCTCTACTTCGCACTC 1385  
QY 1381 AGCAGCCTCACAGCGTGGGCTTCGGCAACAGTGTCCGCCAAACACGAGACCGGAGATC 1440  
Db 1386 AGCAGCCTCACAGCGTGGGCTTCGGCAACAGTGTCCGCCAAACACGAGACCGGAGATC 1445  
QY 1441 TTCTCCATCTGCACCATGCTCATCGSGCGCCTGATGACGCGTGGTGTGGAAACGTG 1500  
Db 1446 TTCTCCATCTGCACCATGCTCATCGSGCGCCTGATGACGCGTGGTGTGGAAACGTG 1505  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCGCGCCTTCTGTACCACAGCCGACCGCGGAC 1560  
Db 1506 ACGGCCATCATCCAGCGCATGTACGCGCGCCTTCTGTACCACAGCCGACCGCGGAC 1565  
QY 1561 CTGCGGCACTACATCCCGCATCCACCGTATCCCCAAGCCCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 1566 CTGCGGCACTACATCCCGCATCCACCGTATCCCCAAGCCCCCTCAAGCAGCGCATGCTGGAG 1625  
QY 1621 TACTTCCAGGCCACTGGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGC 1680  
Db 1626 TACTTCCAGGCCACTGGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGC 1685  
QY 1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGACACTGCACAAGGAGGTCTGCAAGCTG 1740  
Db 1686 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGACACTGCACAAGGAGGTCTGCAAGCTG 1745  
QY 1741 CCACTGTTTGAGGCGCGCAGCGCGCTGCTGCGGCGCACTGTCTCTGGCCCTGCGGCC 1800  
Db 1746 CCACTGTTTGAGGCGCGCAGCGCGCTGCTGCGGCGCACTGTCTCTGGCCCTGCGGCC 1805  
QY 1801 GCCTTCTGCACGCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1860  
Db 1806 GCCTTCTGCACGCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1865  
QY 1861 TTTGTCTGCTCTGGTCCATGGAGGTGCTCAAGGTGGCACCGTGTGCGCCATCCTAGGG 1920  
Db 1866 TTTGTCTGCTCTGGTCCATGGAGGTGCTCAAGGTGGCACCGTGTGCGCCATCCTAGGG 1925  
QY 1921 AAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 1926 AAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGGCCAATGCC 1985  
QY 1981 GACGTGAAGGGGTGACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
Db 1986 GACGTGAAGGGGTGACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2045  
QY 2041 AGCCTTGCCTGTACCCCGAGTTTGGCCGCGCTTCAAGTGTGGCTTCCGAGGGGAGCTC 2100  
Db 2046 AGCCTTGCCTGTACCCCGAGTTTGGCCGCGCTTCAAGTGTGGCTTCCGAGGGGAGCTC 2105  
QY 2101 AGCTAACACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAAGCTCCCTGAGCGGC 2160  
Db 2106 AGCTAACACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAAGCTCCCTGAGCGGC 2165  
QY 2161 GACAATACCTTTATGTCCAGCTGGAGGAGAGGAGACAGATGGGGAGCAGGGCCCCACG 2220  
Db 2166 GACAATACCTTTATGTCCAGCTGGAGGAGAGGAGACAGATGGGGAGCAGGGCCCCACG 2225  
QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTGTGCTGCTGCTGCTGCTGCTG 2280  
Db 2226 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTGTGCTGCTGCTGCTGCTGCTG 2285  
QY 2281 TCATCCTCAGCTGCCAAGCTGCTATCCACGTGCAACAGACACCCCGGCTCGTCTAGGT 2340  
Db 2286 TCATCCTCAGCTGCCAAGCTGCTATCCACGTGCAACAGACACCCCGGCTCGTCTAGGT 2345  
QY 2341 GGCAGAGGAGGCCAGGCGAGGCGAGGGCTTTGAAGGTGAGGCTGAGGCTGAGGCTGAGGCTG 2400



Db 2346 GGCAGAGGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCTCTGTCTCC 2405

QY 2401 CCACGGCCCTAGAGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2460

Db 2406 CCACGGCCCTAGAGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2465

QY 2461 AGCCCCAGGCTAGATGGCATTTGAAGCGGCTGTGGCTCGGACCAAGCCCAAGTTCTCT 2520

Db 2466 AGCCCCAGGCTAGATGGCATTTGAAGCGGCTGTGGCTCGGACCAAGCCCAAGTTCTCT 2525

QY 2521 TTCCGCTGGGCCAGTCTGGCCCCGGGAATGTAGCAGCAGCCCCCTCCCTGGACCAGAGGC 2580

Db 2526 TTCCGCTGGGCCAGTCTGGCCCCGGGAATGTAGCAGCAGCCCCCTCCCTGGACCAGAGGC 2585

QY 2581 GGCCTGCTCACTGTTCCCATGTTGGCCCCAGCGAGGCAAGGAACACACACACTGGACAAG 2640

Db 2586 GGCCTGCTCACTGTTCCCATGTTGGCCCCAGCGAGGCAAGGAACACACACACTGGACAAG 2645

QY 2641 CTTCGGCAGGCGGTGACAGAGCTGTACAGAGCTGTACAGCAGGTGCTGCGGGAAGGACTGCAG 2700

Db 2646 CTTCGGCAGGCGGTGACAGAGCTGTACAGAGCTGTACAGCAGGTGCTGCGGGAAGGACTGCAG 2705

QY 2701 TCACTTCGCCAGGCTGTGCAGCTGTCTCTGGCCCCCAGGAGGGTCCGTGCCCTCGG 2760

Db 2706 TCACTTCGCCAGGCTGTGCAGCTGTCTCTGGCCCCCAGGAGGGTCCGTGCCCTCGG 2765

QY 2761 GCATCGGGAGAGGGGCCGTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820

Db 2766 GCATCGGGAGAGGGGCCGTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2825

QY 2821 GACACTGGGGCATCCTCTACTGCTGCAGCCAGCCAGCCCCAGCTGGCTCTGTGTGTGTG 2880

Db 2826 GACACTGGGGCATCCTCTACTGCTGCAGCCAGCCAGCCCCAGCTGGCTCTGTGTGTGTG 2885

QY 2881 TGGCCCCACCCCTCGTCCGGGCTCTCTCCCTCATGSCACCCCTGGCCCTGGGGTCCCCCA 2940

Db 2886 TGGCCCCACCCCTCGTCCGGGCTCTCTCCCTCATGSCACCCCTGGCCCTGGGGTCCCCCA 2945

QY 2941 GCGTCTCAGAGCTCCCTCGGCTCGAGCCAGCTTTCTGGACCTCCACCTCAGACTCA 3000

Db 2946 GCGTCTCAGAGCTCCCTCGGCTCGAGCCAGCTTTCTGGACCTCCACCTCAGACTCA 3005

QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGTCTGAGCCAGCACCCCTGCCTCCCTCCCTCCT 3060

Db 3006 GAGCCCCCTGCCTCAGGAGACCTCTGTCTGAGCCAGCACCCCTGCCTCCCTCCCTCCT 3065

QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCTGTGAGCCAGGCTGAGGCTACCCAGC 3120

Db 3066 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCTGTGAGCCAGGCTGAGGCTACCCAGC 3125

QY 3121 ACTGGAGAGCCCCACAGGCTCAGGGGCTGCGGCTTGCCCTGGGACCCCCACAGCCTG 3180

Db 3126 ACTGGAGAGCCCCACAGGCTCAGGGGCTGCGGCTTGCCCTGGGACCCCCACAGCCTG 3185

QY 3181 GAGATGGTGCTTATTTGGCTGCCATGGCTCTGSCACAGTCCAGTGGACCCAGGAAGGC 3240

Db 3186 GAGATGGTGCTTATTTGGCTGCCATGGCTCTGSCACAGTCCAGTGGACCCAGGAAGGC 3245

QY 3241 ACAGGGGTCTGA 3252

Db 3246 ACAGGGGTCTGA 3257

RESULT 3

AAZ87712

ID AAZ87712 standard; DNA; 3829 BP.

XX

AC

AAZ87712;

XX

DT 19-MAY-2000 (first entry)

XX

DE Human ESK1 (hESK1) protein encoding DNA.

XX

KW ESK1; eag similar K+ channel; potassium channel associated disorder; neurological; Alzheimer's disease; anxiety; panic; autism; hyperactivity; KW obsessive-compulsive disorder; schizophrenia; Huntington's disease; KW epilepsy; cardiovascular; musculoskeletal; proliferative; cancer; KW ESK channel blocker; nootropic; neuroprotective; antidepressant; KW tranquilizer; neuroleptic; antiParkinsonian; cardiant; cytostatic; KW anticonvulsant; ds.

XX Homo sapiens.

OS  
XX  
FH Location/Qualifiers  
FT 254..3496  
FT /\*tag= a  
FT /product= "ESK1 protein"

XX WO200009534-A1.

XX 24-FEB-2000.

XX 13-AUG-1999; 99WO-US018556.

XX 14-AUG-1998; 98US-0096570P.

XX (ELAN-) ELAN PHARM INC.

XX Forsayeth JR, Zhao BB;

XX WPI; 2000-224270/19.

XX P-PSDB; AAY77738.

XX Novel eag similar potassium channel polypeptide useful for treating various neurological, cardiovascular, musculoskeletal and proliferative disorders.

XX Claim 8; Fig 1A-E; 52pp; English.

XX This DNA encodes a eag similar K+ channel (ESK) polypeptide (hESK1). The hESK1 protein can be expressed by standard recombinant methodology. The ESK polypeptide, polynucleotides and antibodies are useful for treating and diagnosing various potassium channel associated disorders such as neurological disorders, e.g. Alzheimer's disease, depression, anxiety, panic, obsessive-compulsive disorders, attention deficit, epilepsy, hyperactivity disorders, autism, schizophrenia, Huntington's disease and Parkinson's disease, cardiovascular disorders, musculoskeletal disorders and proliferative disorders such as cancer. The ESK polynucleotide is also useful for synthesis of ESK and gene mapping. The polypeptide can be used in an assay to identify molecules such as synthetic drugs, antibodies, peptides or other molecules which have an effect on the activity of the ESK channel

XX Sequence 3829 BP; 650 A; 1302 C; 1202 G; 675 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 3250.4; DB 3; Length 3829;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 3251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60

Db 245 ATGCCGGCCATGCGGGCCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 304

QY 61 CGCTTCGACGGCAGCACAGTAATCTGCTGGGCAACGCCAGGTGGGGCTCTTC 120

Db 305 CGCTTCGACGGCAGCACAGTAATCTGCTGGGCAACGCCAGGTGGGGCTCTTC 364

QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGCTGAGGTC 180

Db 365 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGCGGCTTCTCCCGGCTGAGGTC 424

QY 181 ATGCAGCGGGGCTGTGCCTGCTCCTTCTTATGGGCCACACACAGTGAGTCTGTCGCGC 240

Db 425 ATGCAGCGGGGCTGTGCCTGCTCCTTCTTATGGGCCACACACAGTGAGTCTGTCGCGC 484

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Db 241 CAACAGATCCGCAAGGCCCTGGACGAGCAAAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Qy 301 CGGAAGAGCGGGTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAATGAGAAA 360  
Db 301 CGGAAGAGCGGGTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAATGAGAAA 360  
Qy 361 GGGGAGGTGGCTCTCTTCTTAGTCTCTCACAAAGACATCAGCGAAACCAAGAACCGAGGG 420  
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Qy 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCCGATATGGCCGGCACGATCC 480  
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Db 481 AAAGGCTTCAATGCCAACCGCGCGGAGCCGGSCGTGCTCTACCACTGTCCGGGCAC 540  
Qy 541 CTGCAGAAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600  
Db 541 CTGCAGAAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600  
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Qy 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCACTCTGTGCGCCACACTCTATGTGGCTGTC 720  
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Qy 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCACTCTTGACATTGTGCTGAATTTC 840  
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Db 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCCCTGCTG 1020  
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Db 1021 CGCCTGTGCGCCTGCTTCCGCGGTGGACCGGTACTCGAGTACAGCGCGGTGGTGTG 1080  
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Db 1081 ACATGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCGCTGCGTTTAC 1140  
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Db 1141 ATTGGCCAGCGGAGATCGAGACAGCGAAATCCGAGTGCCTGAGATTGGCTGGCTGCGAG 1200  
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Db 1201 GAGCTGGCCCCGCGACTGGAGACTCCCTACTACTACTGGTGGCGCGAGGCCAGCTGGAGGG 1260  
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QY 481 AAAGGCTTCAATGCCAACCGGCGCGGAGCCGGCGTGTCTACCACTGTCCGGGCAC 540  
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RESULT 6  
AAZ11906  
ID AAZ11906 standard; cDNA; 3857 BP.  
XX  
AC AAZ11906;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human potassium channel K+Hnov14 cDNA.  
XX  
KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;  
KW cardiovascular disorder; CNS disorder; renal disorder; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key  
CDS Location/Qualifiers  
FT 249..3497  
FT /\*tag= a  
FT /product= "Human K+Hnov14 potassium channel"  
FT replace(3168,T)  
FT /\*tag= b  
XX  
PN WO943696-A1.  
XX  
PD 02-SEP-1999.  
XX  
PF 22-FEB-1999; 99WO-US003826.  
XX  
PR 25-FEB-1998; 98US-0076687P.

PR 07-AUG-1998; 98US-0095836P.  
PR 19-JAN-1999; 99US-0116448P.  
XX  
PA (AXYS-) AXYS PHARM INC.  
XX  
PI Miller AP, Curran ME, Hu P, Rutter M, Wang J;  
XX  
DR WPI; 1999-527591/44.  
DR P-PSDB; AAY34128.  
XX  
PT New nucleic acids encoding mammalian K+Hnov potassium channel proteins,  
PT useful for the diagnosis and treatment of episodic ataxia with myokymia,  
PT cardiac arrhythmia, epilepsy and Bartter's syndrome.  
XX  
PS Claim 4; Page 72-76; 112pp; English.  
XX  
CC This sequence represents human potassium channel K+Hnov14 cDNA. K+Hnov  
CC proteins have a high degree of homology to known potassium channels and  
CC may be alpha subunits, which form the functional channel, or accessory  
CC subunits that act to modulate the channel activity. K+Hnov14 is a 6  
CC transmembrane domain, voltage gated potassium channel. The gene's  
CC chromosomal location is 12q14, determined via PCR chromosomal  
CC localisation using primers AAZ11928 and AAZ11929. K+Hnov cDNAs were  
CC isolated by extension of expressed sequence tags (ESTs) which were  
CC related but not identical to known human potassium channels. Potential  
CC polymorphisms detected as sequence variants between multiple independent  
CC clones. Potassium channels have critical roles in various cell types and  
CC biochemical pathways. Defective potassium channels are known to cause  
CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia  
CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium  
CC channels are critical components of virtually all cells, it is likely  
CC that abnormal potassium channels are also implicated in certain renal,  
CC cardiovascular and central nervous system (CNS) disorders. Nucleotides  
CC encoding K+Hnov proteins may be used for identifying homologous or  
CC related proteins and the DNA sequences encoding them. They may be used to  
CC produce compositions that modulate the expression and function of the  
CC K+Hnov protein and in studying the biochemical pathways associated with  
CC it. They may also be used for the recombinant production of K+Hnov  
CC protein in fermentation cultures. Additionally, such nucleotides may be  
CC used in gene therapy protocols for the treatment of diseases associated  
CC with abnormal potassium channels  
XX  
SQ Sequence 3857 BP; 677 A; 1301 C; 1201 G; 678 T; 0 U; 0 Other;

Query Match 99.0%; Score 3218; DB 2; Length 3857;  
Best Local Similarity 99.8%; Pred. NO. 0;  
Matches 3244; Conservative 0; Mismatches 5; Indels 3; Gaps 2;  
QY 1 ATGCCGGCCATGCGGGGCTCCTGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60  
Db 249 ATGCCGGCCATGCGGGGCTCCTGGCGCGCAGAACACCTTCTCTGGACACCATCGCTACG 308  
QY 61 CGCTTCGACGCGCACAGTAACCTCGTCTGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 309 CGCTTCGACGCGCACAGTAACCTCGTCTGGCAACGCC--AGTGGCGGGCTCTT- 365  
QY 121 CCCGTGGTCTACTGCTCTGTATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTGAGGTC 180  
Db 366 CCCGTGGTCTACTGCTCTGTATGGCTTCTGTGACCTCAGGGCTTCTCCGGGCTGAGGTC 425  
QY 181 ATGCAGCGGGGCTGTGCCTGCTCTCTCTTATGGCCAGACACAGTGTGCTGTAC 240  
Db 426 ATGCAGCGGGGCTGTGCCTGCTCTCTCTTATGGCCAGACACAGTGTGCTGTAC 485  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAGGAGTTCAAGCTGAGCTGATCTGTAC 300  
Db 486 CAACAGATCCGCAAGGCCCTGGACGAGCACAGGAGTTCAAGCTGAGCTGATCTGTAC 545  
QY 301 CGGAGAGCGGGCTCCCGTTCTGTGTCTCTCTGGATGTATACCCATAAAGATGAGAAA 360  
Db 546 CGGAGAGCGGGCTCCCGTTCTGTGTCTCTCTGGATGTATACCCATAAAGATGAGAAA 605  
QY 361 GGGAGGTGGCTCTCTTCTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGACCGAGGG 420

Db 606 GGGGAGGTGGCTCTCTTCTCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGGG 665  
QY 421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCGATATGGCCGGGACGATCC 480  
Db 666 GGCCCCGACAGATGGAAGAGACAGGTGGTGGCCGGCCGATATGGCCGGGACGATCC 725  
QY 481 AAAGGCTTCAATGCCAAACCGGCGGAGCGGGCCGCTCTTACACCTGTCCGGGCAC 540  
Db 726 AAAGGCTTCAATGCCAAACCGGCGGAGCGGGCCGCTCTTACACCTGTCCGGGCAC 785  
QY 541 CTGCAGAAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600  
Db 786 CTGCAGAAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 845  
QY 601 AACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCTTTCATCCTGTGCACTGT 660  
Db 846 AACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTGCCTTTCATCCTGTGCACTGT 905  
QY 661 GGGGCACTGAGAGCCACTGGGATGGCTTTCATCCTGTGCGCACACTCTATGTGGCTGTC 720  
Db 906 GGGGCACTGAGAGCCACTGGGATGGCTTTCATCCTGTGCGCACACTCTATGTGGCTGTC 965  
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCCAGTGCCCGCCGCGGCCCG 780  
Db 966 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCCAGTGCCCGCCGCGGCCCG 1025  
QY 781 CCCAGCGTCTGTGACCTGGCCCGTGGAGGTCTCTTTCATCCTTGACATTGTGTAATTTC 840  
Db 1026 CCCAGCGTCTGTGACCTGGCCCGTGGAGGTCTCTTTCATCCTTGACATTGTGTAATTTC 1085  
QY 841 CGTACCACATTCTGTGTCAAGTCCGGCCAGGTGGTGTGTCCTTTCATCCTTGACATTTC 900  
Db 1086 CGTACCACATTCTGTGTCAAGTCCGGCCAGGTGGTGTGTCCTTTCATCCTTGACATTTC 1145  
QY 901 CACTACGTCAACCACTGGTTCTGTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA 960  
Db 1146 CACTACGTCAACCACTGGTTCTGTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA 1205  
QY 961 CATGCCTTCAAGGTCAACGTGTACTTCCGGGCCCATCTGTCTGAAGACGGTGGCCCTGCTG 1020  
Db 1206 CATGCCTTCAAGGTCAACGTGTACTTCCGGGCCCATCTGTCTGAAGACGGTGGCCCTGCTG 1265  
QY 1021 CGCCTGCTGGCCCTGCTTCCGGCGCTGGACCGGTACTCCAGTACAGCCCGCTGTGCTG 1080  
Db 1266 CGCCTGCTGGCCCTGCTTCCGGCGCTGGACCGGTACTCCAGTACAGCCCGCTGTGCTG 1325  
QY 1081 ACACGTGCTCATGGCCGTGTCCGCCCTGCTCGCGCACTGGGTGCTGCTGCTGCTGTTTAC 1140  
Db 1326 ACACGTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGGTGCTGCTGCTGCTGTTTAC 1385  
QY 1141 ATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGTGCCTGAGATTGGCTGGCTGCAG 1200  
Db 1386 ATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGTGCCTGAGATTGGCTGGCTGCAG 1445  
QY 1201 GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGCCGAGGCCAGCTGGAGGG 1260  
Db 1446 GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGCCGAGGCCAGCTGGAGGG 1505  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAAACGGGACGGGGCTG 1320  
Db 1506 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAAACGGGACGGGGCTG 1565  
QY 1321 GAGCTGTGGGCGGCCCGCTGCTGCGCAGCGCCTACATCACCTTCCCTTACTTCGCACCTC 1380  
Db 1566 GAGCTGTGGGCGGCCCGCTGCTGCGCAGCGCCTACATCACCTTCCCTTACTTCGCACCTC 1625  
QY 1381 AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAAACAGGACACCGAGAAGATC 1440  
Db 1626 AGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAAACAGGACACCGAGAAGATC 1685  
QY 1441 TTCTCCATCTGCACCATGTCTATCGCGCCCTGATGACGCGGTGGTGTGGGAAACGTG 1500

Db 1686 TTCTCCATCTGCACCATGTCTCATCGCGCCCTGATGACGCGTGGTGTGGGAAACGTG 1745  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCAAGCCGACGCGCGAC 1560  
Db 1746 ACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCAAGCCGACGCGCGAC 1805  
QY 1561 CTGGCGACTACATCCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 1806 CAGCGCACTACATCCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1865  
QY 1621 TACTTCCAGCCACCTGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGC 1680  
Db 1866 TACTTCCAGCCACCTGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGC 1925  
QY 1681 CTCCTGACGAGCTGCGCGAGACATCGCCATGCACCTGCACAAGGAGGTCTGCAAGCTG 1740  
Db 1926 CTCCTGACGAGCTGCGCGAGACATCGCCATGCACCTGCACAAGGAGGTCTGCAAGCTG 1985  
QY 1741 CCACCTTGTAGCGCGCCAGCCCGGCTGCTGCGGGCACTGTCTCTGGCCCTGCGGCC 2045  
Db 1986 CCACCTTGTAGCGCGCCAGCCCGGCTGCTGCGGGCACTGTCTCTGGCCCTGCGGCC 2045  
QY 1801 GCCTTCTGCACGCGCGCGAGTACCTCATCCACCAAGGCGATGCCCTGAGGCCCTCTAC 1860  
Db 2046 GCCTTCTGCACGCGCGCGAGTACCTCATCCACCAAGGCGATGCCCTGAGGCCCTCTAC 2105  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTGCCATCCTAGGG 1920  
Db 2106 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTGCCATCCTAGGG 2165  
QY 1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGGGAGCAGGTGTTAAAGGCCAATGCC 1980  
Db 2166 AAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGCGGAGCAGGTGTTAAAGGCCAATGCC 2225  
QY 1981 GACGTGAAGGGGTGACGTACTGCGTCTGCAAGTGTCTGAGCTGGCTGGCCCTGCAAGC 2040  
Db 2226 GACGTGAAGGGGTGACGTACTGCGTCTGCAAGTGTCTGAGCTGGCTGGCCCTGCAAGC 2285  
QY 2041 AGCCTTGCCTGTACCCCGAGTTTGCCCGCGCTTCAAGTGTGAGTGTCCGAGGGAGCTC 2100  
Db 2286 AGCCTTGCCTGTACCCCGAGTTTGCCCGCGCTTCAAGTGTGAGTGTCCGAGGGAGCTC 2345  
QY 2101 AGCTACAACTGGTGTGGGGAGGCTCTGCAAGGTGGACACAGCTCCCTGAGCGGC 2160  
Db 2346 AGCTACAACTGGTGTGGGGAGGCTCTGCAAGGTGGACACAGCTCCCTGAGCGGC 2405  
QY 2161 GACAATAACCTTATGTCCAGCTGGAGGAGAGGAGACAGATGGGAGCAGGCCCCACG 2220  
Db 2406 GACAATAACCTTATGTCCAGCTGGAGGAGAGGAGACAGATGGGAGCAGGCCCCACG 2465  
QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCCCTGGCTGCACCTC 2280  
Db 2466 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCCCTGGCTGCACCTC 2525  
QY 2281 TCATCCTCAGTGCCTGCTATCCCCAGTGCAGACAGCACCCCGCCCTCGTCTAGGT 2340  
Db 2526 TCATCCTCAGTGCCTGCTATCCCCAGTGCAGACAGCACCCCGCCCTCGTCTAGGT 2585  
QY 2341 GGCAGAGGGAGGCCAGGCGAGGCGAGGGCTTTGAAGGTGAGGCTGGCCCTCTGCTCCC 2400  
Db 2586 GGCAGAGGGAGGCCAGGCGAGGCGAGGGCTTTGAAGGTGAGGCTGGCCCTCTGCTCCC 2645  
QY 2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2460  
Db 2646 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2705  
QY 2461 AGCCCCAGGGTAGTAGATGGCATTTGAAGACGGCTGTGGCTCGGACAGCCCCAAGTTCTCT 2520  
Db 2706 AGCCCCAGGGTAGTAGATGGCATTTGAAGACGGCTGTGGCTCGGACAGCCCCAAGTTCTCT 2765  
QY 2521 TTCCGCGTGGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCCCTCCCTGGACGAGAGC 2580  
Db 2766 TTCCGCGTGGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCCCTCCCTGGACGAGAGC 2825

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QY 2581 GGCGTGTCTACTGTTCCCATGGGCCCCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2640
Db 2826 GGCGTGTCTACTGTTCCCATGGGCCCCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2885

QY 2641 CTTCCGCAGGCGGTGACAGAGCTGTTCAGAGCAGGTGTCTCAGATGCGGGAAGGACTGCAG 2700
Db 2886 CTTCCGCAGGCGGTGACAGAGCTGTTCAGAGCAGGTGTCTCAGATGCGGGAAGGACTGCAG 2945

QY 2701 TCACCTTCGCCAGGCTGTTCAGAGCTGTTCCTTGGCGCCCCACAGGAGGTCCTCGTCCCTCGG 2760
Db 2946 TCACCTTCGCCAGGCTGTTCAGAGCTGTTCCTTGGCGCCCCACAGGAGGTCCTCGTCCCTCGG 3005

QY 2761 GCATCGGAGAGGGGCGGTGCCCCAGCCAGCACCTCGGGCTTCTGCAGCCTCTGTGTGTG 2820
Db 3006 GCATCGGAGAGGGGCGGTGCCCCAGCCAGCACCTCGGGCTTCTGCAGCCTCTGTGTGTG 3065

QY 2821 GACACTGGGGCATCTCTCTACTGCTGCCTGCAGCCCCCAGCTGGCTCTGTCTTGTGGGACT 2880
Db 3066 GACACTGGGGCATCTCTCTACTGCTGCCTGCAGCCCCCAGCTGGCTCTGTCTTGTGGGACT 3125

QY 2881 TGGCCCCACCCTCGTCGGGGCCTCTCTCCCTCATGCGCACCCCTGGCCCTGGGFTCCCCCA 2940
Db 3126 TGGCCCCACCCTCGTCGGGGCCTCTCTCCCTCATGCGCACCCCGCCCTGGGFTCCCCCA 3185

QY 2941 GCGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000
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QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGTCTGAGCCCGAGCACCCCTGCTCCCTCCCTCCTCCT 3060
Db 3246 GAGCCCCCTGCCTCAGGAGACCTCTGTCTGAGCCCGAGCACCCCTGCTCCCTCCCTCCTCCT 3305

QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC 3120
Db 3306 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC 3365

QY 3121 ACTGGAGAGCCCCACCAGGGTCAAGGGGCTGCGGCTTGCCCTGGGACCCCCACAGCCTG 3180
Db 3366 ACTGGAGAGCCCCACCAGGGTCAAGGGGCTGCGGCTTGCCCTGGGACCCCCACAGCCTG 3425

QY 3181 GAGATGCTGCTATTGGCTGCCATGGCTTGGCACAGTCCAGTGGACCCAGGAAGGC 3240
Db 3426 GAGATGCTGCTATTGGCTGCCATGGCTTGGCACAGTCCAGTGGACCCAGGAAGGC 3485

QY 3241 ACAGGGGTCTGA 3252
Db 3486 ACAGGGGTCTGA 3497
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RESULT 7
AAZ50452
ID AAZ50452 standard; cdNA; 3355 BP.
XX AC
AC AAZ50452;
XX AC
XX 18-MAY-2000 (first entry)
XX DE
DE Monkey potassium channel molecule ERG-LP1 cdNA.
XX KW
KW Monkey; potassium channel molecule; ERG-like protein 1; ERG-LP1;
KW neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;
KW neuroleptic; nootropic; treatment; CNS disorder; central nervous system;
KW potassium channel mediated disorder; epilepsy; Alzheimer's disease;
KW Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia; ss.
XX OS
OS Primates.
```

```
XX Key Location/Qualifiers
FH 5'UTR 1..103
FT /*tag= a
FT 104..3355
FT /*tag= b
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FT /product= "ERG-Lp1"
XX /note= "This region is specifically claimed"
PN WO200005346-A1.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-US016752.
XX
PR 21-JUL-1998; 98US-00119855.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Curtis RAJ;
XX
DR WPI; 2000-182682/16.
DR P-PSDB; AAY44904.
PT Novel gene encoding potassium channel molecule useful in treating central
PT nervous system disorders such as Alzheimer's disease, multiple sclerosis,
PT and schizophrenia.
XX Claim 2; Fig 1; 144pp; English.
XX
CC The present sequence is a cDNA encoding ERG-like protein 1 (ERG-LP1)
CC which is a member of ERG potassium channel family. This sequence is from
CC a full length clone jlkba25d10 which was derived from monkey hippocampal
CC library. ERG-LP1 is expressed exclusively in the brain. Highest
CC expression is found in cortical regions, hippocampus, caudate and
CC amygdala. The protein functions as a potassium channel modulator and has
CC neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
CC neuroleptic and nootropic activities. The present sequence is useful for
CC treating several potassium channel mediated disorders (CNS disorders)
CC such as Alzheimer's disease, Parkinson's disease, multiple sclerosis,
CC epilepsy, depression, schizophrenic disorders and amnesia
XX
SQ Sequence 3355 BP; 580 A; 1128 C; 1041 G; 506 T; 0 U; 0 Other;

Query Match 97.0%; Score 3156; DB 3; Length 3355;
Best local Similarity 98.2%; Pred. No. 0;
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGCCGGCCATCGGGGCTCTCTGATGGCTTCTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180
Db 104 ATGCCGGCCATCGGGGCTCTCTGATGGCTTCTGACCTCACGGGCTTCTCCCGGCTGAGGTC 283
QY 61 CGCTTCGACGGCACGCACAGTAACCTTCTGCTGGGCAACGCCAGGTCGGGGCTCTTC 120
Db 164 CGCTTCGACGGCACGCACAGTAACCTTCTGCTGGGCAACGCCAGGTCGGGGCTCTTC 223
QY 121 CCCGTGTCTACTGCTCTGATGGCTTCTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180
Db 224 CCCGTGTCTACTGCTCTGATGGCTTCTGACCTCACGGGCTTCTCCCGGCTGAGGTC 283
QY 181 ATGCAGCGGGCTGTGCCTGCTCCTTCTCTTATGGCCAGACACAGTGTAGCTCGTCCGC 240
Db 284 ATGCAGCGGGCTGTGCCTGCTCCTTCTCTTATGGCCAGACACAGTGTAGCTCGTCCGC 343
QY 241 CAACAGATCCGCAAGGCCCTTGACGAGCAACAAGGATTCAAGGCTGAGCTGATCCTGTAC 300
Db 344 CAACAGATCCGCAAGGCCCTTGACGAGCAACAAGGATTCAAGGCTGAGCTGATCCTGTAC 403
QY 301 CGAAGAGCGGGCTCCCGTCTGCTGCTCTCTGATGTGATACCCATAAAGAATGAGAAA 360
Db 404 CGAAGAGCGGGCTCCCGTCTGCTGCTCTCTGATGTGATACCCATAAAGAATGAGAAA 463
QY 361 GGGAGGTGGCTCTCTTCTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGACCGAGG 420
Db 464 GGGAGGTGGCTCTCTTCTCTAGTCTCTCACAAGGACATCAGTGAACCAAGACCGAGG 523
QY 421 GGGCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGCCGATATGGCCGGGCACGATCC 480
Db 524 GGGCCCTGACAGATGGAAGGAGACAGGTAGTGGCCGCGCCGATATGGCCGGGCACGATCC 583
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QY	481	AAAGGCTTCAATGTCACCAACCGCGCGGAGCGGGCGGTGCTCTATACCACCTGTCCGGGCAC	540
Db	584	AAAGGCTTCAATGTCACCAACCGCGCGGAGCGGGCTGTCTCTACCACTGTCCGGGCAC	643
QY	541	CTGCAGAGCAGCCCAAGGCAAGCAACAGCTCAATAAGGGGGTGTCTTGGGAGAAACCA	600
Db	644	CTGCAGAGCAGCCCAAGGCAAGCAACAGCTCAATAAGGGGGTGTCTTGGGAGAAACCA	703
QY	601	AACCTTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTGCACTGT	660
Db	704	AACCTTGCTGAGTACAAAGTAGCTGCCATCCGGAAGTCGCCCTTCATCCTGTGCACTGT	763
QY	661	GGGGCAGTGAAGCCACCTGGGATGGCTTCATCCTGCTGCCACACTCTATGTGGCTGTC	720
Db	764	GGGGCGCTGAGGGCCACCTGGGATGGCTTCATCCTGCTGCCACCGCTCTATGTGGCTGTC	823
QY	721	ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCAAGTGCCGCCCGGGGCCG	780
Db	824	ACCGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCAAGTGCCGCCCGGGGCCCA	883
QY	781	CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCATCCTTGACATGTGCTGAATTC	840
Db	884	CCCAGCGTCTGTGACCTGGCTGTGGAGGTCTCTTCATCCTTGACATGTGCTGAATTC	943
QY	841	CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTTCGCCCAAGTCCATTTGCCCTC	900
Db	944	CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTTCGCCCAAGTCCATTTGCCCTC	1003
QY	901	CACATCGTCACCACTGGTTCCTGCTGGATGTCTATCGAGCGCTGCCCTTTGACCTGCTA	960
Db	1004	CACATCGTCACCACTGGTTCCTGCTGGATGTCTATCGAGCGCTGCCCTTTGACCTGCTG	1063
QY	961	CATGCCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCCCTGCTG	1020
Db	1064	CATGCCCTTCAAGGTCAACGTGTACTTCGGGGCCCACTGCTGAAGACGGTGGCCCTGCTG	1123
QY	1021	CGCTGTCTGCGCCTGCTTCGGCGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGCTG	1080
Db	1124	CGCTGTCTGCGCCTGCTTCGGCGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGCTG	1183
QY	1081	ACACTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGTGCCTCGCTCGCTTGTATAC	1140
Db	1184	ACACTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGTGCCTCGCTCGCTTGTATAC	1243
QY	1141	ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG	1200
Db	1244	ATTGGTCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG	1303
QY	1201	GAGTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGCCGGAGGCCAGCTGGAGGG	1260
Db	1304	GAGTGGCCCGCCGACTGGAGACCCCTACTACTTGGTGGGCCGGAGACCAAGCCGGAGGG	1363
QY	1261	AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAAACGGGCGGCTG	1320
Db	1364	AACAGCTCTGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAAACGGGCGGCTG	1423
QY	1321	GAGCTGCTGGGGCGCCGCTGCTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACCTC	1380
Db	1424	GAGCTGCTAGGGCGCCGCTGCTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACCTC	1483
QY	1381	AGCAGCTCACACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGGACACCGAGAAGATC	1440
Db	1484	AGCAGCTCACACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACCGGACACTGAGAAGATC	1543
QY	1441	TTCTCCATCTGCACCATGCTCATCGGGCGCCTGATGCACGCGGTGGTGTGGGAACGTG	1500
Db	1544	TTCTCCATCTGCACCATGCTCATCGGGCGCCTGATGCACGCGGTGGTGTGGGAACGTG	1603
QY	1501	ACGGCCATCATCAGCGCATGTACGCCCGCGCTTTCTGTACCAACAGCCGCGCGCGAC	1560
Db	1604	ACGGCCATCATCAGCGCATGTACGCCCGCGCTTTCTGTACCAACAGCCGCGCGCGAC	1663

Db 2744 CTTCGGCAGCGGTGATGAGAGCTGTGACAGAGCTGTGACAGATGCGGGAAGGACTACAG 2803  
QY 2701 TCACTTCGCCAGGCTGTGAGCTTGTCTCTGGCGCCCAACAGGAGGCTCGGTGCGCTCGG 2760  
Db 2804 TCACTTCGCCAGGCTGTGAGCTTGTCTCTGGCAACCCATAGGAGGCTCCATGCGCTCGG 2863  
QY 2761 GCATCGGAGAGGGGCGGTGCCCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
Db 2864 GCCTCAGGAGAGGGGCCATGCCCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2923  
QY 2821 GACACTGGGGCATCCTCTACTGCTGCTGCAGCCCCCAGCTGGCTCTGTCTTGTAGTGGGACT 2880  
Db 2924 GACACTGGGGCATCCTCTACTGCTGCTGCAGCCCCCAGCTGGCTCTGTCTTGTAGTGGGACT 2983  
QY 2881 TGGCCCCACCTCTGTCGGGGCCTCCTCCCTCATGGCACCCCTGGCCCTGGGTCCTCCCA 2940  
Db 2984 TGGCCCCACCTCTGTCGGGGCCTCCTCCCTCATGGCACCCCTGGCCCTGGGTCCTCCCA 3043  
QY 2941 GCGTCTCAGAGCTCCCTTGGCTCGAGCCACAGCTTCTTGACCTCCACCTCAGACTCA 3000  
Db 3044 GCATCTCAGAGCTCCCTTGGCTCGAGCCACAGCTTCTTGACCTCCACCTCAGACTCA 3103  
QY 3001 GAGCCCCCTGCTCAGGAGACCTCTGCTCTGAGCCAGCACCCCTGCCTCCCTCCTCCT 3060  
Db 3104 GAGCCCCCTGCTCAGGAGACCTCTGCTCTGAGCCAGCACCCCTGCCTCCTCCTCCT 3163  
QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCCGAGAGCTGTGAGCCAGGCTGAGGTACCAGC 3120  
Db 3164 TCTGAGGAAGGGCTAGGACTGGGCCCCGAGAGCTGTGAGCCAGGCTGAGGTACCAGC 3223  
QY 3121 ACTGAGAGCCCCCAGGAGGCTCAGGGGCTTGCGCTTGGACCTCCACAGCCCTG 3180  
Db 3224 ACTGAGAGCCCCCAGGAGTGTGAGGGGCTTGCGCTTGGACCTCCACAGCCCTG 3283  
QY 3181 GAGATGGTGTATTGGCTGCCATGGCTCTGSCACAGTCCAGTGGACCCAGGAAGGC 3240  
Db 3284 GAGATGGTGTATTGGCTGCCACGGCTCTGSCACAGTCCAGTGGACCCAGGAAGGC 3343  
QY 3241 ACAGGGGTCTGA 3252  
Db 3344 ACAGGGGTCTGA 3355

RESULT B  
ACA61728  
ID ACA61728 standard; cDNA; 3355 BP.  
XX  
AC ACA61728;  
XX  
DT 19-AUG-2003 (first entry)  
XX  
DE Monkey ERG-like protein 1 (ERG-LP1) cDNA.  
XX  
KW Monkey; ERG-like protein 1; ERG-LP1; gene; ss; ERG potassium channel;  
KW neuronal cell; muscle cell; potassium channel associated disorder; pain;  
KW neurodegenerative disorder; psychiatric disorder; learning disorder;  
KW memory disorder; obesity; cardiac disorder; gastrointestinal disorder.  
OS Macaca sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 104..3355  
FT /\*tag= a  
FT /product= "Monkey ERG-LP1"  
XX  
PN US6518398-B1.  
XX  
PD 11-FEB-2003.  
XX  
PF 21-JUL-1999; 99US-00358383.  
XX  
PR 21-JUL-1998; 98US-00119855.

XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Curtis RAJ;  
XX  
DR WPI; 2003-455687/43.  
DR P-PSDB; ABU61670.  
XX  
PT New human ERG-like protein (ERG-LP2) potassium channel polypeptide and  
PT nucleic acid, useful for treating or diagnosing e.g. Alzheimer's disease,  
PT schizophrenia, obesity, restenosis, myocardial infarction, Crohn's  
PT disease, pain.  
XX  
PS Example 1; Fig 1; 116pp; English.  
XX  
CC The invention relates to an isolated human ERG-like protein (ERG-LP2) of  
CC the ERG potassium channel family and the nucleic acid encoding it. The  
CC ERG-LP2 polypeptide or nucleic acid is useful for modulating potassium  
CC channel mediated activity in a cell, such as a neuronal cell or a muscle  
CC cell. The ERG-LP2 polypeptide or nucleic acid is particularly useful for  
CC treating potassium channel associated disorders, e.g. neurodegenerative  
CC disorders (e.g. Alzheimer's disease, Parkinson's disease, multiple  
CC sclerosis, amyotrophic lateral sclerosis, supranuclear palsy, epilepsy or  
CC Creutzfeldt-Jakob disease), psychiatric disorders (e.g. depression,  
CC schizophrenia, Korsakoff's psychosis, mania, anxiety or phobias),  
CC learning or memory disorders (e.g. amnesia or age-related memory loss),  
CC obesity, cardiac disorders (e.g. arteriosclerosis, ischaemic reperfusion  
CC injury, restenosis, congestive heart failure, angina, hypertension,  
CC myocardial infarction, coronary artery disease or arrhythmia),  
CC gastrointestinal disorders (e.g. atresia, hiatal hernia, peptic ulcers,  
CC gastritis, stomach tumours, Crohn's disease or ischaemic bowel disease)  
CC or pain (e.g. joint pain, tooth pain or headaches). This sequence  
CC represents cDNA encoding the monkey ERG-like protein 1 (ERG-LP1)  
XX  
SQ Sequence 3355 BP; 580 A; 1128 C; 1041 G; 606 T; 0 U; 0 Other;

Query Match 97.0%; Score 3156; DB 7; Length 3355;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGCCGGCCATCGGGGCGCTCTCTGGCGCTCAGAACACCTTCTTGAGACCATCGCTACG 60  
Db 104 ATGCCGGCCATCGGGGCGCTCTCTGGCGCGCAGAACACCTTCTTGAGACCATCGCTACG 163  
QY 61 CGCTTCGACGGCACGCACAGTAACCTCTGTCTGGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 164 CGCTTCGACGGCACGCACAGTAACCTCTGTCTGGGCAACGCCAGGTGGCGGCTCTTC 223  
QY 121 CCCGTGGTCTACTGCTCTGTAGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
Db 224 CCCGTGGTCTACTGCTCTGTAGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 283  
QY 181 ATGCAGCGGGCTGTGCTGCTCTCTCTTATGGGCCAGACACCATGAGCTCGTCCGC 240  
Db 284 ATGCAGCGGGCTGTGCTGCTCTCTCTTATGGGCCAGACACCATGAGCTCGTCCGC 343  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGATTCAAGGTGAGCTGATCCTGTAC 300  
Db 344 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGATTCAAGGTGAGCTGATCCTGTAC 403  
QY 301 CGGAAGAGCGGCTCCCGTTCTGTGTCTCTCTGGATGTATACCCATAAAGAATGAGAA 360  
Db 404 CGGAAGAGCGGCTCCCGTTCTGTGTCTCTCTGGATGTATACCCATAAAGAATGAGAA 463  
QY 361 GGGAGGTGGCTCTCTTCTAGTCTCTACAAGGACATCAGCGAAACCAAGACCGAGGG 420  
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QY 421 GGCCCGACAGATGGAAGGAGACAGGTGGTGGCGCGCGCGATATGGCCGGCAGCATCC 480  
Db 524 GGCCCTGACAGATGGAAGGAGACAGGTAGTGGCCGCGCGCGATATGGCCGGCAGCATCC 583  
QY 481 AAAGGCTTCAATGCCAACCGGCGGAGCGCGGCGGTGCTTACCACCTGTCCGGGCAC 540

Db 584 AAAGGTTCAATGCCAACCGGCGGAGCCGGGTGTGCTCTACCACTGTCCGGGCAC 643  
QY 541 CTGCAGAGCAGCCCCAAGGCAAGCACCAAGCTCAATAAGGGGGTGTGTTGGGAGAAACCA 600  
Db 644 CTGCAGAGCAGCCCCAAGGCAAGCACCAAGCTCAATAAGGGGGTGTGTTGGGAGAACCA 703  
QY 601 AACTTGGCTGAGTACAAAGTAGTCCGCAATCCGGAAGTCCGCTTCACTCTGCACTGT 660  
Db 704 AACTTGGCTGAGTACAAAGTAGTCCGCAATCCGGAAGTCCGCTTCACTCTGCACTGT 763  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCACTCTGCTCGCCACACTATATGTGGCTGTC 720  
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QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCAAGTCCGCGCCGCGGCCG 780  
Db 824 ACCGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCAAGTCCGCGCCGCGGCCCA 883  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGTCCCTTCACTCTTGACATTTGCTGAATTC 840  
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QY 2581 GGCCTGCTCACTGTTCCCATGGGCCCGAGCGAGGCAAGGAACACAGACACTGGACAAG 2640  
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QY 2701 TCACCTCGCCAGGCTGTGCAGCTTGTCTGGCGCCACAGGAGGCTCCGTGCGCTCGG 2760  
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QY 2761 GCATCGGGAGAGGGCGCTGCCCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
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Db 3284 GAGATGGTGTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGAGCCAGGAAGGC 3343  
QY 3241 ACAGGGGTCTGA 3252  
Db 3344 ACAGGGGTCTGA 3355

RESULT 9  
ADB66794  
ID ADB66794 standard; cDNA; 3355 BP.  
XX ADB66794;  
AC ADB66794;  
XX 04-DEC-2003 (first entry)  
XX cDNA encoding monkey ERG-like protein 1 (ERG-LP1).  
DE Monkey; ERG potassium channel like protein; ERG-LP1; tumour; cytostatic;  
KW gene; ss.  
KW Macaca sp.  
OS  
XX  
XX  
FH Location/Qualifiers  
FT 104..3355  
FT /\*tag= a  
FT /product= "ERG-LP1"  
FT /note= "The coding region given as SEQ ID No:3 is  
specifically claimed in Claim 2"

US2003104429-A1.

05-JUN-2003.

27-JUN-2002; 2002US-00185867.

21-JUL-1998; 98US-00119855.

21-JUL-1999; 99US-00358383.

PA (CURT/) CURTIS R A J.  
XX Curtis RAJ;  
PI  
XX  
DR WPI; 2003-687835/65.  
DR P-PSDB; ADB66795.  
XX  
PT New isolated nucleic acid, useful for producing a polypeptide and  
PT preparing a composition for diagnosing or treating diseases e.g., a  
XX tumor.  
PS Claim 2; Fig 1; 122pp; English.  
XX  
CC The present invention relates to novel ERG potassium channel like  
CC proteins, designated ERG-LPs, and the polynucleotide sequences encoding  
CC them. Also disclosed are: a host cell containing the polynucleotide, an  
CC antibody that selectively binds to the polypeptide, a method for  
CC producing the polypeptide, a method for detecting the presence of the  
CC polypeptide or the nucleic acid in a sample, a method for identifying a  
CC compound that binds to the polypeptide, a method for modulating the  
CC activity of the polypeptide, a method for identifying a compound that  
CC modulates the activity of the polypeptide, and a kit. The polynucleotide  
CC sequences are useful for producing the ERG-LP polypeptides. The ERG-LP  
CC polynucleotide and polypeptide sequences are useful for preparing a  
CC composition for diagnosing or treating diseases e.g. tumours. The present  
CC sequence encodes monkey ERG-LP1.  
XX  
SQ Sequence 3355 BP; 580 A; 1128 C; 1041 G; 606 T; 0 U; 0 Other;

Query Match 97.0%; Score 3156; DB 9; Length 3355;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGCCGGCCATCGGGGCTCTCTGGGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60  
Db 104 ATGCCGGCCATCGGGGCTCTCTGGGCTCAGAACACCTTCTCTGGACACCATCGCTACG 163  
QY 61 CGTTTCGACGGCACGCACAGTAACCTCTGTCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 164 CGTTTCGACGGCACGCACAGTAACCTCTGTCTGGGCAACGCCAGGTGGCGGGCTCTTC 223  
QY 121 CCCGTGCTACTGCTCTGTATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
Db 224 CCCGTGCTACTGCTCTGTATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 283  
QY 181 ATGCAGCGGGCTGTGCTGCTCTCTCTCTTATGGCCAGACACAGTGAGCTCGTCCGC 240  
Db 284 ATGCAGCGGGCTGTGCTGCTCTCTCTCTTATGGCCAGACACAGTGAGCTCGTCCGC 343  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 344 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 403  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCTCTGTGATGATACCCATAAAGAATGAGAAA 360  
Db 404 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCTCTGTGATGATACCCATAAAGAATGAGAAA 463  
QY 361 GGGAGGTGGCTCTCTTCTAGTCTCTCAAGGACATCAGCGCAACCAAGAACCGAGGG 420  
Db 464 GGGAGGTGGCTCTCTTCTAGTCTCTCAAGGACATCAGCGCAACCAAGAACCGAGGG 523  
QY 421 GGCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGCCGATATGCCGGGCACGATCC 480  
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Db 584 AAAGGCTTCAATGCCAACCGGGCGGAGCGCGGCTGTCTACACCTGTCCGGGCAC 643  
QY 541 CTGCAGAACGAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600  
Db 644 CTGCAGAACGAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 703

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QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC 720  
Db 764 GGGGCGCTGAGGGCCACCTGGGATGGCTTCATCCTGCTCGCCACGCTCTATGTGGCTGTC 823  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTGCGGCCCGCGGCCCG 780  
Db 824 ACCGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTGCGGCCCGCGGCCCA 883  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTTTCATCCTTGACATTTGCTGAATTC 840  
Db 884 CCCAGCGTCTGTGACCTGGCTGTGGAGGTCTCTTTTCATCCTTGACATTTGCTGAATTC 943  
QY 841 CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTGTTGCCCCAAAGTCCATTTGCCTC 900  
Db 944 CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTGTTGCCCCAAAGTCCATTTGCCTC 1003  
QY 901 CACTACGTACACCACTGGTTCTCTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGCTA 960  
Db 1004 CACTACGTACACCACTGGTTCTCTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGCTG 1063  
QY 961 CATGCCCTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGGTGGCTGCTG 1020  
Db 1064 CATGCCCTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGCTGAAGACGGTGGCTGCTG 1123  
QY 1021 CGCCTGCTGCGCCTGTTCCGGGGTGGACCGGTACTCGCAGTACAGCGCGGTGGTGGT 1080  
Db 1124 CGCCTGCTGCGCCTGTTCCGGGGTGGACCGGTACTCGCAGTACAGCGCGGTGGTGGT 1183  
QY 1081 ACACCTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTTTAC 1140  
Db 1184 ACACCTGCTCATGGCCGTGTTTGCCTGCTTGGCACTGGGTGCGCTGCTGTTTAC 1243  
QY 1141 ATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCGTGAGATTGGCTGGCTGCAG 1200  
Db 1244 ATTGGTCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCGTGAGATTGGCTGGCTGCAG 1303  
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QY 1621 TACTTCCAGGCCACCTGGGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGC 1680  
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QY 841 CGTACCACATTCTGTCCAAAGTCGGGCCAGGTGGTGTTCGCCCAAAAGTCCATTGCGCTC 900  
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QY 1081 AACTGCTCATGGCCGTGTTGGCCCTGCTCGCGCACTGGGTGCCTGCGTCTGTTTAC 1140  
Db 1081 AACTGCTCATGGCCGTGTTGGCCCTGCTCGCGCACTGGGTGCCTGCGTCTGTTTAC 1140  
QY 1141 AATTGGCCAGCGGAGATCGAGACAGCGAATCCGAGTGCCTGAGATTGGCTGGCTGCAG 1200  
Db 1141 AATTGGCCAGCGGAGATCGAGACAGCGAATCCGAGTGCCTGAGATTGGCTGGCTGCAG 1200  
QY 1201 GAGCTGGCCCGCGGACTGGAGTCCCTACTACTCTGGTGGCGCGGAGCCAGCTGGAGGG 1260  
Db 1201 GAGCTGGCCCGCGGACTGGAGTCCCTACTACTCTGGTGGCGCGGAGCCAGCTGGAGGG 1260  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGACAGCAGCAGCAGCGGCAACCGGAGCGGGCTG 1320  
Db 1261 AACAGCTCCGGCCAGAGTGACAACTGACAGCAGCAGCAGCGGCAACCGGAGCGGGCTG 1320  
QY 1321 GAGCTGTGGGCGGCCCTGCTGCGCAGCGCCTACATCCTCCCTCTACTTCGCACTC 1380  
Db 1321 GAGCTGTGGGCGGCCCTGCTGCGCAGCGCCTACATCCTCCCTCTACTTCGCACTC 1380  
QY 1381 AGCAGCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCCAACCGGACACCGAGAAGATC 1440  
Db 1381 AGCAGCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCCAACCGGACACCGAGAAGATC 1440  
QY 1441 TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGACCGCGGTGGTGTTCGGAAACGTG 1500  
Db 1441 TTCTCCATCTGCACCATGCTCATCGCGCCCTGATGACCGCGGTGGTGTTCGGAAACGTG 1500  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTATCCACAGCGCCACCGCGGAC 1560  
Db 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTATCCACAGCGCCACCGCGGAC 1560  
QY 1561 CTGCGGACTACATCCGCTCCACCGGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
Db 1561 CTGCGGACTACATCCGCTCCACCGGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
QY 1621 TACTTCCAGGCCACTTGGCGGTGAACAATGGCATCGACACCGAGCTGTCAGAGC 1680  
Db 1621 TACTTCCAGGCCACTTGGCGGTGAACAATGGCATCGACACCGAGCTGTCAGAGC 1680  
QY 1681 CTCCTGACGAGCTGGCGGACAGCATCGCCCATGCACCTGCACAAGGAGTCTCTGCAGCTG 1740

Db 1681 CTCCTGACGAGCTGGCGGACAGACATCGCCATGCACCTGCACAAGGAGTCTCTGCAGCTG 1740  
QY 1741 CCACTGTTGAGGGCGCCAGCCGGGCTGCTCGGGCACTGTCTCTGGCCCTCGGGCCC 1800  
Db 1741 CCGCTGTTGAGGCAGCCAGCCGGGCTGCTCGGGCACTGTCTCTGGCCCTCGGGCCC 1800  
QY 1801 GCCTTCTGACGCCCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1860  
Db 1801 GCCTTCTGACGCCCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1860  
QY 1861 TTTGTCTGCTGCTGCTCCATGGAGGTGCTCAAGGGTGGCA CCGTGTCTGCCATCCTAGGG 1920  
Db 1861 TTTGTCTGCTGCTGCTCCATGGAGGTGCTCAAGGGTGGCA CCGTGTCTGCCATCCTAGGG 1920  
QY 1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGGCGGAGCAGGTGTTAAAGGCCAATGCC 1980  
Db 1921 AAGGGTACCTGATCGGCTGTGAGCTGCCCGGAGGAGCAGGTGTTAAAGGCCAATGCC 1980  
QY 1981 GACGTGAAGGGGCTGACGTACTGCGTCTCTGCACTGTCTGAGCTGGCTGGCTGCACGAC 2040  
Db 1981 GATGTGAAGGGGCTGACGTACTGCGTCTCTGCACTGTCTGAGCTGGCTGGCTGCACGAC 2040  
QY 2041 AGCCTTGCGCTGTACCCCGAGTTTGGCCCGGCTTCAGTCTGCGGCTCCGAGGGAGCTC 2100  
Db 2041 AGCCTTGCGCTCTACCCCGAGTTTGGCCCGGCTTCAGTCTGCGGCTCCGAGGGAGCTC 2100  
QY 2101 AGCTAACAACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGCGGC 2160  
Db 2101 AGCTAACAACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGCGGC 2160  
QY 2161 GACAATACCCCTTATGTCCACGCTGGAGGAGAAAGGAGACAGATGGGGAGAGGGCCCAAG 2220  
Db 2161 GACAATACCCCTTATGTCCACGCTGGAGGAGAAAGGAGACAGATGGGGAGAGGGCCCAAG 2220  
QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTACTGTCCCCCTGTTGCACTCC 2280  
Db 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTACTGTCCCCCTGTTGCACTCC 2280  
QY 2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAAACAGCACCCCGGCTCGTCTAGGT 2340  
Db 2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAAACAGCACCCCGGCTCGTCTAGGT 2340  
QY 2341 GGAGAGGGAGGCCAGGAGGGGCTTTGAAGGCTGAGGCTGGCCCCCTCTGCTCCC 2400  
Db 2341 GGAGAGGGAGGCCAGGAGGGGCTTTGAAGGCTGAGGCTGGCCCCCTCTGCTCCC 2400  
QY 2401 CCACGGGCTTAGAGGGGCTAGCGGCTGCCCCCTTGAAGGCTGAGGCTGGCCCCAGATCTG 2460  
Db 2401 CCACGGGCTTAGAGGGGCTAGCGGCTGCCCCCTTGAAGGCTGAGGCTGGCCCCAGATCTG 2460  
QY 2461 AGCCCCAGGGTAGTAGATGGCAATTGAAGACGGCTGTGGCTCGGACCCAGCCAAAGTTCTCT 2520  
Db 2461 AGCCCCAGGGTAGTAGATGGCAATTGAAGACGGCTGTGGCTCGGACCCAGCCAAAGTTCTCT 2520  
QY 2521 TTCCGCTGGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCTTCCCTGGACCCAGAGAGC 2580  
Db 2521 TTCCGCTGGGCCAGTCTGGCCCCGAATGTAGCAGCAGCCCTTCCCTGGACCCAGAGAGT 2580  
QY 2581 GGCCTGCTCACTGTTCCCCATGGGCCAGGCAAGGAACACAGACACACTGGACAAG 2640  
Db 2581 GGCCTGCTCACTGTTCCCCATGGGCCAGGCAAGGAACACAGACACACTGGACAAG 2640  
QY 2641 CTTCCGAGGGCGGTGACAGAGTGTACAGCAGGTGTGCTGAGTGGGGAAGGACTGCAG 2700  
Db 2641 CTTCCGAGGGCGGTGATGGAGCTGTACAAACAGGTGTGCTGAGTGGGGAAGGACTACAG 2700  
QY 2701 TCACCTCGCAGGCTGTGAGCTTGTCTGGCGCCCCACAGGGAGGCTCGTGCCTCGG 2760  
Db 2701 TCACCTCGCAGGCTGTGAGCTTGTCTGGCGCCCCACAGGGAGGCTCGTGCCTCGG 2760  
QY 2761 GCATCGGGAGAGGGCGCTGCCCCAGCCAGCAGCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820

Db 2761 GCCTCAGGAGAGGGCCATGCCAGCCAGCACCTCCGGGCTTCGTGAGCCTCTGTGTGTG 2820  
QY 2821 GACACTGGGGCATCTCTACTGCTGAGAGCCCCAGCTGGCTCTGTCTTTGAGTGGGACT 2880  
Db 2821 GACACTGGGGCATCTCTACTGCTGAGAGCCCCAGCTGGCTCTGTCTTTGAGTGGGACT 2880  
QY 2881 TGGCCCCACCTCTGTCGGGGCCCTCCTCCCTCATGGCACCTGGCCCTGGGGTCCCCCA 2940  
Db 2881 TGGCCCCACCTCTGTCGGGGCCCTCCTCCCTCATGGCACCTGGCCCTGGGGTCCCCCA 2940  
QY 2941 GCGTCTCAGAGCTCCCCCTGGCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000  
Db 2941 GCACTCTCAGAGCTCCCCCTGGCTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCA 3000  
QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCCAGCACCCCTGCCTCCCTCCT 3060  
Db 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCCAGCACCCCTGCCTCCTCCT 3060  
QY 3061 TCTGAGGAAGGGGCTAGGACTGGGCCCCGAGAGCCTGTGAGCCAGGCTGAGGCTACAGC 3120  
Db 3061 TCTGAGGAAGGGGCTAGGACTGGGCCCCGAGAGCCTGTGAGCCAGGCTGAGGCTACAGC 3120  
QY 3121 ACTGGAGAGCCCCCACCAGGCTCAGGGGGCCCTGGCCCTTGCCTGGGACCCCCACAGCCTG 3180  
Db 3121 ACTGGAGAGCCCCCACCAGGCTCAGGGGGCCCTGGCCCTTGCCTGGGACCCCCACAGCCTG 3180  
QY 3181 GAGATGGTGCTTATTGGCTGCCACGGCTCTGGCACAGTCCAGTGGACCCAGGAAGGC 3240  
Db 3181 GAGATGGTGCTTATTGGCTGCCACGGCTCTGGCACAGTCCAGTGGACCCAGGAAGGC 3240  
QY 3241 ACAGGGGTC 3249  
Db 3241 ACAGGGGTC 3249

RESULT 11  
ID AAX84919 standard; DNA; 3715 BP.  
XX  
AC AAX84919;  
XX  
DT 28-SEP-1999 (first entry)  
XX  
DE Rat brain specific potassium channel protein coding sequence.  
XX  
KW Brain specific potassium channel; central nervous system disorder;  
KW dementia; cerebral ischaemic sclerosis; therapy; probe; ss.  
XX  
OS Rattus sp.  
XX  
PN WO9937677-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 20-JAN-1999; 99WO-JP000190.  
XX  
PR 23-JAN-1998; 98JP-00011434.  
PR 04-DEC-1998; 98JP-00346198.  
XX  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
XX  
PI Miyake A, Mochizuki S, Yokoi H;  
XX WPI; 1999-458683/38.  
XX  
PT Potassium channel protein expressed specifically in brain tissue and  
PT method for its production.  
XX  
PS Example 3; Page 54-57; 63pp; English.  
XX  
CC This sequence encodes a rat potassium channel protein, and was used as a  
CC probe to isolate DNA encoding the protein of the invention. The protein  
CC of the invention is a human brain specific potassium channel protein. The

CC protein is used to treat and investigate disorders of the central nervous  
CC system such as dementia and cerebral ischaemic sclerosis  
XX  
SQ Sequence 3715 BP; 735 A; 1167 C; 1090 G; 723 T; 0 U; 0 Other;  
Query Match 81.9%; Score 2664.8; DB 2; Length 3715;  
Best Local Similarity 89.0%; Pred. No. 0;  
Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;  
QY 1 ATGCGGGCCATGCGGGGCTCCTGGCGCCTCAGAACACCTTCTGAGACACCATCGCTACG 60  
Db 156 ATGCGGGCCATGCGGGGCTCCTGGCGCCTCAGAACACCTTCTGAGACACCATCGCCACC 215  
QY 61 CGCTTCGACGGCACGCACAGTAACTTCTGTGGGCAACGCCAGGTGGCGGCTCTTC 120  
Db 216 CGCTTCGACGGCACGCACAGTAACTTCTGTGACCTCACGGTTTCTCCAGAGCTGAGGTC 275  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 180  
Db 276 CCGTGGTCTACTGCTCCGATGGCTTCTGTGACCTCACGGTTTCTCCAGAGCTGAGGTC 335  
QY 181 ATGACGGGGCTGTGCTGCTCTCTCTTCTTATGSGCCAGACACCATGAGCTCGTCCGC 240  
Db 336 ATGACGGAGGCTGTGCTGCTCTCTTCTCTATGSGCCAGACACCATGAGTGGTGGTCCGC 395  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCTGTAC 300  
Db 396 CAACAGATCCGCAAGGCCCTGGATGAGCACAAAGAAATTCAGGCTGAACCTGATCTGTAC 455  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTATACCCATATAAAGATGAGAAA 360  
Db 456 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTATACCTATAAAGAACGAGAAG 515  
QY 361 GGGGAGGTGGCTCTCTCTAGTCTCTCACAAGAGACATCAGCGAAACCAAGACCGAGGG 420  
Db 516 GGGGAGGTGGCCCTCTCTCTGGTCTCTCACAAGAGACATCAGTGAGACCAAGAACCGAGGA 575  
QY 421 GGCCCCGACAGATGGAAGGAGAGAGGTGGTGGCGCGCGCGGATATGSCCGGACGATCC 480  
Db 576 GGCCCTGACAACTGGAAGGAGAGAGGTGGTGGCGCGCGAGATATGGTGGGAGGATCC 635  
QY 481 AAAGGCTTCAATGCAACCGCGCGGAGCGGCGCGGCTGTCTTACCACTGTCTCCGGGCAC 540  
Db 636 AAAGGCTTAAATGCCAATCGGAGGCGCGCGCGGCTGTCTTACCACTGTCTGGTCCAC 695  
QY 541 CTGCAGAGCAGCCCCAAGGCAAGCACAGTCAATAAGGGGTGTTTGGGAGAGAAACCA 600  
Db 696 CTGCAGAGCAACCCCAAGGCAAGCACAAACTCAATAAGGGTGTGTTGGAGAGAAAGCCA 755  
QY 601 AACTTGCTGAGTACAAAGTAGCCGCGCATCCGGAAGTCGCCCTTCAFCCTGTGCACTGT 660  
Db 756 AATTTGCCCGAATAATAAGTCGCTGCTATCCGGAAGTCACCCCTTTATCCTGCTGCACTGT 815  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCACTGCTCGCCACACTCTATGTGGCTGT 720  
Db 816 GGGGCTCTGAGAGCCACCTGGGATGGCTTCACTGCTCGCCACGCTTACGTGGCTGT 875  
QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCCACTGCCCGCCCGGCCG 780  
Db 876 ACTGTGCCATACAGCGTGTGTGAGCACAGCACGGGAGCCCACTGCTGCCCGTGGCCCA 935  
QY 781 CCCAGCGTCTGTGACCTGGCCCTGGAGGTCCTCTTCACTCTTGACATTGTGCTGAATTC 840  
Db 936 CCTAGTGTCTGTGACCTGGCCGTGGAAGTCCTCTTCACTTAGATATTGTGCTGAATTC 995  
QY 841 CGTACCACATTGCTCCAGTCCGGGCCAGGTGGTGTGCTTCACTCTTGACATTGTGCTGAATTC 900  
Db 996 CGTACTACATTGTTGTCCAAGTCAGGCCAGGTGGTATTCGCCCCCAAGTCCATTTGCCTC 1055  
QY 901 CACTACGTCAACCACTGGTTCCTGCTGGATGTATCGCAGCGCTGCCCTTTGACCTGTA 960  
Db 1056 CACTACGTCAACCACTGGTTCCTGCTGGATGTATCGCAGCGACTGCCCTTTGACCTACTA 1115

QY 961 CATGCCCTCAAGGTCAACGTGTAATCTGGGGCCCCATCTGCTGAAGACGGTGGCCCTGCTG 1020  
Db 1116 CATGCCCTCAAGGTCAATGTGTACGTTGGGGCTCACCTACTGAAGACCGTGGGGTGGCTT 1175  
QY 1021 CGCCTGCTGCGCTGCTTCCGCGGCTGGAACGGTACTCGCAGTACAGCGCCGTGGTGTG 1080  
Db 1176 CGGCTGCTGCGCTACTACCAAGACTGGACCGGTACTCTCAGTATAGCGCTGTTGTGCTC 1235  
QY 1081 ACATGCTCATGGCCGTGTTCCGCCCTGCTCGGCACCTGGTGCCTGCTGCTGCTGTTTAC 1140  
Db 1236 ACCTTGCTCATGGCTGTGTTTGCCTGCTCGCCACTGGTGGCTGCGTTGGTTCCTAC 1295  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGTGGCTGCAG 1200  
Db 1296 ATCGGCCAGCAAGAGATTGAGAACAGCGAGTCAGAGCTGCCTGAGATCGGCTGGCTGCAG 1355  
QY 1201 GAGCTGGCCCGGACTGGAGACTCCCTACTACTGGTGGGCGGAGGCCAGCTGGAGGG 1260  
Db 1356 GAGCTGGCACGCGAGGCTGGAGACGCCCTATTACTGGTGAGCCGGAGTCCAGATGGAGGG 1415  
QY 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCA-----GCAGCGAGGCCAACCGGG 1311  
Db 1416 AACAGCTCTGGCCAGAGTGAAAACTGCAGTAGCAGTGGCGGCGGAGCGAAGCAACCGGG 1475  
QY 1312 ACGGGCTGGAGCTGCTGGCGGCGCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTAC 1371  
Db 1476 ACTGGCTGGAGCTGCTGGGTGGCCCATCCCTACCGCAGCGCCTACATCACCTCCTTGTAC 1535  
QY 1372 TTCGCACTCAGCAGCCCTCACCAGCGTGGGCTTCGGCAACGCTGTCGGCCAAACAGGACACC 1431  
Db 1536 TTCGCGCTCAGCAGTCTCACCAGTGTGGGCTTCGGCAATGTGTCCGCTAACACAGACACT 1595  
QY 1432 GAGAAGATCTTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACCGCGTGGTGT 1491  
Db 1596 GAGAAGATTTTCTCCATCTGCACCATGCTTATTGGAGCTCTGATGCATGCAGTGGTGT 1655  
QY 1492 GGGAACTGACGGCCATATCCAGCGCATGTACGCCCGCGCTTCTGTACCAACAGCCGC 1551  
Db 1656 GGGAACTGACAGCCATATCCAGCGCATGTACGCTCGCGCTTCTGTACCAACAGCCGC 1715  
QY 1552 ACGCGCGACCTCGCGACTACATCCGCTATCCCAAGCCCTCAAGCAGCGC 1611  
Db 1716 ACCCGTACCTCGAGACTACATTCGCTATCCCGCATCCCGCATCCCAAGCCCTCAAGCAGCGC 1775  
QY 1612 ATGCTGGAGTACTTCCAGGCCACTGGGCGGTGAACAATGGCATCGACACCGAGCTG 1671  
Db 1776 ATGCTCGAGTACTTCCAGGCCACTGGGCGGTGAACAATGGCATCGATACCATGAGCTG 1835  
QY 1672 CTGACAGCCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGTC 1731  
Db 1836 CTGACAGCCCTTCCGATGAGCTTCGAGCAGACATCGCCATGCACCTGCACAAGGAGTC 1895  
QY 1732 CTGAGCTGCCACTGTTTGAGGCGCCAGCCGGCTGCCTGCGGGCACTGTCTCTGGCC 1791  
Db 1896 CTGAGCTGCCATGTTTCGAGGCGAGCGGCTGGCTGCCTGCGGGCACTGTCTCTGGCC 1955  
QY 1792 CTGCGGCCGCTTCTGCACGCCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAG 1851  
Db 1956 CTGAGGCCGCTTCTTGACGCCGCGGAGTACCTCATTCACCAAGGCGATGCTCTCCAG 2015  
QY 1852 GCCCTCTACTTGTGCTGTGGTCCATGGAGGTGCTCAAGGTGGCACCGTGTCTGCC 1911  
Db 2016 GCTCTCTACTTGTGTGCTCAGGTTCCATGGAGGTCTCAAAGGTGGCACCGTCTCTGCC 2075  
QY 1912 ATCTAGGGAAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAG 1971  
Db 2076 ATTCTAGGGAAGGCTGACCTGATCGGCTGTGAGCTGCCCGCAGCGAGAGCAAGTAGTGAAG 2135  
QY 1972 GCCAATGCCAGCTGAAGGGCTGACGTAAGTGTGCTGCTGCTGAGTGTCTGAGCTGGTGGC 2031  
Db 2136 GCCAATGCCAGCTGAAGGGCTGACATACTGCGTCTTACAGTGCCTGACGTGGCTGGG 2195  
QY 2032 CTGCACGACAGCCCTTGGCTGTATACCCCGAGTTTGGCCCGCGCTTCAGTCTGGCCCTCCGA 2091

Db 2196 CTGCACGAGAGCCCTCGCACTGTACCCCTGAGTTTGGCCCAACGCTTTAGCCGTGGCTCCGA 2255  
QY 2092 GGGAGCTCAGCTAACACCTGGGTGCTGGGGGAGGCTCTGCAGAGGTGGACACCAGCTCC 2151  
Db 2256 GGGAGCTCAGCTAACACCTGGAGCTGGAGGAGTGTCTGCAGAGGTGGATACCAGCTCA 2315  
QY 2152 CTGAGCGGCGACAAATACCCCTTATGTCCACGCTGGAGGAGAAAGGAGACAGATGGGAGCAG 2211  
Db 2316 CTGAGTGGTGACAAACCCCTCATGTCCACACTGGAGGAGAAAGGAGACAGATGGGAGCAA 2375  
QY 2212 GGCCCCACGGTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCTGGC 2271  
Db 2376 GGACACACGATCTCACCAGCCCCAGCAGATGAGCCCTCCAGCCCCCTGCTGTCACTGGC 2435  
QY 2272 TGCACCTCCTCATCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCCCT 2331  
Db 2436 TGTACCTCCTCCTCCTCAGCGGCCAACTACTCTCCCCACGTCGAACCTGCAACCCCGGCCG 2495  
QY 2332 CGTCTAGTGGCAGAGGGAGGCCAGGCGAGGGGCTTTGAAGGCTGAGGCTGGGCCCT 2391  
Db 2496 AGGTGGGTGGCAGAGGGCGGCCAAGTAGGGCAGGGGTTTTGAAGCCTGAGGCTGGTCT 2555  
QY 2392 TCTGCTCCCCACGCGGCCCTAGAGGGGCTACGGGTGCCCCCATGCCATGGAATGTGCC 2451  
Db 2556 TCTGCTCATCCACGGACACTTGATGGGTGCACTGCTGCCCCCATGCCATGGAATGTACT 2615  
QY 2452 CCAGATCTGAGCCCCCAGGGTAGTAGTGGCATTGAAGACGGCTGTGGCTCGGACCCAGCCC 2511  
Db 2616 CCAGACCTGAGCCCCCAGGGTCGTAGATGGCATTTAGGATGGCTGCGGCTCTGACACGAC 2675  
QY 2512 AAGTTCTCTTCCGCGTGGCCAGTCTGGCCCGGAATGTAGCAGAGCCCCCTCCCTGGA 2571  
Db 2676 AAGTTCTCTTCCGCGTGGGTGAGTCTGGCCCGAATGTAGCAGAGCCCCCTCCCGAG 2735  
QY 2572 CCAGAGAGCGGCTGCTCACTGTTCCCATGCGGCCAGGAGGCAAGAAACACAGACACA 2631  
Db 2736 ACAGAGAGTGGCTGCTCACTGTTCCCTTGGTGGCCAGTGAAGGCAAGAAACACAGACACA 2795  
QY 2632 CTGGACAAGCTTCGGCAGGCGGTGACAGAGCTGTGACAGCAGGTGTGAGATGCGGGA 2691  
Db 2796 CTGGACAAGCTACGGCAGGCGGTGACGGAGCTGTCTGAACAGGTGTGAGATGCGAGAG 2855  
QY 2692 GGAATGCACTTCCGCGAGGCTGTGAGCTTGTCTGGCGCCCCACAGGAGGCTCG 2751  
Db 2856 GGAATGCACTTCCGCGAGGCTGTGAGCTTGTCTGGTGGCCCAAGGGAAGGCCAG 2915  
QY 2752 TGCCCTCGGGCATCGGAGAGGCGCCGTGCCCCAGCAGCAGCTCCGGGCTTCTGAGCCT 2811  
Db 2916 TGTCCTCGGGTATCAGGAGAGGCGCCATGCCAGCCACTGCTGCTGGGCTCTGAGCCT 2975  
QY 2812 CTGTGTGTGACACTGGGGCATCTCTCTACTGCTGAGCGCCAGCTGGCTGTCTGTTG 2871  
Db 2976 CTGCGTGTGACACTGGGGCATCATCTACTGCTGAGCGCCAGCAGGTTTCTGTTG 3035  
QY 2872 AGTGGACTTGGCCCCCACCTCTGTCGGGGCT--CCTCCCTCATGGCACCCCTGGCC 2928  
Db 3036 AGTGGACTTGGCCCTCACCCCCCTGTCAGGGCATCCCCCTCCCTCATGGCACCCCTGGCC 3095  
QY 2929 TGGGTCCCCAGCGTCTCAGAGCTCCCCCTGGCTCGAGCCACAGCTTCTGAGCCTCC 2988  
Db 3096 TGGGGCCCCCAGCATCTCAGAGCTCCCCCTGGCTCGAGCCACAGCTTATGAGCCTCC 3155  
QY 2989 ACCTCAGACTCAGAGCCCCCTGGCTCTGAGAGACCTCTGCTGAGCCCCAGCACCCCTGCC 3048  
Db 3156 ACCTCAGACTCAGAGCCCCCTGGCTCTGAGAGACCTCTGCTGAGCCCCAGCACCCAGCC 3215  
QY 3049 TCCCTCCTCTCTGTAGGAAAGGGCTGAGACTGGGCCCGCAGAGCCTGTGAGCCAGGCT 3108  
Db 3216 TCACCCCCCTCTCTGAGGAAAGGAGCTAGGACTCTGCACTCTGTGAGCCAGGCT 3275  
QY 3109 GAGGCTACCAAGCACTGGAGAGCCCCCAACAGGGTCAAGGGGCTGGCCCTGCTGGGAC 3168



Db 3276 GAGGCTACCAGTACTGGAGAGCCCCCTCCGGGGTCAGGGGGCCGAGCCTTGCCCTGGGAT 3335  
QY 3169 CCCCACAGCTGGAGATGGTGTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACC 3228  
Db 3336 CCCCACAGCTAGAGATGGTGTCTATCGCTGCCATGGCCCTGGCTCGGTCCAGTGGACC 3395  
QY 3229 CAGGAAGAAGGCACAGGGGTCTGA 3252  
Db 3396 CAGGAGAGGGCACAGGAGTCTGA 3419

RESULT 12  
ADB58253  
ID ADB58253 standard; DNA; 3715 BP.  
AC ADB58253;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Toxicity-related gene, SEQ ID 3279.  
XX  
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;  
KW drug screening; toxicity assay; ds.  
XX  
OS Unidentified.  
XX  
PN WO2003064624-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-US003194.  
XX  
PR 31-JAN-2002; 2002US-00060087.  
PR 15-MAR-2002; 2002US-0364045P.  
PR 15-MAR-2002; 2002US-0364055P.  
PR 30-DEC-2002; 2002US-0436643P.  
XX  
PA (GENE-) GENE LOGIC INC.  
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
XX WPI; 2003-689530/65.

DR  
XX Predicting a toxic effect of a compound, useful in identifying toxicity  
PT markers in liver tissues or cells for drug screening and toxicity assays,  
PT comprises preparing gene expression profile of tissue or cells exposed to  
PT the compound.

PS Claim 1; SEQ ID NO 3279; 1156pp; English.

XX  
CC The present invention relates to a method for predicting a toxic effect  
CC of a compound. The method comprises preparing a gene expression profile  
CC of a tissue or cell sample exposed to the compound, and comparing the  
CC gene expression profile to a database comprising SEQ ID 1-4925, where  
CC differential expression of the gene indicates at least one toxic effect.  
CC The method is useful for predicting at least one toxic effect of a  
CC compound, predicting hepatotoxicity or the progression of a toxic effect  
CC of a compound, identifying an agent that modulates the onset or  
CC progression of a toxic response, predicting the cellular pathways that a  
CC compound modulates in a cell, and identifying an agent that modulates at  
CC least one activity of a protein. The method and compositions of the  
CC present invention using a database of genes having liver toxin-induced  
CC differential expression, are useful in identifying toxicity markers in  
CC liver tissues or cells for drug screening and toxicity assays. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 3715 BP; 735 A; 1167 C; 1090 G; 723 T; 0 U; 0 Other;

Query Match 81.9%; Score 2664.8; DB 9; Length 3715;  
Best Local Similarity 89.0%; Pred. No. 0;  
Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;

QY 1 ATCCGGCCATGCGGGCCCTCTTGGGCGCTCAGAACACCTTCTCTGGACACCATCGCTACG 60  
Db |||||  
156 ATCCGGCCATGCGGGGCTCTTGGCGCGCAGAACACCTTCTCTGGACACCATCGCCACC 215  
QY 61 CGCTTCGACGGCACGACAGTAACTTCTGTCTGGGCAACGCCCGAGGTGGGGGCTCTTC 120  
Db |||||  
216 CGCTTCGACGGGACGACAGTAACTTCTGTCTGGGCAACGCCCGAGGTGGCGGGCTCTTC 275  
QY 121 CCGGTGCTACTGCTCTGTGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAGGTC 180  
Db |||||  
276 CCTGTGCTACTGCTCCGATGGCTTCTGTGACCTCACGGGTTCTCCAGAGCTGAGGTC 335  
QY 181 ATGCAGCGGGGCTGTGCTGCTCTCTTCTTATGGGCCAGACACAGTGTCTCCGC 240  
Db |||||  
336 ATGCAGCGAGGCTGTGCTGCTCTTCTTCTATGGGCCAGACACAGTGTGTGCTCCGC 395  
QY 241 CAACAGATCCGAAGGCCCTGGACGAGCACAAAGGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db |||||  
396 CAACAGATCCGAAAAGCCCTGGATGAGCACAAAGATTCAAGGCTGAACCTGATCCTGTAC 455  
QY 301 CGGAAGAGCGGGCTCCCGTCTTCTGTGTCTCTCTGGATGTATACCCATAAAGAAATGAGAAA 360  
Db |||||  
456 CGGAAGAGCGGGCTTCCATTCTGTGTCTCTCTGGATGTATACCTATAAAACGAGAAAG 515  
QY 361 GGGGAGGTGGCTCTCTTCTTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db |||||  
516 GGGGAGGTGGCCCTCTTCTGTGTCTCTCACAAGGACATCAGTGAACCAAGAACCGAGGA 575  
QY 421 GGGCCCGACAGATGGAAGGAGACAGGTGTGCGCGGCCGATATGGCCGGGACGATCC 480  
Db |||||  
576 GGGCCCTGACAACTGGAAGGAGAGAGGTGTGCGCGACGAGATATGTCGGGCGAGATCC 635  
QY 481 AAAGGCTTCAATGCCAACCGGGCGGAGCCGGCGGTCTCTACCACTGTCCGGGCAC 540  
Db |||||  
636 AAAGGCTTTAAIGCCAATCGGAGCGCAGCCGGGGTCTCTACCACTCTCTGTGTAC 695  
QY 541 CTGCAGAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600  
Db |||||  
696 CTGCAGAACAACCAAGGGCAAGCACAAACTCAATAAGGGTGTGTTGGAGAGAAAGCCA 755  
QY 601 AACTTGCTGAGTACAAAAGTAGCCGCCATCCGGAAGTCGCCCTTCACTCTGTGCACTGT 660  
Db |||||  
756 AATTGCGCGAATATAAGTCGTCTGTCTCCGGAAGTCACCCCTTTATCTGTGCACTGT 815  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCTCTGCTGCGCACACTCTATGTGGTGTGTC 720  
Db |||||  
816 GGGGCTCTGAGAGCCACCTGGGATGGCTTCACTCTGCTGCGCACGCTCTACGTGGTGTGTC 875  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGAGCCAGTGCOCGCCCGGCCCG 780  
Db |||||  
876 ACTGTGCCATACAGCGTGTGTGTGAGCACAGCACGGAGCCAGTGTGCGTGGCCCA 935  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTCACTCTGACATTTGTGAATTTT 840  
Db |||||  
936 CCTAGTGTGTGACCTGGCCGTGGAAAGTCTCTTCACTCTTAGATATTGTGTAATTTT 995  
QY 841 CGTACCACATTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTTGCCCAAGTCCATTTGCCTC 900  
Db |||||  
996 CGTACTACATTTGTGTCCAAAGTCAGGCCAGGTGGTATTTCGCCCCAAAGTCCATTTGCCTC 1055  
QY 901 CACTACGTCAACCACCTGTTCTCTGCTGGATGTCTATCGAGCGCTGCCCTTTGACCTGCTA 960  
Db |||||  
1056 CACTACGTCAACCACCTGTTCTCTGCTGGATGTCTATAGCACTGCCCCCTTTGACCTACTA 1115  
QY 961 CATGCTTCAAGGTCAACGTGTACTTTCGGGGCCCATCTGTGTAAGACGGTGCCTGTG 1020  
Db |||||  
1116 CATGCTTCAAGGTCAATGTGTACTGTTGGGCTCACCTACTGAAGACCGTGCCTGTGCTT 1175  
QY 1021 CGCCTGTGCGCCTGTCTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTG 1080  
Db |||||  
1176 CGGCTGTGCGCCTACTACCAAGACTGGACCGGTACTCTCAGTATAGCGCTGTTGTGCTC 1235



Db 3396 CAGGAGGGCACAGGAGTCTGA 3419

## RESULT 13

AAx84911

ID AAX84911 standard; DNA; 3064 BP.



AC AAX84911;

XX	
DT	28-SEP-1999 (first entry)
XX	
DE	Human brain specific potassium channel protein coding sequence.
DE	

Brain specific potassium channel; human; central nervous system disorder; dementia; cerebral ischaemic sclerosis; therapy; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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100	100	100

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4.	.3057	

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PN WO9937677-A1.



PD 29-JUL-1999.

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PF 20-JAN-1999: 99W0-TP000190

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PR 23-JAN-1998. 08.TP-000111434

PR 04-DEC-1998: 98JP-00346108  
 22 CIT: 1330; 200F-00011434.

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01 252 1220, 200F-V0346150.

PA (VAMA) VAMANOUT DUTEM GO 1 50

THE LATH / LATHINOCHI PHARM CO LTD.  
XX

PT Mivako & Mochi no Ichi

ИИ  
УУ  
МЛҮАКЕ А, МОЧИЛЗ

XX  
WT 1000 150000

DR WFL; 1999-458683/38.  
XX P-PSDB; AAY22427.  
PT Potassium channel protein expressed specifically in brain tissue and  
PT method for its production.

XXXXXX

PS  
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CC

Claim 6; Page 44-49; 63pp; English.

This sequence encodes the potassium channel protein of the invention, that is expressed specifically in brain tissue. The protein is used to treat and investigate disorders of the central nervous system such as dementia and cerebral ischaemic sclerosis

Sequence 3064 BP; 554 A; 1042 C; 848 G; 620 T; 0 U; 0 Other; XX SQ

Query Match 27.2%; Score 894.8; DB 2; Length 3064;

Best Local Similarity 65.5%; Pred. No. 6.4e-151;

Matches 1408;	Conservative	0;	Mismatches 622;	Indels 120;	Gaps 3;
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1 ATGCCGGCCATGCGGGGCTCTCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60

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db  
4 ATGCCGGTCA TGAAGGGTTGCTGGCCCCGCAAAACACCTTCTTGGACACCATCGCCAC 63

[illegible]

61 CGCTTCGACGGCAGCAGTAACCTTCGTGCTGGGCAAGCCCACTGTCGGCCGCTTTC

12 11 10 9 8 7 6 5 4 3 2 1

64 CGTTTTCGCGAACGCACAGCAACCTTCCTGCTGGCCATACCCGCAACCCCGCGCTTTT

[illegible][illegible]





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Db 856 GTGCGGTCACCGTCCCTTACAACGTCTGCTTCGCTGGTGATGACGACACCCCCATCAG 915

QY 772 CGCGGCCGCCAGCGTCTGTGACCTGGCCGTGGAGGTCCTCTTCACTCCTTGACATTGTG 831

Db 916 TCCGACACACCCCTTGTCACTGACATCGCTGTGGAGATGCTTTCATCCTTGACATCATC 975

QY 832 CTGAATTTCCGTACCACATTCCGTGTCCAAGTCGSGCCAGTGGTGTGTTTGCCCCAAAGTCC 891

Db 976 TTGAACCTCCGCACACCACTACCTGTCCAGTCCGAGCCAGTGTTTCTGCTCCTCGGTCC 1035

QY 892 ATTTGCTCTCCACTACGTACACACCTGGTTCTCTGCTGGATGTATCGCAGCGCTGCCCTTT 951

Db 1036 ATTGGCTCCACTACCTGGCCACCTGGTTCTTTCGTGGACCTCATTTGCTTTGCCCTTT 1095

QY 952 GACCTGTACATGCCCTTCAAGGTCAACGTGTACTTCGGGGCCCCATCTGCTGAAGACGGTG 1011

Db 1096 GACCTGTGTATGTTCTTCAACATCACTGTGACCTCGTGGTACATCTGCTGAACACCGTG 1155

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Db 1336 TGGTTGCATGAGCTGGTAAGCGGCTGGAGAGCCTTATGTCAATGGTC----- 1385

QY 1252 GCTGGAGGGAACAGCTCCGGCCAGAGTGAACAAATGCAGCAGCAGCGAGGCCAACCGG 1311

Db 1386 ----- 1385

QY 1312 ACGGGCTGGAGCTGTGGCGGCGCCGTCGCTGCGCAGCGCCTACATCACTCCCTCTAC 1371

Db 1386 -----GGCCGTTGGACCACTCTGGCGCAGTGCCTACATCGCGCGCTGTAC 1431

QY 1372 TTCGCACTCAGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGACACC 1431

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Db 1792 CTGCAGTGCCTTGTGTTGGAGCAAGCAGGGGCTGCCCTTCGTGCCCTCTCCCTGCAC 1851

QY 1792 CTGCGGCCCCGCTTCTGCAGCGCCGGCGAGTACCTATCCACCAAGCGGATGCCCTGCAG 1851

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QY 1852 GGCCTCTACTTTTGTCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTCGCC 1911

Db 1912 GCACACTACTATGTCTCTCTGGCTCTCTTGAGGTGCTCCGAGACAACACGGTGTCTGGCC 1971

QY 1912 ATCCTAGGGAAGGGCGACCTGATCGGCTGTGAGCTGCCCCCGGGGAGCAG----- 1962

Db 1972 ATCCTTGAAAGGGGACTTGATTGGGGCAGACATCCCTGAGTTGGGGCAGGAGCCTGGG 2031

QY 1963 -----GTGGTAAAGGCCAATGCCGACCTGAAGGGGCTGACGTACTGCGTC 2007

Db 2032 GCAGGGCAGGCTGCTGCTGAAGACCAGCGCTGATGTGAAGCACTGACTTACTGCGGC 2091

QY 2008 CTGCAGTGTCTGCAGCTGGCTGGCTGCACGACAGCCTTTCGCTGTACCCCGAGTTTGC 2067

Db 2092 CTGCAGCAGCTGAGCAGCCGAGGGCTGGCCGAGGTCTTCGGTTGTATCCGGAATATGTG 2151

QY 2068 CCGCGCTTCAGTCTGGCTCCGAGGGGAGCTCAGCTACAACCTGGG 2114

Db 2152 GCTGCCTTCAGGGCTGGCCTACCCCGGACCTAACCTTCAACCTGCG 2198

RESULT 15

ADB53481

ID ADB53481 standard; DNA; 3736 BP.

XX ADB53481;

XX 04-DEC-2003 (first entry)

XX Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4023.

DE toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;

XX toxicity marker; toxicity progression; drug screening;

KW primary rat hepatocyte toxicity modelling; gene; ds.

XX Rattus norvegicus.

XX WO2003065993-A2.

XX 14-AUG-2003.

XX 04-FEB-2003; 2003WO-US003482.

PR 04-FEB-2002; 2002US-0353171P.

PR 13-MAR-2002; 2002US-0363534P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 10-APR-2002; 2002US-0371150P.

PR 11-APR-2002; 2002US-0371413P.

PR 19-APR-2002; 2002US-0373601P.

PR 19-APR-2002; 2002US-0373602P.

PR 22-APR-2002; 2002US-0374139P.

PR 08-MAY-2002; 2002US-0378370P.

PR 09-MAY-2002; 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.

PR 09-MAY-2002; 2002US-0378665P.

PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.

PR 04-SEP-2002; 2002US-0407688P.

PR 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

PI Elashoff M;

XX WPI; 2003-731472/69.

DR









GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 17:10:22 ; Search time 972 Seconds  
(without alignments)  
16465.512 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257  
Perfect score: 3252  
Sequence: 1 atgccggccatgcggggcct.....aagaaggcacaggggtctga 3252

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3245.8	99.8	3249	15	US-10-160-224-2
3	3218	99.0	3857	15	US-10-121-746-19
4	3156	97.0	3355	9	US-09-119-855-1
5	3156	97.0	3355	15	US-10-185-867-1
6	3153	97.0	3249	15	US-10-185-867-3
7	3144	96.7	3240	9	US-09-119-855-3
8	2664.8	81.9	3715	9	US-09-965-830-9
9	884.8	27.2	3064	9	US-09-965-830-5
10	869.8	26.7	3736	9	US-09-965-830-10
11	844.4	26.0	870	9	US-09-119-855-9
12	844.4	26.0	870	15	US-10-185-867-9
13	844.4	26.0	1132	9	US-09-119-855-7
14	844.4	26.0	1132	15	US-10-185-867-7

15	761.2	23.4	3321	15	US-10-185-867-17	Sequence 17, Appl
16	761.2	23.4	5107	15	US-10-185-867-15	Sequence 15, Appl
17	572.8	17.6	1626	9	US-09-119-855-6	Sequence 6, Appl
18	572.8	17.6	1626	15	US-10-185-867-6	Sequence 6, Appl
19	572.8	17.6	2694	9	US-09-119-855-4	Sequence 4, Appl
20	572.8	17.6	2694	15	US-10-185-867-4	Sequence 4, Appl
21	572.8	17.6	5955	15	US-10-185-867-14	Sequence 14, Appl
22	365.6	11.2	2877	15	US-10-192-440-3	Sequence 3, Appl
23	365.6	11.2	2877	15	US-10-325-430-20	Sequence 20, Appl
24	365.6	11.2	3164	15	US-10-192-440-1	Sequence 1, Appl
25	365.6	11.2	3164	15	US-10-325-430-19	Sequence 19, Appl
26	362.4	11.1	2746	17	US-10-432-171-7	Sequence 7, Appl
27	362.4	11.1	2877	13	US-10-332-447-41	Sequence 41, Appl
28	362.4	11.1	2983	17	US-10-432-171-1	Sequence 1, Appl
29	362.4	11.1	2983	17	US-10-432-171-3	Sequence 3, Appl
30	362.4	11.1	3091	17	US-10-432-171-5	Sequence 5, Appl
31	361.6	11.1	3041	15	US-10-188-308-19	Sequence 19, Appl
32	361.6	11.1	3041	15	US-10-188-296-19	Sequence 19, Appl
33	361.6	11.1	3041	15	US-10-188-341-19	Sequence 19, Appl
34	361.6	11.1	3041	15	US-10-188-297-19	Sequence 19, Appl
35	353.6	10.9	3041	15	US-10-188-308-20	Sequence 20, Appl
36	353.6	10.9	3041	15	US-10-188-296-20	Sequence 20, Appl
37	353.6	10.9	3041	15	US-10-188-341-20	Sequence 20, Appl
38	353.6	10.9	3041	15	US-10-188-297-20	Sequence 20, Appl
39	342.8	10.5	3479	10	US-09-758-036-4	Sequence 4, Appl
40	342.8	10.5	3480	9	US-09-735-995-1	Sequence 1, Appl
41	342.8	10.5	3480	17	US-10-696-708-1	Sequence 1, Appl
42	342.8	10.5	3950	9	US-09-735-995-3	Sequence 3, Appl
43	342.8	10.5	3950	17	US-10-696-708-3	Sequence 3, Appl
44	342.8	10.5	4070	13	US-09-795-651-59	Sequence 59, Appl
45	342.8	10.5	4070	17	US-10-483-617-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-965-830-1  
; Sequence 1, Application US/09965830  
; Patent No. US20020177201A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/965,830  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 09/600,776  
; PRIOR FILING DATE: 2001-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3323  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)..(3257)  
US-09-965-830-1

Query Match 100.0%; Score 3252; DB 9; Length 3323;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 ATGCCGCGCATCGGGGCGCTCCTGGCGCCTCAGAACACCTTCTGGACACCATCGTACG 65  
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QY 61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGCAACGCCAGGTGGGGGCTCTTC 120  
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Db 66 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGCAACGCCAGGTGGGGGCTCTTC 125  
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QY 121 CCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
Db 126 CCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 185  
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Db 186 ATGACGGGGCTGTGCCTGCTCTCCTTCTTTATGGCCAGACACCAAGTGTGCTCGCCG 245  
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QY 301 CGGAAGAGCGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGATGAGAAA 360  
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QY 1921 AAGGCGACCTGTATCGGCTGTGAGTGCCTCCCGGGGAGCAGGTGGTAAAGGCCAATGCC 1980  
Db 1926 AAGGCGACCTGTATCGGCTGTGAGTGCCTCCCGGGGAGCAGGTGGTAAAGGCCAATGCC 1985  
QY 1981 GACGTGAAGGGGCTGACGTACTGCTGCTGCTGAGTGTCTGAGTGGCTGGCTGCACGAC 2040  
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QY 2101 AGCTAACACCTGGGTGTGGGGAGGCTCTGCAGAGGTGGACACAGCTCCCTGAGCGGC 2160  
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QY 2221 GTCTCCCGAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCTGGCTGCACCTCC 2280  
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QY 3241 ACAGGGGTCTGA 3252

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RESULT 2

US-10-160-224-2

; Sequence 2, Application US/10160224

; Publication No. US2003007731A1

; GENERAL INFORMATION:

; APPLICANT: Jegla, Timothy J.

; APPLICANT: Wickenden, Alan

; APPLICANT: ICAGEN, Incorporated

; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit

; FILE REFERENCE: 018512-001320US

; CURRENT APPLICATION NUMBER: US/10/160,224

; CURRENT FILING DATE: 2002-05-28

; PRIOR APPLICATION NUMBER: US/09/343,494

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 3249

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3249)

; OTHER INFORMATION: hElk

US-10-160-224-2

Query Match 99.8%; Score 3245.8; DB 15; Length 3249;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 361 GGGAGGTGGCTCTTCTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420

QY 421 GGCCCCGACAGATGAAGGAGACAGGTGTGTGGCCGGCCGATATGGCCGGGACGATCC 480

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Db 2641 CTTCCGCGAGCGGTGACAGAGCTGTGAGCAGGTGCTGAGATGCGGGAAGGACTGCAG 2700  
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Db 2701 TCACCTTCGCGAGGCTGTGAGCTGTGAGCAGTGTCTGGCGCCCCACAGGAGGGTCCGTGCCCTCGG 2760  
QY 2761 GCATCGGAGAGGGGCGGTGCCAGCCAGCACCTCCGGGCTTCTGAGCCCTCTGTGTGTG 2820  
Db 2761 GCATCGGAGAGGGGCGGTGCCAGCCAGCACCTCCGGGCTTCTGAGCCCTCTGTGTGTG 2820  
QY 2821 GACACTGGGGCATCCTCTACTGCTGAGCCCGCCAGCTGGCTGCTTGTAGTGGGACT 2880  
Db 2821 GACACTGGGGCATCCTCTACTGCTGAGCCCGCCAGCTGGCTGCTTGTAGTGGGACT 2880  
QY 2881 TGGCCCCACCTCTGTCGGGGGCTCTCTCCCTCATGGCACCCCTGCGGCTGCCCCCA 2940  
Db 2881 TGGCCCCACCTCTGTCGGGGGCTCTCTCCCTCATGGCACCCCTGCGGCTGCCCCCA 2940



QY 2941 GCGTCTCAGAGTCCCCCTGGCCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCA 3000  
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3181 GAGATGGTGCTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGGSC 3240  
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3241 ACAGGGGTC 3249

RESULT 3

US-10-121-746-19  
; Sequence 19, Application US/10121746  
; Publication No. US20030036648A1  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutter, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels  
; FILE REFERENCE: SEQ-15p  
; CURRENT APPLICATION NUMBER: US/10/121,746  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: US/09/336,643A  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 3857  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (249)...(3495)  
; OTHER INFORMATION: K+Hnov14  
US-10-121-746-19

Query Match 99.0%; Score 3218; DB 15; Length 3857;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3244; Conservative 0; Mismatches 5; Indels 3; Gaps 2;  
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249 ATGCCGGCCATGCGGGCCTCCTGGCGCCGAGAACACCTTCCTGGACACCATCGCTACG 308  
QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTGTGGGCAACGCCAGGTGGCGGGGCTCTTC 120  
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309 CGCTTCGACGGCAGCACAGTAACCTTCGTGTGGGCAACGCC--AGTGGCGGGGCTCTT- 365  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 180

Dbb|||||  
366 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 425  
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426 ATGAGCGGGCTGTGCTGTCTCTTCTTATGGCCAGACACCACTGAGCTCGTCCGC 485  
QY 241 CAACAGATCCGAAGGCCCTGGACGAGCACAAAGGATTCAAGGTGAGCTGATCCTGTAC 300  
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QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTCAAGGACATCAGCGAAACCAAGAAATGAGAAA 360  
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QY 541 CTGCAAGAGCAGCCCCAAGGCAAGCACAAAGCTCAATAAGGGGGTGTGGGGAGAAACCA 600  
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QY 961 CATGCCCTTCAAGGTCAACGTGTACTTCGGGCCCCATCTGCTGAAGACGGTGGCCTGCTG 1020  
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QY 1021 CGCCTGCTGCGCTGCTTCCCGGGTGGACCGGTACTCGCAGTACAGCGCGTGGTGTG 1080  
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1326 ACACGTCTCATGGCCGTGTTTCGCCCTGCTCGCGCACTGGGTGCGCTGCTGTTTAC 1385  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCGGAATCCGAGTCCCTGAGATTTGGTGGCTGCAG 1200  
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1386 ATTGGCCAGCGGAGATCGAGAGCGGAATCCGAGTCCCTGAGATTTGGTGGCTGCAG 1445  
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Db 1446 GAGCTGGCCGCGGACTGGAGACTCCCTACTACCTGGTGGCCGAGGCCAGCTGGAGGG 1505

QY 1261 AACAGCTCCGGCAGAGTGACAACTGCAGCAGCAGCAGCGGCCAACGGGACGGGGCTG 1320

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QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCCCATCTAGGG 1920

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QY 1981 GACGTGAAGGGCTGACGTACTGCTCTGCAGTGTCTGCAGTGGCTGGCTGCACGAC 2040

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QY 2041 AGCCTTGGCTGTACCCCGAGTTTGGCCCGCGCTTCAGTCGTGGCTCCGAGGGGAGCTC 2100

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Db 3066 GACACTGGGGCATCTCTCTACTGCTGCAGCCCGAGCTGTGTCTTGTAGTGGACT 3125

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Db 3186 GCTCTCAGAGCTCCCCCTGGCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCA 3245

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Db 3246 GAGCCCCCTGCCTCAGGAGACCTCTGTCTGTAGCCCAAGCACCTGCTCCCTCCTCCT 3305

QY 3061 TCTGAGGAAGGGCTAGGACTTGGGCCCGCAGAGCCTGTGAGCAGGCTAGGCTACCAGC 3120

Db 3306 TCTGAGGAAGGGCTAGGACTTGGGCCCGCAGAGCCTGTGAGCAGGCTAGGCTACCAGC 3365

QY 3121 ACTGAGAGCCCCCAGGCTCAGGGGTGAGGGGCTTGGCTTGGCTGGGACCCCGACAGCCTG 3180

Db 3366 ACTGAGAGCCCCCAGGCTCAGGGGTGAGGGGCTTGGCTTGGCTGGGACCCCGACAGCCTG 3425

QY 3181 GAGATGCTTATTGGCTGCCATGGCTTGGCACAGTCCAGTGGACCCAGGAAGAGGC 3240

Db 3426 GAGATGCTTATTGGCTGCCATGGCTTGGCACAGTCCAGTGGACCCAGGAAGAGGC 3485

QY 3241 ACAGGGGTCTGA 3252

Db 3486 ACAGGGGTCTGA 3497

RESULT 4  
US-09-119-855-1  
; Sequence 1, Application US/09119855  
; Patent No. US20020099197A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A. J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

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; FILE REFERENCE: mni-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3355
; TYPE: DNA
; ORGANISM: Monkey
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)..(3352)
US-09-119-855-1

Query Match      97.0%; Score 3156; DB 9; Length 3355;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY      1 ATGCGGGCCATGCGGGGCTCTCTGGCGCCTCAGAAACACCTTCCTGGACACCATCGCTACG 60
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Db      224 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 283

QY      181 ATGCAGCGGGGCTGTGCCTGCTCCTTCTCTTATGGGCCAGACACCATGAGCTCGTCCGC 240
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QY      241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGAGTCAAGGCTGAGCTGATCTGTAC 300
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Db      404 CGGAAGAGCGGGCTCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAAATGAGAAA 463

QY      361 GGGGAGGTGGCTCTCTCTAGTCTCTCACAAAGGACATCAGCGAAACCAAGAACCGAGGG 420
Db      464 GGGGAGGTGGCTCTCTCTAGTCTCTCACAAAGGACATCAGTGAACCAAGAACCGAGGG 523

QY      421 GGCCCCGACAGATGGAAGGAGACAGGTGTGTGGCGGCGCCGATATGGCCGGGACGATCC 480
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QY      481 AAAGGCTTCAATGSCAAACCGGCGGAGCCGGGCGCTGCTCTACCACTGTCCGGGCAC 540
Db      584 AAAGGCTTCAATGCCAACCGGCGGAGCCGGGCTGTGCTCTACCACTGTCCGGGCAC 643

QY      541 CTGCAGAAGCAGCCCCAAGGGCAAGCACAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600
Db      644 CTGCAGAAGCAGCCCCAAGGGCAAGCACAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 703

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QY      661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCTCTGTCGCCACACTCTATGTGGCTGTC 720
Db      764 GGGGCGCTGAGGGCCACCTGGGATGGCTTCATCTCTGTCGCCACCGTCTATGTGGCTGTC 823

QY      721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCCAGTGCAGCCCGCCCG 780
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QY      781 CCCAGCGTCTGTGACCTGGCCGCTGGAGTCTCTTCACTCTGACATGTGCTGAATTTC 840
Db      884 CCCAGCGTCTGTGACCTGGCTGTGGAGTCTCTTCACTCTGACATGTGCTGAATTTC 943
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QY      841 CGTACCACATTCGTGTCCAAGTCGGSCCAGGTGGTGTTCGCCCCAAAGTCCATTTGCCTC 900
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QY      901 CACTACGTCAACACCTGGTTCCTGCTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTA 960
Db      1004 CACTACGTCAACACCTGGTTCCTGCTGGATGTATCGCAGCGCTGCCCTTTGACCTGCTG 1063

QY      961 CATGCCTTCAAGGTCAAACGTGTACTTCGGGGCCCCATCTGCTGAAGACGGTGCCTGCTG 1020
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Db      1124 CGCTGCTGCGCCTGCTTCCTGGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGTGCTG 1183

QY      1081 AACTGCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGGGTGCGCTCGTCTGTTTAC 1140
Db      1184 AACTGCTCATGGCCGTGTTCCGCCCTGCTTCGGCACTGGGTGCGCTCGTCTGTTTAC 1243

QY      1141 ATTGGCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGGCTGCAG 1200
Db      1244 ATTGGTCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGGCTGCAG 1303

QY      1201 GAGCTGGCCCCCGACTGGAGACTCCCTACTACCTGGTGGCGCGAGGCCAGCTGGAGGG 1260
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QY      1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAAACGGGACGGGGCTG 1320
Db      1364 AACAGCTCTGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAAACGGGACGGGGCTG 1423

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QY      1381 AGCAGCCTCACAGCGTGGCTTCGGCAACGTTCCGCCAAACACCGGACACCGAGAAGATC 1440
Db      1484 AGCAGCCTCACAGCGTGGCTTCGGCAACGTTCCGCCAAACACCGGACACTGAGAAGATC 1543

QY      1441 TTCTCCATCTGCACCATCTCATCGGCGCCCTGATGCAACGCGGTGGTGTTCGGGAAACGTG 1500
Db      1544 TTCTCCATCTGCACCATCTCATCGGCGCCCTGATGCAACGCGGTGGTGTTCGGGAAACGTG 1603

QY      1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCAACAGCCGACGCGCGAC 1560
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QY      1621 TACTTCCAGGCCACTGGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGC 1680
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QY      1681 CTCCTGACGAGCTGCGCGCAGACATCGCCCATGCACCTGCAACAAGGAGGTCTCTGACAGTG 1740
Db      1784 CTCCTGACGAGCTGCGCGCAGACATCGCCCATGCACCTGCAACAAGGAGGTCTCTGACAGTG 1843

QY      1741 CCACCTGTTGAGGGCGCCAGCGCGGCTGCCTGCGGGCACTGTCTGTGGCCCTGCGGCC 1800
Db      1844 CCGCTGTTGAGGGCAGCCAGCGCGGCTGCCTGCGGGCACTGTCTGTGGCCCTGCGGCC 1903

QY      1801 GCCTTCTGCACGCCGGCGAGTACCTCATCCACCAAGGCGATGCTGAGGCCCTCTAC 1860
Db      1904 GCCTTCTGCACGCCGGCGAGTACCTCATCCACCAAGGCGATGCTGAGGCCCTCTAC 1963

QY      1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCAGCGTGTCTGCCATCCTAGGG 1920
Db      1964 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCAGCGTGTCTGCCATCCTAGGG 2023
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QY 1921 AAGGGCAGCTGATCGGCTGTGAGCTGCCCCGGCGGAGCAGGTGTAAGGCCAATGCC 1980  
D 1922 AAGGGCAGCTGATCGGCTGTGAGCTGCCCCGGCGGAGCAGGTGTAAGGCCAATGCC 1981  
D 1923 AAGGGCAGCTGATCGGCTGTGAGCTGCCCCGGCGGAGCAGGTGTAAGGCCAATGCC 1980  
QY 1981 GACGTGAAGGGCTGACGTACTCGCTCTGAGTGTCTGAGCTGGCTGCGCTGCACGAC 2040  
D 1982 GACGTGAAGGGCTGACGTACTCGCTCTGAGTGTCTGAGCTGGCTGCGCTGCACGAC 2040  
D 1983 GATGTGAAGGGCTGACGTACTCGCTCTGAGTGTCTGAGCTGGCTGCGCTGCACGAC 2143  
QY 2041 AGCCTTGCGCTGTACCCCGAGTTTGGCCCGGCTTCACTGCTGGCTCCGAGGGGAGCTC 2100  
D 2042 AGCCTTGCGCTGTACCCCGAGTTTGGCCCGGCTTCACTGCTGGCTCCGAGGGGAGCTC 2100  
D 2043 AGCCTTGCGCTGTACCCCGAGTTTGGCCCGGCTTCACTGCTGGCTCCGAGGGGAGCTC 2203  
QY 2101 AGCTACAACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAAGCTTCCCTGAGCGGC 2160  
D 2102 AGCTACAACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAAGCTTCCCTGAGCGGC 2160  
D 2103 AGCTACAACTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAAGCTTCCCTGAGCGGC 2263  
QY 2161 GACAATACCCCTTATGTCCACGCTGGAGGAGAGAGACAGATGGGGAGCAGGGCCCCACG 2220  
D 2162 GACAATACCCCTTATGTCCACGCTGGAGGAGAGAGACAGATGGGGAGCAGGGCCCCACA 2323  
QY 2221 GTCTCCCCAGCCCAAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCCCTGGCTGCACCTCC 2280  
D 2222 GTCTCCCCAGCCCAAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCCCTGGCTGCACCTCC 2383  
QY 2281 TCATCTCAGCTGCCAAGCTGTATCCCCACGTGCAACAGCACCCCGGCTCTGTCTAGGT 2340  
D 2282 TCATCTCAGCTGCCAAGCTGTATCCCCACGTGCAACAGCACCCCGGCTCTGTCTAGGT 2443  
QY 2341 GGCAGAGGGAGGCCAGGAGGGCTTTGAAGCTGAGGCTGGCCCCCTCTGTCTCCC 2400  
D 2342 GGCAGAGGGAGGCCAGGAGGGCTTTGAAGCTGAGGCTGGCCCCCTCTGTCTCCC 2503  
QY 2401 CCACGGGGCCCTAGAGGGCTACGGCTGCCCCCATGCAATGATGTGCCCCCAGATCTG 2460  
D 2402 CCACGGGGCCCTAGAGGGCTACGGCTGCCCCCATGCAATGATGTGCCCCCAGATCTG 2563  
QY 2461 AGCCCCAGGGTAGTAGATGGCAATTGAAGACGGCTGTGGCTCGGACCGCCCAAGTTCTCT 2520  
D 2462 AGCCCCAGGGTAGTAGATGGCAATTGAAGACGGCTGTGGCTCGGACCGCCCAAGTTCTCT 2623  
QY 2521 TTCCGGCTGGCCAGCTGTGGCCCGGAAATGTAGCAGCAGCCCTCCCTCGGACCGAGAGC 2580  
D 2522 TTCCGGCTGGCCAGCTGTGGCCCGGAAATGTAGCAGCAGCCCTCCCTCGGACCGAGAGT 2683  
QY 2581 GGCCTGCTCACTGTTCCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2640  
D 2582 GGCCTGCTCACTGTTCCCCATGGGCCAGCGAGGCAAGGAACACAGACACACTGGACAAG 2743  
QY 2641 CTTGCGCAGCGGTGACAGAGCTGTGAGCAGAGGTGTGAGATGCGGGAAGGACTGCGAG 2700  
D 2642 CTTGCGCAGCGGTGATGGAGCTGTGAGAACAGGTGTGAGATGCGGGAAGGACTACAG 2803  
QY 2701 TCATTTGCCAGGGCTGTGAGCTTGTCTGGGGCCCCCAGGGAGGGTCCGTGCCCCCTCGG 2760  
D 2702 TCATTTGCCAGGGCTGTGAGCTTGTCTGGGGCCCCCAGGGAGGGTCCGTGCCCCCTCGG 2863  
QY 2761 GCATCGGAGAGGGGCGGTGCCCCAGCCAGCCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
D 2762 GCATCGGAGAGGGGCGGTGCCCCAGCCAGCCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2923  
QY 2821 GACACTGGGGCATCCTCCTACTGCTGAGCCCCCAGCTGGCTGTGCTTGTAGTGGGACT 2880  
D 2822 GACACTGGGGCATCCTCCTACTGCTGAGCCCCCAGCTGGCTGTGCTTGTAGTGGGACT 2983  
QY 2881 TGGCCCCACCTCGTCCGGGGCTCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA 2940  
D 2882 TGGCCCCACCTCGTCCGGGGCTCCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCCA 3043  
QY 2941 GCGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCA 3000  
D 2942 GCACTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTCTGGACCTCCACCTCAGACTCA 3103  
QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTGTGAGCCCCAGCACCCCTGCCTTCCCCCTCCT 3060

Db 3104 GAGCCCCCTGCCTCAGGAGACCTCTGCTGTGAGCCAGCACCCCTGCCTCACCTCCTCCT 3163  
QY 3061 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCCTGTGAGCCAGGCTGAGGCTACCAGC 3120  
D 3164 TCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCCTGTGAGCCAGGCTGAGGCTACCAGC 3223  
QY 3121 ACTGAGAGCCCCCAGCAGGCTCAGGGGCTGGCCCTTGGGACCCCCACAGCCTG 3180  
D 3224 ACTGAGAGCCCCCGCCAGTGTGAGGGGCTGGCCCTTGGGACCCCCACAGCCTG 3283  
QY 3181 GAGATGCTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC 3240  
D 3284 GAGATGCTGCTTATTGGCTGCCAGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC 3343  
QY 3241 ACAGGGGTCTGA 3252  
D 3344 ACAGGGGTCTGA 3355

RESULT 5  
US-10-185-867-1  
; Sequence 1, Application US/10185867  
; Publication No. US2003010429A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Roy A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/10/185,867  
; CURRENT FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: US/09/358,383  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 3355  
; TYPE: DNA  
; ORGANISM: Macaca sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (104)..(3352)  
US-10-185-867-1

Query Match 97.0%; Score 3156; DB 15; Length 3355;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 3192; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGCGCGCCATGCGGGGCTCCTGGCGCCTCAGAACACCTTCTGGACACCATCGCTACG 60  
D 104 ATGCGCGCCATGCGGGGCTCCTGGCGCCTCAGAACACCTTCTGGACACCATCGCTACG 163  
QY 61 CGCTTCGACGGCACGCACAGTAACCTTGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
D 164 CGCTTCGACGGCACGCACAGTAACCTTGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 223  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 180  
D 224 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 283  
QY 181 ATGAGCGGGCTGTGCTGCTCCCTTATGGCCAGACACAGGTGAGCTCGTCCGC 240  
D 284 ATGAGCGGGCTGTGCTGCTCCCTTATGGCCAGACACAGGTGAGCTCGTCCGC 343  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
D 344 CAACAGATCCGCAAGGCCCTGGACGAGCAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 403  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTATACCCATAAGAAATGAGAAA 360  
D 404 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTATACCCATAAGAAATGAGAAA 463

QY 361 GGGAGGTGGCTCTCTTCCTAGTCTCTCAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db |||||  
QY 464 GGGAGGTGGCTCTCTTCCTAGTCTCTCAAGGACATCAGTGAACCAAGAACCGAGGG 523  
Db |||||  
QY 421 GGCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCGATATGGCCGGGACAGATCC 480  
Db |||||  
QY 524 GGCCCTGACAGATGGAAGGAGACAGGTAGTGGCCGGCCGATATGGCCGGGACAGATCC 583  
QY 481 AAAGGTTCAATGCCAACCCGGGCGGAGCCGGCCGTGCTTACCACTGTCCGGGGCAC 540  
Db |||||  
QY 584 AAAGGTTCAATGCCAACCCGGGCGGAGCCGGGCTGTGCTTACCACTGTCCGGGGCAC 643  
QY 541 CTGCAGAAAGCAGCCCAAGGCAAGCACAAAGCTCAATAAGGGGGTGTTTGGGGAGAAACCA 600  
Db |||||  
QY 644 CTGCAGAAAGCAGCCCAAGGCAAGCACAAAGCTCAATAAGGGGGTGTTTGGGGAGAAACCA 703  
QY 601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAAGTCGCCCTTCACTCTGTTGCACTGT 660  
Db |||||  
QY 704 AACTTGCCTGAGTACAAAGTAGCTGCCATCCGAAAGTCGCCCTTCACTCTGTTGCACTGT 763  
QY 661 GGGGCACTGAGAGCCACCTGGGATGGCTTCACTCTGCTCGCCACACTCTAATGTGGCTGTC 720  
Db |||||  
QY 764 GGGGCGCTGAGGGCCACCTGGGATGGCTTCACTCTGCTCGCCACAGCTCTAATGTGGCTGTC 823  
QY 721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCAAGTCCGCCCGCCCG 780  
Db |||||  
QY 824 ACCGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCAAGTCCGCCCGCCCG 883  
QY 781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCCCTTCACTCTTACATTTGCTGAATTC 840  
Db |||||  
QY 884 CCCAGCGTCTGTGACCTGGCTGTGGAGGTCCCTTCACTCTTGAATTTGCTGAATTC 943  
QY 841 CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTTCGCCCAAGTCCATTTGCCCTC 900  
Db |||||  
QY 944 CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTTCGCCCAAGTCCATTTGCCCTC 1003  
QY 901 CACTACGTCAACCACTGGTTCCTGCTGGATGTCAATCGCAGCGCTGCCCTTTGACCTGCTA 960  
Db |||||  
QY 1004 CACTACGTCAACCACTGGTTCCTGCTGGATGTCAATCGCAGCGCTGCCCTTTGACCTGCTG 1063  
QY 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCACTGCTGAAGACGGTGGCCCTGCTG 1020  
Db |||||  
QY 1064 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCACTGCTGAAGACGGTGGCCCTGCTG 1123  
QY 1021 CGCCTGCTGCGCCTGCTTCGCGGCTGGACCGGCTACTCGCAGTACAGCGCCGTGGTCTG 1080  
Db |||||  
QY 1124 CGCCTGCTGCGCCTGCTTCGCGGCTGGACCGGCTACTCGCAGTACAGCGCCGTGGTCTG 1183  
QY 1081 ACACGTCTATGGCCGTGTTCCGCCCTGCTCGCGCACTGGTTCGCCTGCGTCTGTTTAC 1140  
Db |||||  
QY 1184 ACACGTCTATGGCCGTGTTTGCCTGCTTGGCACTGGTTCCTGCGTCTGTTTAC 1243  
QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCCTGAGATTGGCTGGCTGCAG 1200  
Db |||||  
QY 1244 ATTGGTCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCCTGAGATTGGCTGGCTGCAG 1303  
QY 1201 GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGCCGGAGGCGCAGCTGGAGGG 1260  
Db |||||  
QY 1304 GAGCTGGCCCGCGACTGGAGACCCCTACTACTTGGTGGCCGGAGACCAAGCGGAGGG 1363  
QY 1261 AACAGCTCCGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCCAAGCGGACGGGGCTG 1320  
Db |||||  
QY 1364 AACAGCTCTGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCCAAGCGGACGGGGCTG 1423  
QY 1321 GAGCTGTGGCGGCCCGCTGCTGCTGCGCAGCGCCTACATCACCTCCCTACTTTCGCACTC 1380  
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QY 1424 GAGCTGTAGCGGCCCGCTGCTGCTGCGCAGCGCCTACATCACCTCCCTACTTTCGCACTC 1483  
QY 1381 AGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCCAACACGGACACCGAGAATC 1440  
Db |||||  
QY 1484 AGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCCAACACGGACACTGAGAATC 1543  
QY 1441 TTCTCCATCTGCACCATGTCTCATCGCGGCCCTGTGATGCACGCGGTGGTGTGGGAACGTG 1500  
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Db 1544 TTCTCCATCTGCACCATGTCTCATCGGCGCCCTGATGCACGCGTGGTGTTCGGAACGTG 1603  
QY 1501 ACGGCCATCATCCAGCGCATGTACGCCCGCCCGCGCTTCTGTACACAGCCGACCGCGGAC 1560  
Db |||||  
QY 1604 ACGGCCATCATCCAGCGCATGTACGCCCGCCCGCGCTTCTGTACACAGCCGACCGCGGAC 1663  
QY 1561 CTGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620  
Db |||||  
QY 1664 CTGCGGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1723  
QY 1621 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCAACGAGCTGCTGCAGAGC 1680  
Db |||||  
QY 1724 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCAACGAGCTGCTGCAGAGC 1783  
QY 1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGACCTGCACAAGGAGGTCTCTGCAGCTG 1740  
Db |||||  
QY 1784 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGACCTGCACAAGGAGGTCTCTGCAGCTG 1843  
QY 1741 CCACCTGTTGAGGCGGCAGCCCGGCTGCCCTGCGGCACTGTCTCTGGCCCTGCGGCC 1800  
Db |||||  
QY 1844 CCGCTGTTTGAGGCAGCAGCCCGGCTGCCCTGCGGCACTGTCTCTGGCCCTGCGGCC 1903  
QY 1801 GCCTTCTGCACGCGCGGAGTACCTCATCCACCRAAGCGATGCCCTGCAGGCCCTCTAC 1860  
Db |||||  
QY 1904 GCCTTCTGCACGCGCGGCGAGTACCTCATCCACCRAAGCGATGCCCTGCAGGCCCTCTAC 1963  
QY 1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTGCCCATCTTAGGG 1920  
Db |||||  
QY 1964 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGTCTGCCCATCTTAGGG 2023  
QY 1921 AAGGGCGACCTGTATCGGCTGTGAGCTGCCCGGGGAGCAGGTGTTAAAGGCCAATGCC 1980  
Db |||||  
QY 2024 AAGGGTGACCTGTATCGGCTGTGAGCTGCCCGGGGAGCAGGTGTTAAAGGCCAATGCC 2083  
QY 1981 GACGTGAAGGGGTGACGTACTGCGTCTCTGCAGTGTCTGCAGTGGTGGCTGCACGAC 2040  
Db |||||  
QY 2084 GATGTGAAGGGGTGACGTACTGCGTCTCTGCAGTGTCTGCAGTGGTGGCTGCACGAC 2143  
QY 2041 AGCCTTGCCTTACCCCGAGTTTGCCCGCGCTTCAGTCTGGCTCCGAGGGAGCTC 2100  
Db |||||  
QY 2144 AGCCTTGCCTTACCCCGAGTTTGCCCGCGCTTCAGTCTGGCTCCGAGGGAGCTC 2203  
QY 2101 AGCTACAACCTTGTCCACCGCTGGAGGAGGCTCTGCAGAGGTGGACACCAAGCTCCCTGAGCGGC 2160  
Db |||||  
QY 2204 AGCTACAACCTTGTCCACCGCTGGAGGAGGAGACAGATGGGAGCAGGGCCCCACA 2263  
QY 2161 GACAATACCTTATGTCCACCGCTGGAGGAGGAGACAGATGGGAGCAGGGCCCCACG 2220  
Db |||||  
QY 2264 GACAATACCTTATGTCCACCGCTGGAGGAGGAGACAGATGGGAGCAGGGCCCCACA 2323  
QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGTGTCTCCCTGGCTGCACCTCC 2280  
Db |||||  
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QY 2281 TCATCCTCAGTGCCTAAGCTGCTATCCACAGTTCGAAACAGCACCCCGGCTCGTCTAGGT 2340  
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QY 2461 AGCCCCAGGGTAGTAGTGGCATTTGAAGACGGCTGTGGTCCGACAGCCCCAAGTTCTCT 2520  
Db |||||  
QY 2564 AGCCCCAGGGTAGTAGTGGCATTTGAAGACGGCTGTGGTCCGACAGCCCCAAGTTCTCT 2623  
QY 2521 TTCCCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGC 2580  
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Db 2624 TTCCGCATGGCCAGTCTGGCCCGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGT 2683  
QY 2581 GGCCTGCTCACTGTTCCCATGGGCCAGGAGGCAAGAAACACAGACACACTGGACAAG 2640  
Db 2684 GGCCTGCTCACTGTTCCCATGGGCCAGGAGGCAAGAAACACAGACACACTGGACAAG 2743  
QY 2641 CTTCCGCGAGGCGGTACAGAGCTGTTCAGAGCAGGTGCTGCAGATGCGGGAAGGACTGCAG 2700  
Db 2744 CTTCCGCGAGGCGGTGATGAGCTGTTCAGAACAGGTGCTGCAGATGCGGGAAGGACTACAG 2803  
QY 2701 TCACCTCGCCAGGCTGTGCAGCTTGTCTCGGCCCCACAGGAGGCTCGTGCCTCGG 2760  
Db 2804 TCACCTCGCCAGGCTGTGCAGCTTGTCTCGGCCCCACAGGAGGCTCGTGCCTCGG 2863  
QY 2761 GCATCGGAGAGGGCCGTGCCCCAGCCAGCACTCCGGGCTTCTGCAGCCTCTGTGTGTG 2820  
Db 2864 GCCTCAGGAGAGGGGCATGCCAGCTTGTCTCGGCCCCACAGCAGCTCCGGGCTTCTGCAGCCTCTGTGTGTG 2923  
QY 2821 GACACTGGGGCATCCTCTACTGCTGCTGCAGCCCGCAGCTGGCTCTGTCTTGAGTGGGACT 2880  
Db 2924 GACACTGGGGCATCCTCTACTGCTGCTGCAGCCCGCAGCTGGCTCTGTCTTGAGTGGGACT 2983  
QY 2881 TGGCCCCACCCCTCGTCCGGGGCCCTCCTCCCTCATGSCACCCCTGGCCCTGGGCTCCCCCA 2940  
Db 2984 TGGCCCCACCCCTCGTCCGGGGCCCTCCTCCCTCATGSCACCCCTGGCCCTGGGCTCCCCCA 3043  
QY 2941 GCGTCTCAGAGCTCCCTCGGCTCGAGCCACAGCTTCTTGACCTCCACCTCAGACTCA 3000  
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QY 3001 GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCAGCACCCCTGCCTCCCTCCTCCT 3060  
Db 3104 GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCAGCACCCCTGCCTCCTCCTCCT 3163  
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QY 3181 GAGATGCTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC 3240  
Db 3284 GAGATGCTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC 3343  
QY 3241 ACAGGGGTCTGA 3252  
Db 3344 ACAGGGGTCTGA 3355

RESULT 6  
US-10-185-867-3  
; Sequence 3, Application US/10185867  
; Publication No. US2003010429A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-055CP  
; CURRENT APPLICATION NUMBER: US/10/185,867  
; CURRENT FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: US/09/358,383  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: USSN 09/119,855  
; PRIOR FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 3249  
; TYPE: DNA  
; ORGANISM: Macaca sp.  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: (1)...(3249)  
US-10-185-867-3  
Query Match 97.0%; Score 3153; DB 15; Length 3249;  
Best local Similarity 98.2%; Pred. No. 0;  
Matches 3189; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
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QY 61 CGCTTCGACCGGACGACAGTAACTTCGTCTGGCAACGCCAGGTGGCGGGCTCTTC 120  
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QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCCGGCTGAGGTC 180  
Db 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCCGGCTGAGGTC 180  
QY 181 ATGCAGCGGGCTGTGCTGCTCTCTCTTATATGGGCCAGACACAGTGAGCTCGTCCGC 240  
Db 181 ATGCAGCGGGCTGTGCTGCTCTCTCTTATATGGGCCAGACACAGTGAGCTCGTCCGC 240  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGAGTCAAGGCTGATCTCTGTAC 300  
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QY 301 CGGAAGAGCGGGCTCCGCTTCTGGTGTCTCTCTGATGTATACCCATAAAGAAATGAGAAA 360  
Db 301 CGGAAGAGCGGGCTCCGCTTCTGGTGTCTCTCTGATGTATACCCATAAAGAAATGAGAAA 360  
QY 361 GGGGAGGTGGCTCTCTCTAGTCTCTCACAAAGGACATCAGCGAAACCAAGAACCGAGGG 420  
Db 361 GGGGAGGTGGCTCTCTCTAGTCTCTCACAAAGGACATCAGTGAAACCAAGAACCGAGGG 420  
QY 421 GGGCCCGACAGATGGAAGGACAGGTGGTGGCCCGGCGCGATATGGCCGGGACGATCC 480  
Db 421 GGGCCCGACAGATGGAAGGACAGGTAGTGGCCCGGCGCGATATGGCCGGGACGATCC 480  
QY 481 AAAGGCTTCAATGCCAACCGCGCGGAGCGCGCTTACACCTGTCCGGGCAC 540  
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QY 541 CTGCAGAAGCAGCCCCAAGGCAAGCAAGCTCAATAAGGGGTGTTGGGAGAAACCA 600  
Db 541 CTGCAGAAGCAGCCCCAAGGCAAGCAAGCTCAATAAGGGGTGTTGGGAGAAACCA 600  
QY 601 AACTTGCCTGAGTACAAAGTAGTGCCTATCCGGAAGTGCCTTTCATCTGTGCACTGT 660  
Db 601 AACTTGCCTGAGTACAAAGTAGTGCCTATCCGGAAGTGCCTTTCATCTGTGCACTGT 660  
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QY 841 CGTACCACATTCGTGTCCAAGTCCGGCCAGGTGGTGTGTTGCCCAAGTCCATTTGCCTC 900  
Db 841 CGTACCACATTCGTGTCCAAGTCCGGCCAGGTGGTGTGTTGCCCAAGTCCATTTGCCTC 900  
QY 901 CACTACGTCACACCTGGTTCCTGCTGGATGTATCGCAGCGCTGCTGACCTGCTA 960  
Db 901 CACTACGTCACACCTGGTTCCTGCTGGATGTATCGCAGCGCTGCTGACCTGCTG 960  
QY 961 CATGCCCTCAAGGTCAAGTGTACTTCGGGGCCCATCTGTGAAGACGGTGGCCTGCTG 1020  
Db 961 CATGCCCTCAAGGTCAAGTGTACTTCGGGGCCCATCTGTGAAGACGGTGGCCTGCTG 1020



Db 961 CATGCCCTCAAGGTCAACGTGTACTTCGGGGCCCCACCTGCTGAAGACGGTGGCGCTGCTG 1020

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QY 1141 ATTGGCCAGCGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCGAG 1200

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QY 1261 AACAGCTCCGGCCAGAGTGAACAACTGCAGCAGCAGCAGCGGCAACCGGACGGGGCTG 1320

Db 1261 AACAGCTCTGGCCAGAGTGAACAACTGCAGCAGCAGCAGCGGCAACCGGACGGGGCTG 1320

QY 1321 GAGCTGCTGGCGGCCCGTGCCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC 1380

Db 1321 GAGCTGCTAGCGGCCCGTGCCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC 1380

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Db 1381 AGCAGCCTCACACGCTGGGCTTCGGCAACGTGTCGCGCAACACCGACACTGAGAAGATC 1440

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Db 1561 CTGCGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAG 1620

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Db 1621 TACTTCCAGGCCACTGGCGGTTGAACAATGGCATCGACACCACCGAGCTGTCAGAGC 1680

QY 1681 CTCCCTGACGAGTGGCGCAGACATCGCCATGCACCTGCACAAGGAGTCTTCAGCTG 1740

Db 1681 CTCCCTGACGAGTGGCGCAGACATCGCCATGCACCTGCACAAGGAGTCTTCAGCTG 1740

QY 1741 CCACCTGTTTAGCGGCCAGCCGCGGCTGCCCTGCGGGCACTGTCTCTGGCCCTGCGGCC 1800

Db 1741 CCGCTGTTTAGCGAGCCAGCCGCGGCTGCCCTGCGGGCACTGTCTCTGGCCCTGCGGCC 1800

QY 1801 GCCTTCTGCACGCCGGCGAGTACCTCATCCACCAAGCGATGCCCTGGAGGCCCTCTAC 1860

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QY 1861 TTTGTCTGCTCTGGCTCCATGGAGTGTCAAGGGTGGCACCGTGTGCGCCATCCTAGGG 1920

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QY 1921 AAGGGCAGCTGATCGGCTGTGAGTGCCTGCGGGGAGCAGGTGGTAAAGGCCAATGCC 1980

Db 1921 AAGGGTGACCTGATCGGCTGTGAGTGCCTGCGGGGAGCAGGTGGTAAAGGCCAATGCC 1980

QY 1981 GACGTGAAGGSGTACGTACTGCGTCTCTGAGTGTCTGCAGCTGGCTGGCCTGCACGAC 2040

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QY 2041 AGCCTTGCGTGTACCCCGAGTTTGGCCCGCGCTTCAGTCTGTCGTCCTCCGAGGGGAGCTC 2100

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Db 2161 GACAAATACCCTTATGTCCACGCTGGAGGAGAAAGGAGACAGATGGGAGCAGGGCCCCACA 2220

QY 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCCCTGGCTGCACCTCC 2280

Db 2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTACTGTCCCCCTGGTTGCACCTCC 2280

QY 2281 TCATCTCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCCGGCCTCGTCTAGGT 2340

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QY 2461 AGCCCCAGGCTAGTAGATGGCATTGAAGACGCTGTGGCTCGGACCCAGCCCAAGTTCTCT 2520

Db 2461 AGCCCCAGGCTAGTAGATGGCATTGAAGACGCTGTGGCTCGGACCCAGCCCAAGTTCTCT 2520

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Db 3121 ACTGAGAGCCCCCGCCAGTGTACGGGGGCTGGCCCTTGGCCCTGGGACCCCCACAGCCTG 3180

QY 3181 GAGATGGTGTATTGGTGCCTGCTGGCCACAGTCCAGTGGACCCAGGAAGAAGGC 3240  
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3181 GAGATGGTGTATTGGTGCCTGCTGGCCACAGTCCAGTGGACCCAGGAAGAAGGC 3240  
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3241 ACAGGGGTC 3249

RESULT 7  
US-09-119-855-3  
; Sequence 3, Application US/09119855  
; Patent No. US20020099197A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: mni-055  
; CURRENT APPLICATION NUMBER: US/09/119,855  
; CURRENT FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 3240  
; TYPE: DNA  
; ORGANISM: Monkey  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3240)  
US-09-119-855-3

Query Match 96.7%; Score 3144; DB 9; Length 3240;  
Best Local Similarity 98.1%; Pred. No. 0;  
Matches 3180; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY 70 GGCACGCACAGTAACCTTGTGCTGGGCAACGCCAGTGGCGGGGCTCTTCCCGTGGTC 129  
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QY 130 TACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTCTATGACGGG 189  
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QY 190 GGCTGTGCTGCTCCTTCTTATGGCCAGACACCAAGTGGTCTCGTCCGCCAACAGATC 249  
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181 GGCTGTGCTGCTCCTTCTTATGGCCAGACACCAAGTGGTCTCGTCCGCCAACAGATC 240  
QY 250 CGCAAGGCGCTGGACGAGCAACAGGATTCAGGCTGAGTCTCTGTACCGGGAAGGC 309  
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241 CGCAAGGCGCTGGACGAGCAACAGGATTCAGGCTGAGTCTCTGTACCGGGAAGGC 300  
QY 310 GGGCTCCGTTCTGGTGTCTCTCAGAGGATTCAGGCTGATACCCATAAAGATGAGAAAGGGAGGTG 369  
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301 GGGCTCCGTTCTGGTGTCTCTCAGAGGATTCAGGCTGATACCCATAAAGATGAGAAAGGGAGGTG 360  
QY 370 GCTCTCTCTAGTCTCTCAGAGGATTCAGGCTGATACCCATAAAGATGAGAAAGGGAGGTG 429  
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361 GCTCTCTCTAGTCTCTCAGAGGATTCAGGCTGATACCCATAAAGATGAGAAAGGGAGGTG 420  
QY 430 AGATGGAAGGAGACAGGTGGTGGCGGCGCGGATATGGCGGCGACGATCCAAAGGCTTC 489  
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421 AGATGGAAGGAGACAGGTGGTGGCGGCGCGGATATGGCGGCGACGATCCAAAGGCTTC 480  
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481 AATGCCAACCGGCGGAGCGCGGCTGTCTACCTACCTGTCCGGGACCTGACAGAG 540  
QY 550 CAGCCCAAGGGCAAGCAAGCTCAATAGGGGGTGTGGGAGAGAAACCAACTTGCCT 609  
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601 GAGTACAAAGTAGCCGCATCCGGAAGTGCCTTTCATCTCTGTTGCACTGTGGGCGCTG 660  
QY 670 AGAGCCACCTGGGATGGCTTCATCTCTGCTGCCACACTCTATGTTGGTGTACTGTGCCC 729  
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661 AGGGCCACCTGGGATGGCTTCATCTCTGCTGCCACGCTCTATGTTGGTGTACCGTGCCT 720  
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721 TACAGCGTGTGTGAGCACAGCACGGGAGCCAGTCCCGCCCGCCCGCCAGCGTC 780  
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781 TGTGACCTGGCTGTGGAGGTCTCTTCATCTCTTGACATTGTGCTGAATTTCCGTACCACA 840  
QY 850 TTCGTGTCCAAAGTCCGGCCAGGTGGTGTTCGCCCCAAAGTCCATTTCCTCCACTACGTC 909  
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841 TTCGTGTCCAAAGTCCGGCCAGGTGGTGTTCGCCCCAAAGTCCATTTCCTCCACTACGTC 900  
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901 ACCACCTGGTTCCTGCTGGATGTATCGAGCGCTGCCCTTTGACCTGCTACATGCCTTC 960  
QY 970 AAGGTCAACGTGTACTTCGGGGCCCATCTGTGAAGACGGTGCCTGCTGCGCTGCTG 1029  
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961 AAGGTCAACGTGTACTTCGGGGCCCATCTGTGAAGACGGTGCCTGCTGCGCTGCTG 1020  
QY 1030 CGCCTGCTTCCGGGCTGGACCGGTACTCGACGACAGCGCGCTGGTGTGACACTGCTC 1089  
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1021 GCGCTGCTTCCGGGCTGGACCGGTACTCGCAGTACAGCGCGTGGTGTGACACTGCTC 1080  
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1081 ATGGCCGTGTTTCCGCTGCTTGGCACTGGGTGCGTCTGGTTTTACATTGCTCAG 1140  
QY 1150 CGGGAGATCGAGAGACGCAATCCGAGTCCCTGAGATTGGCTGGCTGCAGGAGCTGGCC 1209  
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1141 CGGGAGATCGAGAGACGCAATCCGAGTCCCTGAGATTGGCTGGCTGCAGGAGCTGGCC 1200  
QY 1210 GCGCGACTGGAGACTCCCTACTACTTGGTGGCGGAGCCAGCTGGAGGGAACAGCTCC 1269  
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QY 1270 GGCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCAACAGGACGGGCTGGAGCTGCTG 1329  
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1261 GGCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCAACAGGACGGGCTGGAGCTGCTA 1320  
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1321 GCGGCGCGCTGCTGCGCAGCGCCTACATCACCTCCCTCTACTTTCGCACTCAGCAGCTC 1380  
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QY 2290 GCTGCCAAGCTGTATCCCCACGTGCAACAGCACCCCGGCTCGTCTAGGTGGCAGAGGG 2349  
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QY 2410 CTAGAGGGGTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCCAGG 2469  
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RESULT 8  
US-09-965-830-9  
; Sequence 9, Application US/09965830  
; Patent No. US20020177201A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/965,830  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 09/600,776  
; PRIOR FILING DATE: 2001-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 3715  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-09-965-830-9  
Query Match 81.9%; Score 2664.8; DB 9; Length 3715;  
Best Local Similarity 89.0%; Pred.No. 0;  
Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;  
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QY 216 CGCTTCGACGGGACGCACAGTAACTTCGTCTGGCAACGCCAGGTGGCAGGGCTCTTC 275  
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QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180  
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QY 276 CCTGTGGTCTACTGCTCCGATGGCTTCTGTGACCTCACGGGTTCCTCCAGAGCTGAGGTC 335  
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QY 181 ATGCAGCGGGGCTGTGCCCTGCTCCTTCTCTTTATGGGCCAGACACCATGAGCTCGTCCGC 240  
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QY 336 ATGCAGCGAGGCTGTGCCTGCTCCTTCTCTATGGGCCAGACACCATGAGTTGGTCCGC 395





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QY 2632 CTGGACAAGCTTCGGCAGGCGGTGACAGAGCTGTGAGCAGAGTGTGAGATGCGGGAA 2691  
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QY 2692 GGAATGCACTCACTTCGCCAGGTGTGAGCTTGTCTGCGGCCCCACAGGGAGGGTCCG 2751  
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QY 2872 AGTGGGACTTGGGCCACCCCTCGTCCGGGCGCT---CCTCCCTCATGGCACCCCTGGCCC 2928  
Db 3036 AGTGGGACCTGGCCTCACCCCGCTCCAGGGCATCCCGCTCCCTCATGGCACCCCTGGCCC 3095  
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QY 2989 ACCTCAGACTCAGAGCCCGCTGCTCAGGAGACCTCTGCTCTGAGCCCGCAGACCCCTGCC 3048  
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RESULT 9

US-09-965-830-5  
; Sequence 5, Application US/09965830  
; Patent No. US20020177201A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/965,830  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 09/600,776  
; PRIOR FILING DATE: 2001-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-346198

; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 3064  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (4)..(3057)  
US-09-965-830-5

Query Match 27.2%; Score 884.8; DB 9; Length 3064;  
Best Local Similarity 65.5%; Pred. No. 8.7e-215;  
Matches 1408; Conservative 0; Mismatches 622; Indels 120; Gaps 3;

QY 1 ATGCGGCCCATGCGGGGCCTCCTGGCGCCTCAGAAACACCTTCCTGGACACCATCGCTACG 60  
Db 4 ATGCGGGTCAATGAAGGGTTGCTGGCCCCGCAAAACACCTTCCTGGACACCATCGCCACC 63  
QY 61 CGTTTCGACGGCACGCACAGTAACCTTCGTCTGGGCAACGCCACAGTGGCGGGCTCTTC 120  
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QY 181 ATGCAGCGGGCTGTGCTGCTCTTCCCTTTATGGGCAGACACCCAGTGAGCTCGTCCGC 240  
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QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGAGTTCAAGGTGAGCTGATCCTGTAC 300  
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QY 415 CGAGGGGCCCCGACAGATGAAGGAGACAGGTGGTGGCCGGCCGCGGATATGCGCCGGCA 474  
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QY 715 GCTGTCACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGAGCCAGTGCCGCCCGC 774  
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QY 775 GGGCCGCCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTTCATCTTGACATTGTGCTG 834  
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1963 -----GTGGTAAAGGCAATGCCGACGTCGTGAAGGGGCTGACGTACTGC 2004  
1900 GGAGCAGACCAAACTTCGTGCTAAAGACCAAGTGTGATGTGAAAGCTCTGACCTACTGT 1959  
2005 GTCCTGACGTGCTGAGCTGGCTGGCTGACGACGACGCTTTCGCTGTACCCCGAGTTT 2064  
1960 GGCCTGACGAGCTGAGCAGCCGAGGGCTGGCTGAGGTCTCTGAGGCTCTATCTGAGTAT 2019  
2065 GCCCGCGCTTCACTGCTGGCTCCGAGGGGAGCTCAGCTACAACCTGGG 2114  
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RESULT 10  
US-09-965-830-10  
; Sequence 10, Application US/09965830  
; Patent No. US20020177201A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A novel potassium channel protein  
; FILE REFERENCE: Y9903-PCT  
; CURRENT APPLICATION NUMBER: US/09/965,830  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 09/600,776  
; PRIOR FILING DATE: 2001-07-21  
; PRIOR APPLICATION NUMBER: JP P1998-346198  
; PRIOR FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 3736  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-09-965-830-10

Query Match 26.7%; Score 869.8; DB 9; Length 3736;  
Best Local Similarity 65.3%; Pred. No. 5.8e-211;  
Matches 1403; Conservative 0; Mismatches 627; Indels 117; Gaps 4;

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196 CGCTTTCGACGGCAGCAGACGTAATCTTCTTGCCCAATGCCAGGGCCCAACGGGGTTT 255  
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316 ATGCAGAAACCTGTAGCTGCCGCTTCTCTATGGCCAGAGACAGTGGCCGCTTG 375  
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955 CTGCTACATGCTTCAAGGTCAAGTGTACTTGGGGCCCATCTGCTGAAGACGGTGGC 1014  
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1435 AAGATCTTCTCCATCTGCACCATGCTCATCGGGCGCCCTGATGACGCGGTGTTTGGG 1494  
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QY	472	GCACGATCCAAAGGCTTCAATGCCAACCGCGCGGAGCCGGSCCGTGCTCTACCACTG	531
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QY	532	TCCGGCACCTGCAGAGCAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGGTGTTTGGG	591
Db	676	ACTGGCCACTTTGGTCGCCGGGACAGGGAAGCGTGAAAGCCAAATAGTAACGTGTTTGAG	735
QY	592	GAGAAACCAAACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTTCATCCTG	651
Db	736	CCAAAGCCATCAGTGCCTGAGTACAAAGTGGCCTCCGTGGGGGCTCCCGTGCCTGCTC	795
QY	652	TTGCACTGTGGGGCACTGAGAGCCACCTGGGATGGCTTTCATCCTGCTCGCCACACTCTAT	711
Db	796	CTCCACTACAGCATCCCCAAGGCTGTCTGGGACGGTCTCATCTTCTCGCTACGTTCTAC	855
QY	712	GTGGCTGTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGTGCCTGC	771
Db	856	GTGCGGTCAACCGTCCCTTACAACTGTCTTTCGCTGGTATGACGACACCCCATCAG	915
QY	772	CGCGGCCCGCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTTCATCCTTGACATTTG	831
Db	916	TCCCGACACACCTTGTTCAGTGACATCGCTGTGGAGATGCTCTTTCATCCTGGACATCATC	975
QY	832	CTGAATTTCCGTACCACTTCGTGTCCAAGTCGGGCCAGGTGGTGTTTTGCCCAAGTCC	891
Db	976	TTGAATTTCCGACACCACTACGTGTCCAGTCGGGCCAGGTGGTGTTCGTCTCCTCGGTCC	1035
QY	892	ATTGCTCTCCACTACGTCAACACCTGGTTCTCTGCTGGATGTTCATCGCAGCGCTGCCCTTT	951
Db	1036	ATTGGCTCTCCACTACCTGGCCACCTGGTTCTTCGTGGACCTCATTTGCTGCTTTGCCCTTT	1095
QY	952	GACCTGTACATGCCCTTCAAGGTCAAAGTCAACGTGATCTTTCGGGGCCCATCTGCTGAACGGTG	1011
Db	1096	GACCTGTGTATGTCTTCAACATCACTGTGACCTCGCTGGTACATCTGCTGAACACCGTG	1155
QY	1012	CGCTGTGCGCCTGTGCGCCTGCTTCCGCGGTGGACCGGTACTCGCAGTACAGCGCC	1071
Db	1156	CGGCTCCTGCGGTTGCTGAGGCTGCTGCAGAAAGCTAGAGCGGTACTCTCAGTCAGCGCG	1215
QY	1072	GTGGTGTGACACTGCTCATGGCCCGTGTTCGCCCTGTTCGGCACCTGGGTGCGCTGCGTC	1131
Db	1216	GTGGTGTCAACGCTGCTCATGTCCGTCTTTGCACTCTTTCGCCACTGGATGGCTGCGTC	1275
QY	1132	TGGTTTTACATTTGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCCTGAGATTGGC	1191
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QY	1192	TGGCTGCAGGAGCTGCGCCCGCGCACTGGAGACTCCCTACTACCTGGTGGGCGGAGGCCA	1251
Db	1336	TGGTTGCATGATGGGTAGCGGCTGGAGGAGCTTATGTCAATGGTCTC-----	1385
QY	1252	GCTGGAGGGAACAGCTCCGCGCCAGAGTGACAATGCACTGACAGCAGCAGCGAGGCCAACGGG	1311
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QY	1312	ACGGGGCTGGAGCTGTGGCGGCCCGCTCGCTGCGCAGCGCCTACATCACTCCCTCTAC	1371
Db	1386	-----GGCCGGTGGACCATCTCGGCGCAGTGCCTACATCGCCGCGCTGTAC	1431
QY	1372	TTGCGCACTCAGCAGCCTCACAGCGTGGGCTTCGGCAACGTGTCCGCCAACACACGACACC	1431
Db	1432	TTACCGCTGACAGCCCTCACAGTGTAGGCTTCGGCAACGTTTGTGCCAACACTGACGCT	1491
QY	1432	GAGAAGATCTTCTCCATCTGCACCATGTCTCATCGCGCCCTGTATGCACGCGTGGTGT	1491
Db	1492	GAGAAGATCTTCTCCATCTGCACGATGTCTATAGGCGGCTGTATGCACGCGTGGTGT	1551
QY	1492	GGGAACGTGACGGCCATCATCCAGCGCATGTATCGCCCGCCGCTTTCTGTACCAACAGCCGC	1551
Db	1552	GGGAATGTCACAGCCATCATCCAGCGCATGTACTCCCGAGCTCGCTCTACCAACAGCCGC	1611
QY	1552	ACGCGGACCTGCGGCACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGC	1611

RESULT 11

US-09-119-855-9

; Sequence 9, Application US/09119855

; Patent No. US20020099197A1

GENERAL INFORMATION:

APPLICANT: CURTIS, RORY A. J.

1. TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

; FILE REFERENCE: mni-055

; CURRENT APPLICATION NUMBER: US/09/119,855

; CURRENT FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9

; LENGTH: 870

TYPE: DNA

ORGANISM: Homo sapiens

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; FEATURE;
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; NAME/KEY: CDS

LOCATION: (1) : (870)

US-09-119-855-9

### Query Match

Query Match

Best Local Similarity 99.9%; Pred. No. 1.4e-204;

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61 CGCTTCGACGGCAGCACAGTAACTTCGTGCTGGCAACGCCAGGTGGCGGGCTCTTC 120

QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGCTTCTCCCGGGCTGAGGTC	180
Db	121		
QY	181	ATGCAGCGGGCTGTGCCTGCTCCTTCTCTTTATGGGCCAGACACCAGTGAGCTCGTCCGC	240
Db	181		
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Db	361		
QY	421	GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCCCGATATGGCCGGGCACGATCC	480
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QY	541	CTGCAGAAGCAGCCCCAAGGCAAGCAAGCTCAATAAGGGGTGTTGGGGAGAAACCA	600
Db	541		
QY	601	AACCTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCACTCTGTGTGCACTGT	660
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QY	661	GGGCACTGAGAGCCACCTGGATGGCTTCATCCTGCTCGCCACACTCATGTGGCTGTC	720
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Db	841		

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RESULT 12
US-10-185-867-9
; Sequence 9, Application US/10185867
; Publication No. US2003010429A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens

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[illegible]

RESULT 13  
US-09-119-855-7  
; Sequence 7, Application US/09119855





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Db 983 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGGGAGCCCACTGTCGCCCGCGGCGCG 1042

QY 781 CCCAGCGTCTGTGACCTGGCGCGTGGAGGTCCTCTTCATCCTTGACATTGTGTAATTTC 840

Db 1043 CCCAGCGTCTGTGACCTGGCGCGTGGAGGTCCTCTTCATCCTTGACATTGTGTAATTTC 1102

QY 841 CGTACC 846

Db 1103 CGTACC 1108

RESULT 15

US-10-185-867-17

; Sequence 17, Application US/10185867

; Publication No. US20030104429A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

; FILE REFERENCE: MNI-055CP

; CURRENT APPLICATION NUMBER: US/10/185,867

; CURRENT FILING DATE: 2002-06-27

; PRIOR APPLICATION NUMBER: US/09/358,383

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: USSN 09/119,855

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17

; LENGTH: 3321

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3321)

US-10-185-867-17

Query Match 23.4%; Score 761.2; DB 15; Length 3321;

Best Local Similarity 62.2%; Pred. No. 2.3e-183;

Matches 1319; Conservative 0; Mismatches 708; Indels 93; Gaps 4;

QY 1 ATGCCGCGCATGCGGGCCTCTGGCGCCTCAGAACACCTTCTGACACCATCGCTACG 60

Db 1 ATGCCGCTTATGAAAGGATTACTGGCGCGCAAAACACCTTCTGACACCATCGCCACC 60

QY 61 CGCTTCGACGGCACGCACAGTAATTCGTGCTGGGCAACGCCAGTGCGGGCTCTTC 120

Db 61 CGTTTTCGCGAACAACATAGCAACTTCATCTTGCATATGCCAATGCCAGGTGGCTAAGGGTTTC 120

QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180

Db 121 CCCATAGTCTACTGTTCCGATGGCTTCTGCGAGCTTGCTGGATTGCGCGAACTGAAGTC 180

QY 181 ATGCAGCGGGCTGTGCCTGCTCTCTTCTTATGGGCCAGACACCAAGTGAAGTCTGTC 240

Db 181 ATGCAGAGAGTTGTAGTCAAGTTCTTTATTTGGGTTGAAACCAATGACCAACTGATG 240

QY 241 CAACAGATCCGCAAGCCCTGGACGAGCACAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300

Db 241 CTTCAATAGAAAAGTCACTGGAGGAGAAAACAGAATTTCAAAGGAGAAATATGTTCTAC 300

QY 301 CGGAAGAGCGGGCTCCGTTCTGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360

Db 301 AAGAAAAACGGGTCTCCATTTTGGTGCCTACTGGATATTGTTCCCATAAAGAATGAAAA 360

QY 361 GGGGAGGTGGCTCTCTTCTTAGTCTCTCACAAAGGACATCAGCGAAACCAAGAACCGAGGG 420

Db 361 GGAGATGTACTACTTTTCTGGCCCTCGTTCAAAGATATAACAGATA-CAAAAGTGAAGAT 419

QY 421 GGGCCCGACAGATGAAGGAGACAGGTGGTGGCCGGCGCGGATATGGCCGGGCACGATCC 480

Db 420 TACTCCAGAGATAAAAAAGAGACAAAGTCAAAGGAAGATCAAGAGAGGAGGCCCA--- 476

QY 481 AAAGGCTTCAATGCCAACCCGGCGGAGCGGGCGGTGCTCTTACACCTGTCCGGGCAC 540

Db 477 -----CTTTGACTCAGCCCGGAGACGGAGTCGAGCAGTCTTTATCACATCTCTGGGCAC 531

QY 541 CTGCAGAGAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAAAAACCA 600

Db 532 CTGCAAGAGAGAGAAAAAGAACAAATTGAAATAAATAACAATGTTTTTGTAGATAAACCA 591

QY 601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCTCTGTGCACTGT 660

Db 592 GCATTTCCGGAGTATAAAGTTTCTGATGCAAAAAAAGTCCAAATTCATACCTCTGCAATTT 651

QY 661 GGGGCACTGAGAGCACTGGGATGGCTTCTATCCTGCTGCCACACTCTATGTGGCTGTC 720

Db 652 AGCACTTTTAAAGCTGGCTGGGACTGGCTTATTTTGTGGCAACGTTTTATGTTGCTGTG 711

QY 721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGGAGCCCAAGTGCCTGCGGCGGCGCG 780

Db 712 ACTGTACCTTACAACGTTTGTCTTATTGGCAATGAGACCTGTCCACAACCTCGGAGC--- 768

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Db 769 ACAACCGTCAGTGACATTGAGTGGAGATTCTTTTATTATAGATATTATTTAAATTC 828

QY 841 CGTACCACATTCTGTCCAAAGTCGGGCCAGGTGGTGTGTTGCCCCAAAGTCCATTTGCCTC 900

Db 829 CGAACAACTTATGTACGAAAGTCTGGCCAAAGTTATCTTTGAAGCAAGATCAATTTGCATC 888

QY 901 CACTACGTCAACACCTGGTCTCTGCTGGATGTATCGAGCGCTGCCCTTTGACCTGCTA 960

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QY 961 CATGCTTCAAGGTCAACGTGTAATTCGGGGCCCACTGCTGAAGACGGTGGCGCTGCTG 1020

Db 949 TATGCTTCAACGTCAAGTGTGTCTCTGTCATCTTTAAAGACAGTGGCGCTCTTG 1008

QY 1021 CGCCTGCTGCGCTGCTTCCGGGCTGGACCGGTACTCGAGTACAGCGCCGCTGGTGTG 1080

Db 1009 CGTCTTTGCGTCTGCTGCAGAAAGTAGACCGCTATTCCCAACACAGTACTATCGTCTG 1068

QY 1081 ACACCTGCTATGGCCGTGTTCCGCTGCTCGCGCACTGGGTGCGCTGCTGCTGTTTAC 1140

Db 1069 ACTCTGCTCATGTCCATGTTTGCACTCTTGCACACTGGATGGCGTGTATCTGGTACGTC 1128

QY 1141 ATTGGCAGCGGGAGATCGAGAGCAGCAATCCGAGCTGCCTGAGATTGGTGGTGCAG 1200

Db 1129 ATTGGAATAATGGAGAGGGAAGACAACAGCCCTTCTGAAGTGGGAAGTTGGTGGCTCAT 1188

QY 1201 GAGTGGCCCGCACTGGAGACTCCCTACTACCTGTTGGGCCGAGGCCAGCTGGAGGG 1260

Db 1189 GAGTTGGGAAGAGACTGGAATCTCCATACTAT----- 1221

QY 1261 AACAGCTCCGGCCAGAGTGACAACTGACAGCAGCAGCGAGGCCAACGGGACGGGGCTG 1320

Db 1222 -----GGCAAC 1227

QY 1321 GAGCTGCTGGCGGCGCGTCTGCTGCGCAGCGCCTACATCACCTCCCTTACTTCCGCACTC 1380

Db	1228	AATACCTTGGGGGGCCCGTCGATCCGAAAGTGCCTATATTGCCGCTCTGTACTTCAAGCTG	1287
QY	1381	AGCAGCCTCACCAGCGGTGGGCTTCGGCAACGTGTCCGCCAACACGACACCCGAGAAGATC	1440
Db	1288	AGCAGCCTCACCAGCGTGGGTTTTGGGAACGTCTCTGCTAATACAGATGCAGAAAAGATC	1347
QY	1441	TTCTCCTATCTGCACCATGCTCATCGGCGCCCTGATGCACGGGTGGTGTTTGGGAACGTG	1500
Db	1348	TTCTCCATCTGCACCATGCTGATTGGTGCCTTGATGCACGCTTGGTGTTTGGAAACGTG	1407
QY	1501	ACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTATCACAGCCGCACCGCGGAC	1560
Db	1408	ACAGCAATCATACAGAGGATGTACTCCAGATGGTCCCTCTATCACACTAGAACTAAGGAT	1467
QY	1561	CTGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCCCTCAAGCAGCGCATGCTGGAG	1620
Db	1468	CTGAAAGATTTCATCCGTGTCCATCACTTGTCCCAACAACTCAAGCAGAGGATGCTCGAA	1527
QY	1621	TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGC	1680
Db	1528	TATTTTCAACAACCTGGTCAGTCAACAATGGAATAGATTCAAAATGAGCTTTTGAAAGAC	1587
QY	1681	CTCCCTGACGAGCTGCGGCGGAGACATCGCCATGCCATGCACACCAAGGAGGTCTGCAAGCTG	1740
Db	1588	TTTCCAGATGAACCTGCGTTCTGACATCACTATGCACTTGAACAAGGAGATCTTACAGTTG	1647
QY	1741	CCACTGTTTGAGGGCGCCAGCGCGGCTGCCCTGCGGCACTGTCTCTGGCCCTGCGGCC	1800
Db	1648	TCCCTTTTGAATGTCCAGCCGGGCTGCCCTCAGGTCTCTGTCTCTACACATCAAAACC	1707
QY	1801	GCCTTCTGCACGCCGGGAGTACCTCATCCACCAAGCGATGCCCTGCAGGCCCTCTAC	1860
Db	1708	TCTTCTGTGCTCCGGGGAGTATCTGCTGCGTCAAGGGATGCTTTGCAGGCCATCTAC	1767
QY	1861	TTTGTCTGCTCTGGTCCATGGAGGTGCTCAAGGGTGGCACCGTGCTCGCCATCCTAGGG	1920
Db	1768	TTTGATGCTCGGGCTCCATGGAAGTTCTTAAAGACAGCATGGTGTGGCTATTCTTGGG	1827
QY	1921	AAGGGCACCTGATCGGCTGTGAGCTGCCCGGGGAGCAGGTGGTAAAGGCCAATGCC	1980
Db	1828	AAAGGGATTTTAATTGGAGCAAAATCTATCAATTAAAGACCAAGTGATCAAGACCAATGCA	1887
QY	1981	GACGTGAAGGGGTGACGTACTGCGTCTGTGAGTGTCTGCAGCTGGCTGGCCTGCACGAC	2040
Db	1888	GATGTAAGGCTTTAACCCTACTGTGATCTCCAGTGTATCATCCTCAAAGGACTCTTTGAA	1947
QY	2041	AGCCTTGGCTGTACCCCGAGTTTGCCTCCCGGCTTCAGTCGTGGCCTCCGAGGGAGCTC	2100
Db	1948	GTGCTAGACCTTTACCCAGAAATATGCTCACAAATTCGTGGAAGACATTCAGCATGACCTC	2007
QY	2101	AGCTACAACCTGGGTGCTGG	2120
Db	2008	ACATACAACCTCCGAGAAGG	2027

Search completed: September 1, 2004, 21:04:19  
Job time : 982 secs





GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 1, 2004, 15:01:21 ; Search time 107.5 Seconds  
(without alignments)  
5819.811 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257

Perfect score: 6089

Sequence: 1 atgccggccatgcggggcct.....aagaaggcacaggggtctga 3252

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p\_model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US09965830/runat\_01092004\_160110\_4809/app\_query.fasta\_1.3399  
-DB=PIR\_78 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09965830@cgn\_1\_1\_163@runat\_01092004\_160110\_4809 -NCPU=6 -ICPU=3  
-NO\_MMAL -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_78:\*

1: pir1:\*\n2: pir2:\*\n3: pir3:\*\n4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5428	89.1	1087	2 T31100	probable potassium
2	2515	41.3	1102	2 T17367	potassium channel
3	2439.5	40.1	1017	2 T31354	probable potassium
4	1901	31.2	1284	2 T13168	probable potassium
5	1551	25.5	1159	2 I38465	probable potassium
6	1390	22.8	1174	2 A40853	potassium channel
7	1380.5	22.7	962	2 I53197	potassium channel
8	1371.5	22.5	989	2 I48912	potassium channel
9	1257	20.6	934	2 T42394	potassium channel
10	1029.5	16.9	514	2 T19579	hypothetical prote
11	439	7.2	706	2 A55251	cyclic nucleotide-
12	423.5	7.0	735	2 I50630	alpha subunit of c
13	421.5	6.9	665	2 S52072	DmCNGC protein - f
14	421.5	6.9	691	2 JC6509	rod cyclic nucleot

15	420	6.9	695	2	S74179	cyclic nucleotide-
16	416.5	6.8	732	2	S35691	cyclic nucleotide-
17	414.5	6.8	682	1	JH0560	cyclic nucleotide-
18	414	6.8	688	2	B42161	cGMP-gated cation
19	413.5	6.8	690	1	S07103	cGMP-gated ion cha
20	413	6.8	686	1	A44842	cGMP-gated ion cha
21	411	6.7	645	2	I50680	alpha subunit of r
22	407	6.7	690	2	A42161	cGMP-gated cation
23	401	6.6	1414	1	S23809	collagen alpha 2(I
24	393	6.5	664	2	S11517	cyclic nucleotide-
25	391.5	6.4	663	2	S11521	cAMP-gated channel
26	391	6.4	1453	2	S21626	collagen alpha 1(I
27	389.5	6.4	1464	1	CGHU1S	collagen alpha 1(I
28	386.5	6.3	787	2	S68699	potassium channel
29	371	6.1	3570	2	T45025	mucin MUC5B, trach
30	370	6.1	1464	1	CGHU1S	collagen alpha 1(I
31	369.5	6.1	575	2	I59327	olfactory cyclic n
32	368.5	6.1	733	2	E85357	hypothetical prote
33	367.5	6.0	1042	1	CGCH1S	collagen alpha 1(I
34	365	6.0	738	2	E86294	hypothetical prote
35	361	5.9	880	2	F85381	potassium channel-
36	361	5.9	916	2	T05360	probable potassium
37	361	5.9	1106	2	JQ0405	hypothetical 119.5
38	360	5.9	1042	1	CGCH1S	collagen alpha 1(I
39	358.5	5.9	1453	2	S21626	collagen alpha 1(I
40	357	5.9	1418	2	T45467	collagen alpha 1(I
41	356.5	5.9	710	2	T52573	cyclic nucleotide
42	356.5	5.9	1486	1	B40333	collagen alpha 1(I
43	354.5	5.8	1414	1	S23809	collagen alpha 2(I
44	353.5	5.8	747	2	T52572	cyclic nucleotide
45	352	5.8	1806	1	CGHU1E	collagen alpha 1(X

ALIGNMENTS

RESULT 1

T31100  
probable potassium channel 2 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
C;Accession: T31100  
R;Engeland, B.; Neu, A.; Ludwig, J.; Roeper, J.; Pongs, O.  
submitted to the EMBL Data Library, July 1998  
A;Description: Identification of three rat potassium channel genes homologous to D. melar  
A;Reference number: Z20983  
A;Accession: T31100  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 1-1087 <ENG>  
A;Cross-references: EMBL:AJ007627; NID:el329995; PID:el329996; PIDN:CAA07586.1  
A;Experimental source: cortex  
C;Genetics:  
A;Gene: elk2  
C;Keywords: potassium channel

Alignment Scores:

Pred. No.: 6.73e-274 Length: 1087  
Score: 5428.00 Matches: 1039  
Percent Similarity: 96.60% Conservative: 11  
Best Local Similarity: 95.58% Mismatches: 33  
Query Match: 89.14% Indels: 4  
DB: 2 Gaps: 2

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x T31100 (1-1087)

QY 1 ATGCCGCCATCGGGGGCTCTCTGGCGCCTCAGAACACCTTCTCTGGACACCATCGCTACG 60

Db 1 MetProAlaMetArgGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

QY 61 CGTTTCGACGGCACGACAGTAACTTCGTGTGGCAACGCCAGGTGGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe 40



Db 761 CysThrSerSerSerAlaAlaLysLeuSerProArgArgThrAlaProArgPro 780  
QY 2332 CGTCTAGGTGGCAGAGGGAGGCCAGGACGGGCTTTGAAGGCTGAGGCTGGCCCC 2391  
Db 781 ArgLeuGlyGlyArgGlyArgProSerArgAlaGlyValLeuLysProGluAlaGlyPro 800  
QY 2392 TCTGTCCTCCACGGCCCTAGAGGGGCTACGGGTGCCCCCCTGCTGCTGGAATGTGCC 2451  
Db 801 SerAlaHisProArgThrLeuAspGlyLeuGlnLeuProProMetProTrpAsnValPro 820  
QY 2452 CCAGATCTGAGCCCCCAGGGTAGTATGATGGCATTGAAGACGGGTGTGGCTCGGACCGCCC 2511  
Db 821 ProAspLeuSerProArgValValAspGlyIleGluAspGlyCysGlySerAspGlnHis 840  
QY 2512 AAGTTCTCTTCCGGCTGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCCTCCCTGGA 2571  
Db 841 LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerProSerProGly 860  
QY 2572 CCAGAGAGCGGCTGCTCACTGTTCCCATGGGCCAGCAGGCAAGGAACACAGACACA 2631  
Db 861 ThrGluSerGlyLeuLeuThrValProLeuValProSerGluAlaArgAsnThrAspThr 880  
QY 2632 CTGGACAAGCTTCGGCAGCGGTGACAGAGCTGTACAGCAGGTGCTGCAGATGCGGAAA 2691  
Db 881 LeuAspLysLeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGlu 900  
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Db 901 GlyLeuGlnSerLeuArgGlnAlaValGlnLeuIleLeuValProGlnGlyGluGlyGln 920  
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Db 921 CysProArgValSerGlyGluGlyProCysProAlaThrAlaSerGlyLeuLeuGlnPro 940  
QY 2812 CTGTGTGGACACTGGGCGATCCTCCTACTGCTGACGCCCCCAGCTGGCTGTGTCTTG 2871  
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QY 2872 AGTGGACTTGGCCCCACCCTCGTCCGGGG---CCTCCTCCCTCATGGCACCTGGCCCC 2928  
Db 961 SerGlyThrTrpProHisProArgProGlyHisProProLeuMetAlaProTrpPro 980  
QY 2929 TGGGGTCCCCCAGGCTCTCAGAGCTCCCCCTGGCTCGAGCCACAGCTTCTGGACCTCC 2988  
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QY 2989 ACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGCTGTAGCCCCAGACCCCTGCC 3048  
Db 1001 ThrSerAspSerGluProProGlySerGlyAspLeuCysSerGluProSerThrProAla 1020  
QY 3049 TCCCTCCTCCTTCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCCCTGTGAGCCAGGCT 3108  
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Db 1041 GluAlaThrSerThrGlyGluProProProGlySerGlyArgAlaLeuProTrpAsp 1060  
QY 3169 CCCCACAGCTGGAGATGGTCTTATGGCTGCCATGGCTCTGGCAGCTCCAGTGGACC 3228  
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QY 3229 CAGGAAGAGCACAGGGGTC 3249  
Db 1081 GlnGluGluGlyThrGlyVal 1087

RESULT 2  
T17367

potassium channel protein elk1 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T17367  
R;Shi, W.; Wang, H.S.; Pan, Z.; Wymore, R.; Cohen, I.S.; McKinnon, D.; Dixon, J.E.

J. Physiol. 511, 675-682, 1998  
A;Title: Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution in  
A;Reference number: Z18731; MUID:98382545; PMID:9714851  
A;Accession: T17367  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1102 <SHI>  
A;Cross-references: EMBL:AF061957; NID:g3659689; PID:g3659690; PIDN:AAC61520.1  
C;Genetics:  
A;Gene: elk1  
C;Function:  
A;Description: may play a role in the sympathetic nervous system  
C;Keywords: potassium channel

Alignment Scores:  
Pred. No.: 5.97e-123 Length: 1102  
Score: 2515.00 Matches: 551  
Percent Similarity: 62.00% Conservative: 149  
Best Local Similarity: 48.80% Mismatches: 295  
Query Match: 41.30% Indels: 134  
DB: 2 Gaps: 24

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x T17367 (1-1102)

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Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGGCAGCACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCAGGGGCTTCTCCCGGGCTGAGGTC 180  
Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuAlaGlyPheAlaArgThrGluVal 60  
QY 181 ATGACAGCGGGGCTGTGCCTGTCTCCTTCTTATGGGCCACAGACACAGTGAGCTCGTCCGC 240  
Db 61 MetGlnLysSerCysSerCysLysPheLeuPheGlyValGluThrAsnGluGlnLeuMet 80  
QY 241 CAACAGATCCGCAAGCCCTGGACGAGCACAAAGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 81 LeuGlnIleGluLysSerLeuGluLysValGluPheLysGlyGluIleMetPheTyr 100  
QY 301 CGGAAGAGCGGCTCCGTTCTGTGTCTCTGATGATGATACCCATATAAGAAATGAGAAA 360  
Db 101 LysLysAsnGlyAlaProPheTrpCysLeuLeuAspIleValProIleLysAsnGluLys 120  
QY 361 GGGGAGGTGGCTCTTCTCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGA--- 417  
Db 121 GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140  
QY 418 GGGGGCCCCGACAGATGGAAGGACAGAGTGGTGGCCCGCCGATATGGCCGGGCACGA 477  
Db 141 ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly----- 157  
QY 478 TCCAAAGGCTTCAATGCCAACCGGGCGGAGCGCGGCTGTCTTACCACTGTCCGGG 537  
Db 158 ---SerHisPheAspSerAlaArgArgSerArgAlaValLeuTyrHisIleSerGly 176  
QY 538 CACCTGCAGAAGCAGCCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTGGGAGAAA 597  
Db 177 HisLeuGlnArgArgGluLysAsnLysLeuLysIleAsnAsnValPheValAspLys 196  
QY 598 CCAAACTTGCCTGAGTACAAAGTAGCCGCCATCCGGGAAGTCGCCCTTCATCTGTTCAC 657  
Db 197 ProAlaPheProGluTyrLysValSerAspAlaLysLysSerLysPheIleLeuLeuHis 216  
QY 658 TGTGGGCGACTGAGAGCCACCTGGGATGGCTTCATCTCCTGCTGCCACACTCTATGTGGCT 717  
Db 217 PheSerThrPheLysAlaGlyTrpAspTrpLeuIleLeuLeuAlaThrPheTyrValAla 236  
QY 718 GTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCCACTGTCGCCCGCGC 777





QY 2851 CCCCCAGCT-----GGCTCTGTCTTGTAGTGGAGCTTGGCCCCAC 2889  
Db 937 LeuGlnAlaAsnGlyAlaHisLeuTyrHisGlyAsnValThrSerAspIleTrp----- 954  
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Db 955 -----SerValAspProSerLeuValGlySerAsnProGlnArgThrGluAlaHisGlu 972  
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Db 973 GlnSerProValAspSerGluLeuHisHisSerProAsnLeuAlaTyrSerProSerHis 992  
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Db 993 CysGlnValIleGlnGluGlyHisLeuGlnPheLeuArgCysIleSerProHisSerAsp 1012  
QY 2974 GCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAG 3033  
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Db 1033 SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGluGlySerIleThrHis 1052  
QY 3082 GGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGCACTGGAGAGCCCCCACCAGGG 3141  
Db 1053 GlyProValSerSerPheSerLeu-----GluAsnLeuProGly 1065  
QY 3142 TCAGGGGGCCTGGCCTTGCCCTGGGAG 3168  
Db 1066 Ser-----TrpAsp 1068

RESULT 3  
T31354  
probable potassium channel elk chain 1 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C;Accession: T31354  
R;Engelard, B.; Neu, A.; Ludwig, J.; Roeper, J.; Pongs, O.  
submitted to the EMBL Data Library, July 1998  
A;Description: Identification of three rat potassium channel genes homologous to D. mela  
A;Reference number: Z20983  
A;Accession: T31354  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1017 <ENG>  
A;Cross-references: EMBL:AJ007628; NID:e1329997; PID:e1329998; PIDN:CAA07587.1  
A;Experimental source: cortex  
C;Genetics:  
A;Gene: elk1  
C;Keywords: potassium channel

Alignment Scores:  
Pred. No.: 4.86e-119 Length: 1017  
Score: 2439.50 Matches: 532  
Percent Similarity: 60.00% Conservative: 131  
Best Local Similarity: 48.14% Mismatches: 244  
Query Match: 40.06% Indels: 198  
DB: 2 Gaps: 23

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x T31354 (1-1017)

QY 1 ATGCGGGCCATGCGGGGCCTCCTGGCGCTCAGAACACCTTCCTGGACACCATCGCTACG 60  
Db 1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
QY 61 CGCTTCGACGCGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGGGGCTCTTC 120  
Db 21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyProArgGlyPhe 40  
QY 121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180

Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuThrGlyTyrGlyArgThrGluVal 60  
QY 181 ATGCAGCGGGGCTGTGCCTGTCTCCTTCTTATGGGCCAGACACCATGAGCTCGTCCGC 240  
Db 61 MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGluThrSerGluProAlaLeu 80  
QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCTGTAC 300  
Db 81 GlnArgLeuGlnLysAlaLeuGluGlyHisGlnGluHisArgAlaGluIleCysPheTyr 100  
QY 301 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCTCTGATGTGATACCCATAAAGATGAGAA 360  
Db 101 ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetMetProIleLysAsnGluLeu 120  
QY 361 GGGGAGGTGGCTCTCTTCTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGG 420  
Db 121 GlyGluValValLeuPheLeuPheSerPheLysAspIleSerGlnSerGlyGlyProGly 140  
QY 421 -----GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGC 459  
Db 141 LeuGlySerProGlyIleHisGlyAspAsnAsnHisGluAsnSerLeuGlyArg--- 159  
QY 460 CGATATGGCCGGCAGATCCAAAGGCTTCAATGCCAACCGGCGGAGCGCGGCGCTG 519  
Db 160 -----ArgGlyAlaSerSerArgLeuArgSerThrArgArgGlnAsnArgThrVal 176  
QY 520 CTCTACCACCTGTCCGGGACCTGCAGAAGCAGCCCCAAGGCAAGCACAAGCTCAATAAG 579  
Db 177 LeuHisArgLeuThrGlyHisPheGlyArgArgAspGlnGlySerValLysAlaAsnSer 196  
QY 580 GGGGTGTTTGGGAGAAACAAACTTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCG 639  
Db 197 AsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGlySer 216  
QY 640 CCCTTCATCCTGTGCACTGTGGGCACCTGAGAGCCACCTGGATGGCTTCATCTCTGCTC 699  
Db 217 ArgCysLeuLeuHisTyrSerIleProLysAlaValTrpAspGlyLeuIleLeuLeu 236  
QY 700 GCCACACTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAG 759  
Db 237 AlaThrPheTyrValAlaValThrValProTyrAsnValCysPheAlaGlyAspAsp 256  
QY 760 CCCAGTCCCGCCCGCCCGCCCTGTGTGACCTGGCCGTGGAGTCTCTTTCATC 819  
Db 257 ThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPheIle 276  
QY 820 CTTGACATTGTGCTGAATTTCCGTACCACTTCGTGTCCAAAGTCGGGCCAGGTGGTGT 879  
Db 277 LeuAspIleIleLeuAsnPheArgThrThrTyrValSerGlnSerGlyGlnValValSer 296  
QY 880 GCCCAAAGTCCATTTCCTCCACTACCTACCCACCTGGTTCTCTGTGATGTATCGCA 939  
Db 297 AlaProArgSerIleGlyLeuHisTyrLeuAlaThrTrpPhePheValAspLeuIleAla 316  
QY 940 GCGCTGCCCTTTGACCTGTACATGCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTG 999  
Db 317 AlaLeuProPheAspLeuLeuTyrValPheAsnIleThrValThrSerLeuValHisLeu 336  
QY 1000 CTGAAGACGGTGGCCTGTGCGCTGTGCTGCGCTCTTCCGCGGTGGACCGGTACTCG 1059  
Db 337 LeuLysThrValArgLeuLeuArgLeuLeuArgLeuLeuGlnLysLeuGluArgTyrSer 356  
QY 1060 CAGTACAGCGCGTGGTGTGACTGTCTCATGGCCGTGTTCCGCCCTGCTCGCGCACTGG 1119  
Db 357 GlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHisTrp 376  
QY 1120 GTCGCTGCTGTGGTTTACATTGGCCAGCGGGAGATCGAGACGAGCAATCCGAGCTG 1179  
Db 377 MetAlaCysValTrpTyrValIleGlyArgArgGluMetGluAlaAsnAspProLeuLeu 396  
QY 1180 CCTGAGATTGGCTGGCTGAGGAGCTGGCCCGCAGCTGAGACTCCCTACTACCTGGTG 1239  
Db 397 TrpAspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluGluProTyr----- 413

QY	1240	GGCCGAGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGACAACACTGCAGCAGCAGC	2299
Db	413	-----	413
QY	1300	GAGGCCAACGGACGGGGCTGGAGCTGTGGGGGGCCCGTCTGGCGAGCGCCTACATC	3359
Db	414	-----ValAsnGlySerAla-----GlyGlyProSerArgArgSerAlaTyrIle	428
QY	1360	ACCTCCCTCTACTTCGCACTCAGCAGCCCTCACCAGCGTGGGCTTCGGGAACGTGTCCGCC	4419
Db	429	AlaAlaLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCysAla	448
QY	1420	AACACGGACACCGAGAAGATCTTCTCCATCTGCACCATGTCTATCCGGCGCCTGTATGCAC	4479
Db	449	AsnThrAspAlaGluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHis	468
QY	1480	GCGGTGGTGTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCGCTTCTGT	5339
Db	469	AlaValValPheGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgArgSerLeu	488
QY	1540	TACCACAGCCGACCGCGACCTGCGCGACTACATCCGCACTCCACCGTATCCCGCAAGCCC	5599
Db	489	TyrHisSerArgMetLysAspLeuLysAspPheIleArgValHisArgLeuProArgPro	508
QY	1600	CTCAAGCAGCGCATGTGAGTACTTCCAGGCCACCTGGCGGTGAACAATGGCATCGAC	5659
Db	509	LeuLysGlnArgMetLeuGluTyrPheGlnThrThrTrpAlaValAsnSerGlyIleAsp	528
QY	1660	ACCACCGAGCTGTGCAGAGCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTG	5719
Db	529	AlaAsnGluLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHisLeu	548
QY	1720	CACAAGGAGTCTGCACTGCCACTGTTTGGGGCGGCAGCGCGGTGCCTGCGGCA	5779
Db	549	AsnArgGluIleLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArgAla	568
QY	1780	CTGTCTGTGCCCTGCGGCCCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5839
Db	569	LeuSerLeuHisIleLysThrSerPheCysAlaProGlyGluPheLeuLeuArgArgGly	588
QY	1840	GATGCTGTGAGCCCTCTACTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5899
Db	589	AspAlaLeuGlnAlaHisTyrTyrValCysSerGlySerLeuGluValLeuArgAspAsn	608
QY	1900	ACCGTGTCCGCATCTAGGGAAGCGGACCTGATCGGCTGTGCTGCTGCTGCTGCTGCTG	5959
Db	609	ThrValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspIleProGluLeuGly	628
QY	1960	CAG-----GTGGTAAAGGCCAATGCCAGCTGAAGGGGCTG	5995
Db	629	GlnGluProGlyAlaGlyAlaGlyCysValLeuLysThrSerAlaAspValLysAlaLeu	648
QY	1996	ACGTACTGCGTCTGCACTGTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6055
Db	649	ThrTyrCysGlyLeuGlnLeuSerSerArgGlyLeuAlaGluValLeuArgLeuTyr	668
QY	2056	CCCGAGTTTGGCCCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6115
Db	669	ProGluTyrValAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPheAsnLeuArg	688
QY	2116	GCTGGGGGA-----GGCTCTGCA	6133
Db	689	GlnGlySerGluAsnAsnGlyLeuGlyArgPheSerArgSerProArgLeuSerGlnAla	708
QY	2134	GAGGTGGACACCACTCCCTGAGCGGGGCAATACCTTATGTCCACGCTGGAGGAGAAG	6213
Db	709	ArgSerAspThrLeuGlySerSerSerAspLysThrLeuProSerIle-----Thr	725
QY	2194	GAGACAGATGGGAGCAGGGCCCCACGGTCTCCCGAGCCCCAGCTGATGAGCCCTCCAGC	6253
Db	726	GluThrGluGly-----GlyMetGluProGlyAlaGlySerLysProArgArg	741
QY	2254	CCCCTGCTGTCCCTGGCTGCACCTCTCTCATCTCTCAGCTGCCAAGCTG	2301
Db	742	ProLeuLeuLeuProAsnLeuSerProAlaArgProArgGlySerLeuValSerLeuLeu	761
QY	2302	-----CTATCCCCACGTCGA	2316
Db	762	GlyGluGluLeuProPheSerAlaLeuValSerSerProSerLeuSerPro-----	779
QY	2317	ACAGCACCCCGCCTCGTCTAGGTGGCAGAGGAGGCCAGGCAGGAGGGGCTTTGAAG	2376
Db	780	---ThrProSerProAlaLeuAlaGlyArgGly-----	789
QY	2377	GCTGAGGCTGCCCTCT-----GCTCCCCACGGGCCCTAGAGGGG	2418
Db	790	-----SerSerProSerLeuHisGlyProProArgGlySerAlaAlaTrpLysProPro	807
QY	2419	---CTACGGCTGCCCGCATGCCATGGATGTGCCCCCAGATCTGAGCCCCCAGGGTAGTA	2475
Db	808	GlnLeuLeuThrProProLeuGlyThrPheGlyProProAspLeuSerProTrpIleVal	827
QY	2476	GATGGCATTAAGACGGCTGTGGC---TCGACACAGCCCCAAGTTCTCTTCCGCGTGGGC	2532
Db	828	AspGlyIleGluAspSerSerAsnThrAlaGluAlaProThrPheArgPhe-----	844
QY	2533	CAGTCTGGCCCGAATGTAGCAGCAGCCCCCTCCCTGGACCAGAGCGGCTGCTCACT	2592
Db	845	SerLysArgProGluProThrArgThrArgSerGlnAlaProLeuSer-----	860
QY	2593	GTTCCCCATGGGCCAGCAGGCAAGAAC-----ACAGACACACTGGACAAGCTTCGG	2646
Db	861	-----GlyProArgLeuSerArgGluLeuAlaThrGluAlaGluValLys	877
QY	2647	CAGGCGGTGACAGAGCTGTGACAGCAGGTGTGTCAGATGCGGGAAGGACTGCAGTCACTT	2706
Db	878	GluLysValCysArgLeuAsnGlnGluIleSerArgLeuAsnGlnGluValSerGlnLeu	897
QY	2707	CGCCAGGCTGTGAGCTGTCTGCTGGCGCCCCACAGGGAGGCTCCGTGCCCTCGGGCATCG	2766
Db	898	SerArgGluLeuArgGlnValMet-----	905
QY	2767	GGAGAGGGCGGTGCCAGCCAGCAGCAGCTCCGGGCTTCTGACGCTCTGTGTGTGGACACT	2826
Db	906	-----GlyLeuLeuGlnAlaArg-----	911
QY	2827	GGGGCATCTCTACTGCTGCTGACGCCCGCCAGCTGGCTCTGTCTGTAGTGGGACTTGGCCC	2886
Db	912	-----LeuGlyProProSer-----	916
QY	2887	CACCTCTGTCGGGGCTCTCTCCCTCATGTCACCCCTGGCCCTGGGGTCCCCAGCGTCT	2946
Db	917	HisPro-----ProAsp-SerThrTrpLeuProAspLeuProCysProHis-----	931
QY	2947	CAGAGTCCCGCTGGCCTCGAGCCACAGCTTCTTGACCTCCACCTCAGACTCAGAGC--	3004
Db	932	-GlnArgProProCysIleSerProHisMetSerGlyProProGlyLeuGlnAsnTh	951
QY	3004	-----	3004
Db	951	rThrLeuAlaValValHisCysProAlaSerValGlyThrValGluIleGlyAlaThrPr	971
QY	3005	-----CCCCTGCCCTCAGGAGACCTCTGTCTGTAGCCCC	3036
Db	971	oSerGluLeuArgSerSerMetValProProPheProSerGluProAspProLeuGlyPr	991
QY	3037	AGCACCCCTGCCT	3049
Db	991	oSerProValPro	995
RESULT 4			
T13168			
probable potassium channel elk chain - fruit fly (Drosophila melanogaster)			
C;Species: Drosophila melanogaster			
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000			



C;Accession: T13168  
R;Warmke, J.W.; Ganetzky, B.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994  
A;Title: A family of potassium channel genes related to eag in Drosophila and mammals.  
A;Reference number: A54953; MUID:94211879; PMID:8159766  
A;Accession: T13168  
A;Status: preliminary; translated from GB/EMBL/DBDJB  
A;Molecule type: mRNA  
A;Residues: 1-1284 <WAR>  
A;Cross-references: EMBL:U04246; NID:9487735; PID:9487736; PIDN:AAA62472.1  
C;Genetics:  
A;Gene: elk  
A;Cross-references: FlyBase:FBgn0011589  
A;Map position: 2R

Alignment Scores:  
Pred. No.: 3.95e-91 Length: 1284  
Score: 1901.00 Matches: 455  
Percent Similarity: 53.85% Conservative: 146  
Best Local Similarity: 40.77% Mismatches: 273  
Query Match: 31.22% Indels: 242  
DB: 2 Gaps: 31

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x T13168 (1-1284)

QY	1	ATCGGGGCATCGGGGCTCCTGGCGCTCAGAACACCTTCTCGGACACCATCGTACG	60
Db	1	MetProAlaArgLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr	20
QY	61	CGCTTCGACGGCACGACAGTAACCTTCGTGCTGGGCAACGCCAGGTGGCGGCTCTTC	120
Db	21	ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn	39
QY	121	CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC	180
Db	40	ProIleValTyrCysSerAspGlyPheValAspLeuThrGlyTyrSerArgAlaGlnIle	59
QY	181	ATGCAGCGGGGCTGTGCCGTGCTCCTTTATGGGCCAGACACCACTGAGCTCGTCCGC	240
Db	60	MetGlnLysGlyCysSerCysHisPheLeuTyrGlyProAspThrLysGluHisLys	79
QY	241	CAACAGATCCGCAAGGCCCTGGACGACACAAGAGTTCAAGGCTGAGCTGATCCTGTAC	300
Db	80	GlnGlnIleGluLysSerLeuSerAsnLysMetGluLeuLysLeuGluValIlePheTyr	99
QY	301	CGGAAGAGCGGGCTCCCGCTTCTGGTGTCTCCTGGATGTGATACCCATAAAGATGAGAAA	360
Db	100	LysLysGluGlyAlaProPheTrpCysLeuPheAspIleValProIleLysAsnGluLys	119
QY	361	GGGAGGTGGCTCTCTTCCTAGTCTCTCACAGGACATCAGCGAAACCAAG	411
Db	120	ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGlu	139
QY	411	-----	411
Db	140	MetAsnValAsnGluGluCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGlyAla	159
QY	412	-----	412
Db	160	ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyLeuProGlyLeuGly	179
QY	421	GGCCCC-----GACAGATGGAAGGAGACAGGTGGTGGCGCGCGGATATGGCCGG	471
Db	180	GlyProAlaAlaSerAspGlyAspThrGluAlaGlyGluGlyAsnAsnLeuAspValPro	199
QY	472	GCACGATCCAAAGGCTTCAATGCCAACCGCGCGGAGCGCGGCGGTGCTTACACACCTG	531
Db	200	Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValLeuTyrGlnLeu	216
QY	532	TCCGGGCACCTGCAGAAGCAGCCCAAGGC---AAGCACAAAGCTCAATAAGGGG	582
Db	217	SerGlyHisTyrLysProGluLysGlyGlyValLysThrLysLeuLysLeuGlyAsnAsn	236

QY	583	---GTGTTTGGGAGAAACCAAACTTGCCCTGAGTACAAAGTAGCCCATCCGGAAGTCG	639
Db	237	PheMetHisSerThrGluAlaProPheProGluTyrLysThrGlnSerIleLysLysSer	256
QY	640	CCCTTCATCCTGTGCACTGTGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTC	699
Db	257	ArgLeuIleLeuProHisTyrGlyValPheLysGlyIleTyrAspTyrValIleLeuVal	276
QY	700	GCCACACTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTGAGCAGCAGCGGAG	759
Db	277	AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg	296
QY	760	CCCAGTGGCGCGCGCGCCCGCTGTGTGACCTGGCCGTGGAGTCTCTTCATC	819
Db	297	GlnThr-----LysValSerAspValIleValGluAlaLeuPheIle	310
QY	820	CTTGACATTTGCTGAATTTCCGTACCACATTCGTGTCCAAGTCGGGCCAGGTGTTT	879
Db	311	ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyGluValValSer	330
QY	880	GCCCCAAAGTCCATTGCTCCACTACGTACCACCTGGTTCCTGTGGATGTATCGCA	939
Db	331	AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTyrPheAlaLeuAspLeuLeuAla	350
QY	940	GCGTGGCCTTTGACCTGTACATGCCTTCAAGGTCAACGTGTACTTCGGG	990
Db	351	AlaLeuProPheAsp-----HisLeuTyrAlaSerAspLeuTyrAspGlyGluAspSer	368
QY	991	---GCCCATCTGCTGAAGACGGTGGCTGCTGCTGGCCCTGTGCGCCTGCTTCCGGGGCTG	1047
Db	369	HisIleHisLeuValLysLeuThrArgLeuLeuArgLeuAlaArgLeuGlnLysIle	388
QY	1048	GACCGGTACTCGCAGTACAGCGCGGTGGTGTGACACTGCTCATGGCCGTGTTCCGCCCTG	1107
Db	389	AspArgTyrSerGlnHisThrAlaMetIleLeuThrLeuLeuMetPheSerPheThrLeu	408
QY	1108	CTCGCGCACTGGTGGCTCGCTGCTGTTTATATGGCCAGCGGAGATCGAGAGCAGC	1167
Db	409	AlaAlaHisTrpLeuAlaCysIleTrpTyrValIleAlaValLysGluTyrGlu-----	426
QY	1168	GAATCCGAGCTGCCTGAG-----ATTGGTGGCTGTGAGGAGTGGCCCGCGACTGGAG	1221
Db	427	-----TrpPheProGluSerAsnIleGlyTrpLeuGlnLeuAlaGluArg-----	442
QY	1222	ACTCCCTACTACCTGGTGGCGCGAGGCCAGCTGGAGGGAACAGCTCCGGCCACAGTGAC	1281
Db	442	-----	442
QY	1282	AACGTCAGCAGCAGCAGCGAGGCCAACCGGGACGGGGCTGGAGCTGCTGGGCGGCCGTCG	1341
Db	443	-----LysAsnAlaSerValAlaIleLeuThrThrAlaGlu-----	454
QY	1342	CTGCGCAGCGCCTTACATCACCTCCCTCTACTTTCGCACTCAGCAGCCTCACCAGCGTGGC	1401
Db	455	-----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly	471
QY	1402	TTCGGCAACGTGTCCGCCAACACCGGACACCGAGAAGATCTTCTCCATCTGCACCATGCTC	1461
Db	472	PheGlyAsnValSerAlaAsnThrThrAlaGluLysValPheThrIleMetMetLeu	491
QY	1462	ATCGCGCGCCTGATGCACGGGTGGTGTGGAAACGTGACGGCCATCATCCAGCGCATG	1521
Db	492	IleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMet	511
QY	1522	TACGCCCGCGCTTTCTGTACCACAGCCGACCGCGACCTGGCGACTACATCCGCATC	1581
Db	512	TyrSerArgSerLeuTyrGluSerLysTrpArgAspLeuLysAspPheValAlaLeu	531
QY	1582	CACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGCG	1641
Db	532	HisAsnMetProLysGluLeuLysGlnArgIleGluAspTyrPheGlnThrSerTrpSer	551
QY	1642	GTGAACAATGGCATCGACACCCAGAGCTGCTGCAGAGCCTCCCTGACGAGCTCGCGGCA	1701



QY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300  
Db 80 AlaGlnIleAlaGlnAlaLeuLeuGlyAlaGluGluArgLysValGluIleAlaPheTyr 99  
QY 301 CGGAAGAGCGGGCTCCCGTCTCTGCTCTGCTGATGATACCCATAAAGATGAGAAA 360  
Db 100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValProValLysAsnGluAsp 119  
QY 361 GGGGAGGTGGCTCTCTCTA-----GTCTCTCACAGGACATC----- 399  
Db 120 GlyAlaValIleMetPheIleLeuAsnPheGluValMetGluLysAspMetValGly 139  
QY 400 -----ACGGAACCAAGAACCGAGGGGGCCCGACAGATGG----- 435  
Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyArg 159  
QY 435 ----- 435  
Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179  
QY 436 ---AAGGAGACAGGTGGTGGCGGCGCGGATATGGCCGGC---ACGATCCAAAGGCTTC 489  
Db 180 ValArgSerGlyGlyAlaGly-GlyAlaGlyAla-ProGlyAlaValValAspVala 199  
QY 490 AATGCCAAACGGCG----- 503  
Db 199 spLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMetA 219  
QY 504 -----GCGGAGCCGGCGCTGCTCTA----- 524  
Db 219 spAsnHisValAlaGlyLeuGlyProAlaGluGluArgAlaLeuValGlyProGlys 239  
QY 525 --CCACCTGTCCGGGCACCTGCAGAAGCAGCCCAAGGCAAG---CACAAAGTCAAT--- 576  
Db 239 erProProArgSerAlaProGlyGlnLeu-ProSerProArgAlaHisSerLeuAsnPro 258  
QY 576 ----- 576  
Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAlaSer 278  
QY 577 -----AAGGGGTGTTGGGGAG 594  
Db 279 ValArgArgAlaSerSerAlaAspAlleGluAlaMetArgAlaGlyValLeuProPro 298  
QY 595 AAACCAAC----- 603  
Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318  
QY 603 ----- 603  
Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338  
QY 603 ----- 603  
Db 339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358  
QY 603 ----- 603  
Db 359 IleAlaProLysIleLysGluArgThrHisAsnValThrGluLysValThrGlnValLeu 378  
QY 604 -----TTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTC 645  
Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp 398  
QY 646 ATCCTGTGCACTGTGGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACA 705  
Db 399 ThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuVal 418  
QY 706 CTCTATGTGGCTGTCACTGTGCCCTACAGCGTGTGTGTG-----AGCACAGCACGG 756  
Db 419 IleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGluGlu 438

QY 757 GAGCCCAAGTGCC-----GCCCGCGGCCCGCCCGAGCGTCTGTGACCTGGCC 801  
Db 439 GlyProProAlaThrGluCysGlyTyrAlaCysGlnProLeuAlaValValAspLeuIle 458  
QY 802 GTGGAGGTCTCTTTCATCCTTGACATTGTGTAATTTCCGTACCAATTCGTGTCCAAG 861  
Db 459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsnAla 478  
QY 862 TCGGGCCAGGTGGTGTTCGCCCAAGTCCATTTCCTCCACTACGTACCCACCTGGTTC 921  
Db 479 AsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrpPhe 498  
QY 922 CTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGTCTACATGCTTCAAGGTCAACGTG 981  
Db 499 LeuIleAspMetValAlaAlaIlePropheAspLeuLeu----- 511  
QY 982 TACTTCGGGGCC-----CATCTGCTGAAGACGGTGCCTGTGCGC 1023  
Db 512 IlePheGlySerGlySerGluGluLeuIleGlyLeuLysThrAlaArgLeuLeuArg 531  
QY 1024 CTGCTGCGCCTGCTTCCGGCGGTGGACCGGTACTCGCAGTACAGCCGCGTGGTGACA 1083  
Db 532 LeuValArgValAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551  
QY 1084 CTGCTCATGGCCGTGTTGCGCCTGCTCGCGCACTGGTGGCTGCTGCTGTTTACATT 1143  
Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIle 571  
QY 1144 GGCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCTGAGATTGGCTGGTGCAGGAG 1203  
Db 572 GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTrpLeuHisAsn 588  
QY 1204 CTGGCCCGCGACTGGAGACTCCCTACTACTCTGTTGGGCGGAGCCAGCTGGAGGGAAC 1263  
Db 589 LeuGlyAspGlnIleGlyLysProTyr-----Asn 598  
QY 1264 AGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGGAGGCCAACCGGACGGGCTGGAG 1323  
Db 599 SerSerGly----- 601  
QY 1324 CTGCTGGCGGCGCGTGGTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAGC 1383  
Db 602 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPheSer 620  
QY 1384 AGCTCACCAAGGTGGCTTCGGCAACGTGTCCGCCAACACCGGACACCGAGAAGATCTTC 1443  
Db 621 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe 640  
QY 1444 TCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGGTGTGGGAACGTGACG 1503  
Db 641 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer 660  
QY 1504 GCCATCATCCAGCGCATGTACGCCCGCGCTTCTGTACCACAGCGCAGCGCGACCTG 1563  
Db 661 AlaIleIleGlnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArgVal 680  
QY 1564 CGCGACTACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTAC 1623  
Db 681 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluTyr 700  
QY 1624 TTCAGGCCACCTGGCGGTGAACAATGGCATCGACACCGAGCTGCTGCAGAGCCTC 1683  
Db 701 PheGlnHisAlaTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe 720  
QY 1684 CCGTACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCTCTGCAG---CTG 1740  
Db 721 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuHisCys 740  
QY 1741 CCACTGTTTGGCGGCCAGCGCGGTGCCTGCGGGCACTGTCTCTGCGCCCTGCGGCC 1800  
Db 741 LysPropheArgGlyAlaThrLysGlyCysLeuArgAlaLeuAlaMetLysPheLysThr 760  
QY 1801 GCCTTCTGCACGCCGGCGAGTAGTACCTCATCCACCAAGCGCATGCCCTGCAGGCCCTCTAC 1860



1074 Db ValProProAlaTyrSerAla-- 1080  
2812 QY CTGTGTGTGGACACTGGGGCATCCTCTACTGCTGAGCCCGCCAGCTGCTGTCTTG 2871  
1081 Db ValThrThrProGlyProGlyProThrSerThrSerProLeuLeuProValSerPr 1099  
2872 QY AGTGGGACTGGCCCCCACCCTCGTCCGGGGCCTCTCCCTCATGGCACCCTGGCCCTGG 2931  
1099 Db ProThrLeuThrLeuAspSerLeuSerGln----- 1110  
2932 QY GGTCCCCCAGCGTCTC-----AGAGCTCCCCCTGGCCTCGAGCCACAGCTTTCTGG 2982  
1111 Db ValSerGlnPheMetAlaCysGluGluLeuProProGly--AlaProGluLeuProGl 1129  
2983 QY ACCTCCACCTCAGACTCAGAGCCCCCTGCTCAGGAGACCTCTGCTCTGAGCCACAGCACC 3042  
1129 Db nGluGlyProThrArgLeuSerLeuProGlyGlnLeuGlyAlaLeuThrSerGlnPr 1149  
3043 QY CCTG 3046  
1149 Db oLeu 1150  
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A40853  
potassium channel protein eag - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 24-Sep-1998  
C;Accession: A40853  
R;Warmke, J.; Drysdale, R.; Ganetzky, B.  
Science 252, 1560-1562, 1991  
A;Title: A distinct potassium channel polypeptide encoded by the Drosophila eag locus.  
A;Reference number: A40853; MUID:91262635; PMID:1840699  
A;Accession: A40853  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1174 <WAR>  
A;Cross-references: GB:M61157; NID:gl57311; PID:gl57312  
C;Genetics:  
A;Gene: FlyBase:eag  
A;Cross-references: FlyBase:FBgn0000535  
C;Keywords: transmembrane protein  
Alignment Scores:  
Pred. No.: 1.19e-64 Length: 1174  
Score: 1390.00 Matches: 390  
Percent Similarity: 47.57% Conservative: 198  
Best local Similarity: 31.55% Mismatches: 398  
Query Match: 22.83% Indels: 250  
DB: 2 Gaps: 42  
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QY 1 ATGCCG---GCCATGGGGGCTCTGCGCCCTCAGAACACCTTCTCTGACACCATCGCT 57  
Db 1 MetProGlyGlyArgGlyLeuValAlaProGlnAsnThrPheLeuGluAsnIle 20  
QY 58 ACGCGCTTCGACGGC---ACGCACAGTAATCTGCTGGGCAACGCCAGGTGGCGGG 114  
Db 21 ArgArgSerAsnSerGlnProAspSerSerPheLeuLeuAlaAsnAlaGlnIleValAsp 40  
QY 115 CTCTTCCCGTGGTCTACTGCTGTGATGGCTTCTGTGACCTCAGGGCTTCTCCCGGCT 174  
Db 41 ---PheProIleValTyrCysAsnGluSerPheCysLysIleSerGlyTyrAsnArgAla 59  
QY 175 GAGGTCTATGACGGGGCTGT-----GCCTGCTCTTCTCTTTATGGCCACACACCATG 228  
Db 60 GluValMetGlnLysSerCysArgTyrValCysGlyPheMetTyrGlyGluLeuThrAsp 79  
QY 229 GAGCTCGTCCGCCAACACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGCTGAG 288  
Db 80 LysGluThrValGlyArgLeuGluTyrThrLeuGluAsnGlnGlnAspGlnPheGlu 99  
QY 289 CTGATCTGTACCGGAAGAGCGGGCTC----- 315

761 Db ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuLeuThrAlaLeuTyr 780  
1861 QY TTTGTCTGCTCTGCTCCATGGAGGTGCTCAAGGTGGACACCGTCTGCTCGCCATCTAGGG 1920  
781 Db PheIleSerArgGlySerIleGluIleLeuArgGlyAspValValAlaIleLeuGly 800  
1921 QY AAGGGCGACCTGATCGGTGTGAGTGCCTCCCGGGGAGCAGGTGTAAAGGCCAATGCC 1980  
801 Db LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly 820  
1981 QY GACGTGAAGGGGTGACGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
821 Db AspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeuGlu 840  
2041 QY AGCCTTGGCTGATCCCGAGTTTCCCGCGCTTTCAGTCTGCTGCTGCTGCTGCTGCTGCT 2100  
841 Db ValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu-----GluIle 858  
2101 QY AGCTACAACCTG-----GGTGTGGGGAGGCTCTGCGAGAGGTGGAC 2142  
859 Db ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu 878  
2143 QY ACCAGCTCCCTGAGCGGCGACAATACCTTATGTCACCGCTGGAGGAGAGGACAGAT 2202  
879 Db GlyGlyPheSerArgGlnArgLysArgLysLeuSerPheArgArgArgThrAspLysAsp 898  
2203 QY GGGGAGCAGGGCCCCACGGTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGCCCCCTGCTG 2262  
899 Db ThrGluGln----- 901  
2263 QY TCCCTGGCTGACCTCTCATCTCCTCAGCTGCCAAGCTGCTATCCCGACGTGCAACAGCA 2322  
902 Db ---ProGlyGluValSerAla-----LeuGlyProGlyArgAlaGly 914  
2323 QY CCGCGGCTCTAGTGGGACAGGGAGGCGGAGGCGGAGGCGGCTTTGAAGGCTGAG 2382  
915 Db AlaGlyPro-----SerSerArgGlyArgProGlyGlyProTrpGlyGluSerProSer 932  
2383 QY GGTGGCCCTCTGCTCCCGCA-----CGGGCCCTAGAGGGG 2418  
933 Db SerGlyProSerSerProGluSerSerGluAspGluGlyProGlyArgSerSerPro 952  
2419 QY CTACGGCTG-----CCCCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCC 2466  
953 Db LeuArgLeuValProPheSerSerProArgProProGlyGluProProGlyGlyGluPro 972  
2467 QY AGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCGACCCCAAG----- 2514  
973 Db ---LeuMetGluAspCysGluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe 991  
2515 QY TTTCTTTT-----CGGTGGGCCAGTCT 2538  
992 Db SerGlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyArgGlnTyrGlnGlu 1011  
2539 QY GGGCCGGAATGTACGAGCAGCCCCCTCCCTGGACGAGAGCGGCTGCTCACTGTT--- 2595  
1012 Db LeuProArgCys-----ProAlaProThrProSerLeuLeuAsnIlePro 1026  
2596 QY CCCCCGCCCCAGGAGGCAAGGAACACACACACTG 2634  
1027 Db LeuSerSerProGlyArgProArgProArgGlyAspValGluSerArg-----Leu 1042  
2635 QY GACAAGCTTCGGCAGGGGTGACAGAGTGTACAGCAGGTG---CTGCAGATCGGGAA 2691  
1043 Db AspAlaLeuGlnArgGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThr 1062  
2692 QY GGAATGACATCTCGCCAGGCTGTGACGCTTGTCTGCGGCCCCACAGGAGGCTCCG 2751  
1063 Db ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu----- 1073  
2752 QY TGCCCTCGGCATCGGGAGAGGGCGCTGCCCCAGCCAGCAGCTCCGGGCTTCTGACGCT 2811







Db 175 GlyGluAsnValHisLysHisSerArgLeuAlaGluValLeuGlnLeuGlySerAspIle 194  
QY 586 TTTGGGGAGAAACCAAACTTGCCTGAGTACAAAGTAGCCGCCCATCCGGAAGTGCCTTC 645  
Db 195 -----LeuProGlnTyrLysGlnGluAlaProLysThrProHis 208  
QY 646 ATCTGTGTCACCTGTGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTGCCACA 705  
Db 209 IleIleLeuHisTyrCysValPheLysThrThrTrpAspTrpIleIleLeuIleLeuThr 228  
QY 706 CTCATGTGGTGTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCAGT 765  
Db 229 PheTyrThrAlaIleLeuValProTyrAsnValSerPheLysThr---ArgGlnAsnAsn 247  
QY 766 GCCGCCCGCGCGCCAGCGTCTGTGACCTGGCCGTGGAGGTCCCTCTTCATCCTTGAC 825  
Db 248 ValAlaTrp-----LeuValValAspSerIleValAspValIlePheLeuValAsp 264  
QY 826 ATTGTGCTGAATTCGGTACCACTACCACTTCGTGTCCAAAGTCGGGCCAGGTGTGTTGCCCA 885  
Db 265 IleValLeuAsnPheHisThrThrPheValGlyProAlaGlyGluValIleSerAspPro 284  
QY 886 AAGTCCATTGCTCCACTACGTACCACTGCTGTTTCTGCTGATGTCATCGCAGCGCTG 945  
Db 285 LysLeuIleArgMetAsnTyrLeuLysThrTrpPheValIleAspLeuLeuSerCysLeu 304  
QY 946 CCCTTTGACCTGTACATGCCTTCAAG-----GTCAACGTGTACTTCGGG 990  
Db 305 ProTyrAspValIleAsnAlaPheGluAsnValAspGluGlyIleSerSerLeuPheSer 324  
QY 991 GCCCATCTGCTGAAGACGGTGGCGCTGCTGCGCTGTGCTGCGCTGCTTCCGGCGGTGGAC 1050  
Db 325 Ser-----LeuLysValValArgLeuLeuArgLeuGlyArgValAlaAlaArgLysLeuAsp 342  
QY 1051 CGGTACTCGCAGTACAGCGCGCTGGTGTGACACTGTCTCATGGCCGTGTTCCGCCCTGCTC 1110  
Db 343 HisTyrIleGluTyrGlyAlaAlaValLeuValLeuValCysValPheGlyLeuAla 362  
QY 1111 GCGCACTGGTTCGCTCGCTGCTGGTGTATATTGGCCAGCGGAGATCGAGAGCAGCGAA 1170  
Db 363 AlaHisTrpMetAlaCysIleTrpTyrSerIleGlyAspTyrGluIlePheAspGluAsp 382  
QY 1171 TCCGAG---CTGCCTGAGATTGGCTGGCTGCAGGAGTGGCCCGCCGACTGGAGACTCCC 1227  
Db 383 ThrLysThrIleArgAsnAsnSerTrpLeuTyrGlnLeuAlaLeuAspIleGlyThrPro 402  
QY 1228 TACTACCTGGTGGCGCGGAGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGACAACTGC 1287  
Db 403 TyrGlnPhe-----AsnGlySerGlySerGlyLysTrpGlu----- 414  
QY 1288 AGCAGCAGCAGCGAGGCGCAACGGGACGGGCTGGAGCTGGCGGCGCCCGCTCGCTGCGC 1347  
Db 415 -----GlyGlyProSerLysAsn 420  
QY 1348 AGCGCCTACATCACTCCCTCTACTTCGCACTCAGCAGCCCTCACCAGCGTGGGCTTCGGC 1407  
Db 421 SerValTyrIleSerSerLeuTyrPheThrMetThrSerLeuThrSerValGlyPheGly 440  
QY 1408 AACGTGTCCGCCAACACGGACACCGAGAGATCTTCTCCATCTGCACCACTGCTCATCGGC 1467  
Db 441 AsnIleAlaProSerThrAspIleGluLysIlePheAlaValAlaIleMetMetIleGly 460  
QY 1468 GCCCTGATGCACGGTGGTGTGTTGGGAACGTGACGGCCCATCATCCAGCGCATGTACGCC 1527  
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QY 1528 CGCCGCTTCTGTACCAACAGCCGACCGGACCTGCGGACTACATCCGCACTCCACCGT 1587  
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QY 1588 ATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGCGGTGAAC 1647  
Db 501 ValProLysGlyLeuSerGluArgValMetAspTyrIleValSerThrTrpSerMetSer 520

QY 1648 AATGGCATCGACACCAACCGAGCTGCTGCAGAGCCCTCCCTGACGAGCTGCGCGCAGACATC 1707  
Db 521 ArgGlyIleAspThrGluLysValLeuGlnIleCysProLysAspMetArgAlaAspIle 540  
QY 1708 GCCATGCACCTGCACAAGGAGGTCTCTG---CAGCTGCCACTGTTTGTAGGGCGGCGAGCGC 1764  
Db 541 CysValHisLeuAsnArgLysValPheLysGluHisProAlaPheArgLeuAlaSerAsp 560  
QY 1765 GGCTGCCTGCGGCACTGTCTCTGGCCCTGCGGCCCGCCCTTCTGCACGCGCGGCGAGTAC 1824  
Db 561 GlyCysLeuArgAlaLeuAlaMetGluPheGlnThrValHisCysAlaProGlyAspLeu 580  
QY 1825 CTCATCCACCAAGCGCATGCCCTGCGAGGCCCTCTACTTTGTCTGCTCTGCTCCATGGAG 1884  
Db 581 IleTyrHisAlaGlyGluSerValAspSerLeuCysPheValValSerGlySerLeuGlu 600  
QY 1885 GTGCTCAAGGGTGGCACCGTCTCGCCATCCTAGGGAAGGGCGACCTGATCGGCTGTGAG 1944  
Db 601 ValIleGlnAspAspGluValValAlaIleLeuGlyLysGlyAspValPheGlyAspVal 620  
QY 1945 CTGCCCCGCGGAGCAGGTGGTAAAGGCCAAATGCCGACGTGAAGGGGTGACGTACTGC 2004  
Db 621 PheTrpLysGluAlaThrLeuAlaGlnSerCysAlaAsnValArgAlaLeuThrTyrCys 640  
QY 2005 GTCTGCACTGTCTGCAGCTGGCTGGCCTGCACGACAGCCCTTGGCTGTACCCCGAGTTT 2064  
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QY 2065 GCCCCGCGCTTCAGTCTGCTGGCTCCGAGGGGAGCTCAGCTACAAC----- 2109  
Db 661 SerHisSerPheSerArgAsnLeu-----IleLeuThrTyrAsnLeuArgLysArgIle 678  
QY 2109 ----- 2109  
Db 679 ValPheArgLysIleSerAspValLysArgGluGluGluArgMetLysArgLysAsn 698  
QY 2109 ----- 2109  
Db 699 GluAlaProLeuIleLeuProAspHisProValArgArgLeuPheGlnArgPheArg 718  
QY 2110 -----CTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAAGTCC 2151  
Db 719 GlnGlnLysGluAlaArgLeuAlaAlaGluArgGlyGlyArgAspLeuAspLeuAsp 738  
QY 2152 CTGAGCGGCGACAATACCTTATGTCC---ACGCTGGAGGAGAAGGAGACAGATGGGGAG 2208  
Db 739 ValGluLysGlyAsnAlaLeuThrAspHisThrSerAlaAsnHisSerLeuValLysAla 758  
QY 2209 CAGGGCCCCACGGTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCCT 2268  
Db 759 SerValValThrValArgGluSerProAlaThrProValSerPheGlnAlaAlaSer--- 777  
QY 2269 GGCTGCACCTCCTCATCTCAGCTGCCAAGCTGCTATCCCCACGTCGAAACAGACACCCCG 2328  
Db 778 ---ThrSerThrValSerAspHisAlaLysLeuHisAlaProGlySerGluCysLeuGly 796  
QY 2329 CCTCGTCTAGGTGGCAGAGGAGGCCAGGCAGGCAGGGCAGGG----- 2367  
Db 797 ProLysAlaGlyGlyGlyAspProAlaLysArgLysGlyTrpAlaArgPheLysAspAla 816  
QY 2368 -----GCTTTGAAGGCTGAGGCTGGCCCTCTGTCTCCC 2400  
Db 817 CysGlyLysGlyGluAspTrpAsnLysValSerLysAlaGluSerMetGluThrLeuPro 836  
QY 2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCCCATGCCATGGAATGTGCCCCAGATCTG 2460  
Db 837 GluArgThr-----LysAla 841  
QY 2461 AGCCCCAGGGTAGTAGATGGCAATTGAAGACGGCTGTGGCTCGGACCAAGTTCTCT 2520  
Db 842 SerGlyGluAlaThrLeuLysLysThrAspSerCysAspSerGlyIleThrLysSerAsp 861

QY 2521 TTCCGGCTGGCCAGTCTGGCCCGAATGTAGCAGCAGCCCTCCCTGGACCAGAGAGC 2580  
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Db 862 LeuArgLeuAsnValGly-----GluAlaArgSerProGlnAspArgSer 877  
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Db 878 ProIleLeuAlaGluValLysHisSerPheTyrProIleProGluGlnThrLeuGlnAla 897  
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QY 2617 AGGAACACAGACACACTGGACAAGCTTCGGAGGCGGTGACAGAGCTGTACAGCAGGTG 2676  
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Db 898 ThrValLeuGluValLysHisGluLeuLysGluAspIleLysAlaLeuAsnAlaLysMet 917  
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QY 2677 CTGCAGATGCGGGAAGGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTGGCGCCC 2736  
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Db 918 ThrSerIleGluLysGlnLeuSerGluIleLeuArgIleLeuMet----- 932  
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QY 2737 CACAGGAGGGTCCGTGCCCTCGGGCATCGGAGAGGGCGGTGCCAGCCAGCACCTCC 2796  
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Db 933 -----SerArgGlySerSerGlnSerProGlnAspThrCys 944  
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Db 945 GluValSerArgPro 949  
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RESULT 8  
I48912  
potassium channel subunit - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I48912  
R:Warme, J.W.; Ganetzky, B.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994  
A:Title: A family of potassium channel genes related to eag in Drosophila and mammals.  
A:Reference number: A54953; MUID:94211879; PMID:8159766  
A:Accession: I48912  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-989 <RES>  
A:Cross-references: EMBL:U04294; NID:G487739; PIDN:AAA62474.1; PID:G487740  
C:Genetics:  
A:Gene: m-eag

Alignment Scores:  
Pred. No.: 1.07e-63 Length: 989  
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Percent Similarity: 50.14% Conservative: 189  
Best local Similarity: 32.26% Mismatches: 310  
Query Match: 22.52% Indels: 217  
DB: 2 Gaps: 31

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x I48912 (1-989)

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QY 73 ACGCACAGTAACCTCGTGGGCAACGCCAGGTGGGGCTCTTCCCGTGGTCTAC 132  
|||::: |||  
Db 28 Thr-----AsnPheValLeuGlyAsnAlaGlnIleValAsp---TrpProIleValTyr 44  
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QY 133 TGCTCTGATGGTCTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTCTATGACGGGGC 192  
|||::: |||  
Db 45 SerAsnAspGlyPheCysLysLeuSerGlyTyrHisArgAlaGluValMetGlnLysSer 64  
|||::: |||  
QY 193 TGTGCTGCTCCTTCTTATGGCCAGACACCATGAGCTCGTCCGCCAACAGATCCGC 252  
|||::: |||  
Db 65 SerAlaCysSerPheMetTyrGlyGluLeuThrAspLysAspThrValGluLysValArg 84  
|||::: |||  
QY 253 AAGGCCCTGGACGACACAAGGATTCAAGGCTGAGCTGATCCTGTACCGGAAGAGCGGG 312  
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Db 85 GlnThrPheGluAsnTyrGluMetAsnSerPheGluLeuLeuMetTyrLysLysAsnArg 104  
|||::: |||  
QY 313 CTCCCGTTCTGTGTCTCTCGATGTGATACCCATAAAGATGAGAAAGGGGAGGTGGCT 372  
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Db 105 ThrProValTrpPhePheValLysIleAlaProIleArgAsnGluGlnAspLysValVal 124  
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QY 373 CTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGGGCCCCGACAGA 432  
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Db 125 LeuPheLeuCysThrPheSerAspIleThrAlaPheLysGlnProIleGluAspAspSer 144  
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QY 433 TGAAGGAGACAGGTGGTGGCCGG---CGCGCATATGGCCGGCACGATCCAAAGGCTTC 489  
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Db 145 CysLys-----GlyTrpGlyLysPheAlaArgLeuThrArgAlaLeuThrSer----- 160  
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QY 490 AATGCCAACCGCGCGGAGCGCGGTCTGTACACCTGTCCGGGACCTGCAGAGAAG 549  
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Db 161 -----SerArgGlyValLeuGlnGlnLeuAlaProSerValGlnLys 174  
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QY 550 ---CAGCCCCAAGGCAAGCAC-----AAGCTCAATAAGGGGGTG 585  
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Db 175 GlyGluAsnValHisLysHisSerArgLeuAlaGluValLeuGlnLeuGlySerAspIle 194  
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QY 586 TTTGGGGAGAAACCAAACTTGCCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTTC 645  
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Db 195 -----LeuProGlnTyrLysGlnGluAlaProLysThrProProHis 208  
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QY 646 ATCTGTGTGCACTGTGGGCACTGAGAGCCACCTGGGATGGCTTCATCTGCTGCCACA 705  
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Db 209 IleIleLeuHisTyrCysValPheLysThrThrTrpAspTrpIleIleLeuIleLeuThr 228  
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QY 706 CTCTATGTGGTGTACTGTGCTTACAGCGTGTGTGAGCACAGCAGGGAGCCCACT 765  
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Db 229 PheTyrThrAlaIleLeuValProTyrAsnValSerPheLysThr---ArgGlnAsnAsn 247  
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QY 766 GCGCGCGCGCGCCCGCTGTGTGACCTGGCGCGGAGGTCTCTTCACTCTGAC 825  
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Db 248 ValAlaTrp-----LeuValValAspSerIleValAspValIlePheLeuValAsp 264  
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QY 826 ATTGTGCTGAATTTCCGTACCATTCGTGTCCAAGTCGGGCGAGGTGGTGTTCGCCCA 885  
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QY 886 AAGTCCATTGCTCCACTACCTACCCACCTGGTTCCTGCTGGATGTATCGCAGCGCTG 945  
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Db 285 LysLeuIleArgMetAsnTyrLeuLysThrTrpPheValIleAspLeuLeuSerCysLeu 304  
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Db 305 ProTyrAspValIleAsnAlaPheGluAsnValAspGluValSerAlaPheMetGlyAsp 324  
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QY 990 ----- 990  
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QY 1036 CTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCGCTGGTGTGCTGACACTGCTCATGGCC 1095  
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Db 365 AlaArgLysLeuAspHisTyrIleGluTyrGlyAlaAlaValLeuValLeuValCys 384  
|||::: |||  
QY 1096 GTGTTGCGCTGCTCGGCACCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTG 1155  
|||::: |||  
Db 385 ValPheGlyLeuAlaAlaHisTrpMetAlaCysIleTrpTyrSerIleGlyAspTyrGlu 404  
|||::: |||  
QY 1156 ATCGAGAGCAGCGAATCCGAG---CTGCCTGAGATTGGCTGGCTGGCTGGCTGGCTGGC 1212  
|||::: |||  
Db 405 IlePheAspGluAspThrLysThrIleArgAsnAsnSerTrpLeuTyrGlnLeuAlaLeu 424  
|||::: |||  
QY 1213 CGACTGGAGACTCCCTACTACTGTTGGTGGCGCGGAGCCAGCTGGAGGGAACAGCTCCGC 1272  
|||::: |||  
Db 425 AspIleGlyThrProTyrGlnPhe-----AsnGlySerGlySerGly 438  
|||::: |||  
QY 1273 CAGAGTGACAACTGCAGCAGCAGCAGCAGCGAGGCGCAACGGGACGGGCTGGAGCTGCTGGC 1332  
|||::: |||

Db 439 LysTrpGlu-----Gly 442

QY 1333 GGCCCGTCGCTGGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTCAC 1392  
|||||  
Db 443 GlyProSerLysAsnSerValTyrIleSerSerLeuTyrPheThrMetThrSerLeuThr 462

QY 1393 AGCGTGGGTTCCGCAACGTGTCCGCCAACACGACACCGAGAGATCTTCTCCATCTGC 1452  
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Db 463 SerValGlyPheGlyAsnIleAlaProSerThrAspIleGluLysIlePheAlaValAla 482

QY 1453 ACCATGCTCATCGGCCCTGTATGCACGCGGTGGTGTTTGGGAACGTGACGGCCATCATC 1512  
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Db 483 IleMetMetIleGlySerLeuLeuTyrAlaThrIlePheGlyAsnValThrThrIlePhe 502

QY 1513 CAGCGCATGTAGCCCGCCGCTTTCTGTACCACAGCCGCGACCTGCGCGACTAC 1572  
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Db 503 GlnGlnMetTyrAlaAsnThrAsnArgTyrHisGluMetLeuAsnSerValArgAspPhe 522

QY 1573 ATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCC 1632  
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Db 523 LeuLysLeuTyrGlnValProLysGlyLeuSerGluArgValMetAspTyrIleValSer 542

QY 1633 ACCTGGCGGTGAACAATGGCATCGACACACCGAGCTGCTGCAGAGCCTCCCTGACGAG 1692  
|||||  
Db 543 ThrTrpSerMetSerArgGlyIleAspThrGluLysValLeuGlnIleCysProLysAsp 562

QY 1693 CTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGTCCCTG--CAGCTGCCACTGTTT 1749  
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Db 563 MetArgAlaAspIleCysValHisLeuAsnArgLysValPheLysGluHisProAlaPhe 582

QY 1750 GAGCGGCCAGCGCGCTGCTGCGGCACCTGTCTCGCCCTGCGGCCCGCTTCTGC 1809  
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Db 583 ArgLeuAlaSerAspGlyCysLeuArgAlaLeuAlaMetGluPheGlnThrValHisCys 602

QY 1810 ACGCCGGCGAGTACCTCATCCACCAAGCGATGCCCTGCAGGCCCTCTACTTTGCTGC 1869  
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Db 603 AlaProGlyAspLeuIleTyrHisAlaGlyGluSerValAspSerLeuCysPheValVal 622

QY 1870 TCTGGCTCCATGGAGGTCTCAAGGTGGCACCGTGTCTGCCATCCTTAGGGAAGGCGAC 1929  
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Db 623 SerGlySerLeuGluValIleGlnAspAspGluValValAlaIleLeuGlyLysGlyAsp 642

QY 1930 CTGATCGGCTGTGAGTGCCTCCCGCGGAGCAGGTGGTAAAGGCCAATGCCGACGTGAAG 1989  
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Db 643 ValPheGlyAspValPheTrpLysGluAlaThrLeuAlaGlnSerCysAlaAsnValArg 662

QY 1990 GGGCTGACGTACTGCTGCTGCAGTGTCTGCAGCTGGCTGGCTGCACGACGCTTGGC 2049  
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Db 663 AlaLeuThrTyrCysAspLeuHisValIleLysArgAspAlaLeuGlnLysValLeuGlu 682

QY 2050 CTGTACCCCGAGTTTGGCCCGCGCTTCAGTCTGGCCCTCCGAGGGGAGCTCAGCTACAAC 2109  
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Db 683 PheTyrThrAlaPheSerHisSerPheSerArgAsnLeu-----IleLeuThrTyrAsn 700

QY 2109 ----- 2109

Db 701 LeuArgLysArgIleValPheArgLysIleSerAspValLysArgGluGluGluArg 720

QY 2109 ----- 2109

Db 721 MetLysArgLysAsnGluAlaProLeuIleLeuProProAspHisProValArgArgLeu 740

QY 2110 -----CTGGGTGCTGGGGAGGCTCTGCAGAG 2136  
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Db 741 PheGlnArgPheArgGlnGlnLysGluAlaArgLeuAlaAlaGluArgGlyGlyArgAsp 760

QY 2137 GTGGAC-----ACCAGCTCCCTGAGCGGCGACAAT 2166  
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Db 761 LeuAspAspLeuAspValGluLysGlyAsnAlaLeuThrAspHisThrSerAlaAsnHis 780

QY 2167 ACCCTTATG-----TCCACGCTGGAGGAGGAGACAGATGGGGAGGAGGCCCCACG 2220  
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Db 781 SerLeuValLysAlaSerValValThrValArgGluSer----- 793

QY 2221 GTCTCCCGAGCCCGAGCTGATGAGCCCTCCAGCCCTCTGCTGTCCCTGGCTGCACCTCC 2280  
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Db 794 -----ProAlaThrProValSerPheGlnAlaAlaThrThr 805

QY 2281 TCA-----TCCTCAGCTGCCAAGCTG-----CTATCCCCACGT 2313  
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Db 806 SerThrMetSerAspHisAlaLysLeuHisAlaProGlySerGluCysLeuGlyProLys 825

QY 2314 CGAACAGCA-----CCCCGGCTCGTCTAGGT-----GGC 2343  
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Db 826 AlaValSerCysAspProAlaLysArgLysGlyTrpAlaArgPheLysAspAlaCysGly 845

QY 2344 AGAGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCTCTGTCTCCCCA 2403  
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Db 846 LysGlyGluAspTrpAsnLys---ValSerLysAlaGluSerMetGluThrLeuProGlu 864

QY 2404 CGGGCCCTAGAGGGGTACGGGTGCCCCCATGCCATGCCATGGAATGTGCCCCAGATCTGAGC 2463  
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Db 865 ArgThr-----LysAlaProGlyGluAlaThr 873

QY 2464 CCCAGGTAGTAGATGGCATTTGAAGACGGCTGTGGCTCGGACAGCCCAAGTTCTCTTTC 2523  
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Db 874 LeuLysLysThr-----AspSerCysAspSerGlyIleThrLysSerAspLeu 889

QY 2524 CGCGTGGGCCAGTCTGSCCCGGAATGTAGCAGCAGGCCCTCCCTGGACCAGAGCGGC 2583  
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QY 2584 CTGCTCACT-----GTCCCCATGGGCCCGAGCGAGGAAGG 2619  
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Db 906 IleLeuAlaGluValLysHisSerPheTyrProIleProGluGlnThrLeuGlnAlaThr 925

QY 2620 AACACAGACACACTGGACAAGCTTCGGCAGGCGGTGACAGAGCTGTGACAGAGGTGCTG 2679  
|||||  
Db 926 ValLeuGluValLysTyrGluLeuLysGluAspIleLysAlaLeuAsnAlaLysMetThr 945

QY 2680 CAGATCGGGAAGGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTGGCGCCAC 2739  
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Db 946 SerIleGluLysGlnLeuSerGluIleLeuArg-----IleLeuMetSerArg 961

QY 2740 AGGAGGGTCCGTGCTCGCTCGGCATCGGAGAGGGCGCTGCCAGCCAGC 2790  
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Db 962 GlySerAlaGlnSerProGlnGluThrGlyGluIleSerArgProGlnSer 978

RESULT 9  
T42394

potassium channel protein eag homolog - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C;Accession: T42394

R;Waterston, R.

submitted to the EMBL Data Library, June 1999

A;Reference number: Z22153

A;Accession: T42394

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-934 <WAT>

A;Cross-references: EMBL:AF036695; PIDN:AAB88348.1

C;Genetics:

A;Introns: 27/1; 66/2; 104/1; 147/1; 164/3; 222/2; 263/3; 301/3; 410/1; 468/2; 667/3; 76  
A;Note: F16B3.1

Alignment Scores:

Pred. No.:	9.14e-58	Length:	934
Score:	1257.00	Matches:	336
Percent Similarity:	48.09%	Conservative:	180
Best local Similarity:	31.31%	Mismatches:	332
Query Match:	20.64%	Indels:	225
DB:	2	Gaps:	33

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x T42394 (1-934)



QY 1 ATGCGG---GCCATGCGGGGCTCCTGGCGCCTCAGAACACCTTCTCTGGACACCATCGCT 57  
Db 1 MetProValGlyLysArgGlyLeuValAlaProGlnAsnThrPheLeuGluAsnValIle 20  
QY 58 ACGCGCTTCGACGGCACGCACAGTAACCTGCTGGCAACGCCAGTGGCGGGCTC 117  
Db 21 ArgArgCysAsnAsnAlaAspThrSerPheIleLeuAlaAsnAlaGlnValValAsp--- 39  
QY 118 TTCCCGCTGCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGCTGAG 177  
Db 40 TyrProIleValTyrCysAsnAspGlyPheSerLysLeuValGlyTyrThrArgAlaGlu 59  
QY 178 GTCATGACGGGGCTGTGCCTGCTCCTTCTTATGGCCAGACACACAGTGTGCTCGTC 237  
Db 60 IleMetGlnLysProCysSerLeuAlaPheMetHisGlyGluHisGlyGluValGlySer 79  
QY 238 CGCCAACAGATCCGCAAGGCCCTGGACGAGCACAAAGGAGTTCAAGGCTGATGATCCTG 297  
Db 80 LeuGlnLysMetGlnGluAlaLeuGluAsnAlaArgThrGluGlnAlaGluIleGlyLeu 99  
QY 298 TACCGAAGAGCGGGCTCCGTTCTGTGTCTCTGTGATGTGATACCCATAAAGATGAG 357  
Db 100 CysLysLysAsnLysThrProIleTrpLeuLeuValHisLeuAlaProIleLysAsnHis 119  
QY 358 AAAGGGGAGGTGCTCTCTCTAGTCTCTACAAGGACATCAGCGAAACCAAGAACCGA 417  
Db 120 LysAspAlaValValLeuTyrLeuCysGlnPheLysAspIleThrProLeuLysGlnPro 139  
QY 418 GGGGGCCCGACAGATGGAAGGAG-----ACAGGTGGTGGCGCGCGCGATAT 465  
Db 140 LeuAspAspGluAsnAsnLysAlaLeuPheCysValThrGlyLysAla----- 155  
QY 466 GGCCGGGCACGATCCAAAGGCTTCAATGCCAACCGGGCGGGAGCCGGCGCTGCTCTAC 525  
Db 156 -----AsnAlaValGluGluValThrArgValValMet--- 166  
QY 526 CACCTGTCCGGGCACCTGCAGAAAGCAGCCCAAGGGCAACACAAAGCTCAATAAGGGGTG 585  
Db 167 AsnLeuGlyGlyAspMet----- 172  
QY 586 TTTGGGGAGAAACCAACTTGCTGAGTACAAAGTAGCGGCCATCCGGAAGTCGCCCTTC 645  
Db 173 -----LeuProGlnTyrArgGlnGluThrProLysThrSerProHis 186  
QY 646 ATCTGTGTGCTGTGGGCACTGAGAGCCACCTGGGATGGCTTCTCTGCTCGCCACA 705  
Db 187 IleIleLeuHisTyrSerSerPheLysThrIleTrpAspTrpSerIleLeuAlaLeuThr 206  
QY 706 CTCATGTGGTGTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCACT 765  
Db 207 PheTyrThrAlaPheMetValProPheAsnIleAlaPheLysAsnSerSerArgGluAsn 226  
QY 766 GCCGCCCGCGCGCCCGCTGTGT-----GACCTGGCCGTGGAGGTCTCTTTCATC 819  
Db 227 ProGlyGlyGlyIleAspSerValAlaLeuMetAspSerIleValAspValIlePhePhe 246  
QY 820 CTTGACATGTGCTGAATTTCCGTACCACTTCGTGTCCAAAGTCCGGCCAGGTGGTGT 879  
Db 247 AlaAspIleLeuLeuAsnPheHisThrThrPheValGlyProGlyGlyGluValIle 266  
QY 880 GCCCCAAAGTCCATTTGCTCCCTACCTACCTGATCACCACCTGTTCTGTGATGATCGCA 939  
Db 267 GluProSerValIleArgGlnAsnTyrPheLysSerTrpPheLeuIleAspLeuLeuSer 286  
QY 940 GCGCTGCCCTTTGACCTGTACATGCTTCAAG-----GTCAACGTGTAC 984  
Db 287 CysLeuProTyrAspIlePheTyrMetPheLysArgAspAspGluArgIleGlySerLeu 306  
QY 985 TTCGGGGCCCATCTGCTGAAGACGGTGGCTGTGCGCTGTGCGCTGTGCGCTTCCGCGG 1044  
Db 307 PheSerAla-----LeuLysValValArgLeuLeuArgLeuGlyArgValAlaArgLys 324  
QY 1045 CTGGACCGGTACTTCGAGTACAGCGCCCGTGGTGTGCTGACACTGCTCATGCGCGTGTTCGCC 1104

Db 325 LeuAspAsnTyrLeuGluTyrGlyAlaAlaThrLeuLeuLeuLeuCysAlaTyrVal 344  
QY 1105 CTGCTCGGCACACTGGTGCCTGCCTGCTGCTGTTTACATTGGCCAGCGGGAGATC----- 1158  
Db 345 IleValAlaHisTrpLeuAlaCysValTrpPheTrpIleGlyAspSerGluValArgLeu 364  
QY 1159 GAGAGCAGCGAATCCGAGTGCCTGAGATTGGCTGGCTGCAGGAGTGGCCCGCCGACTG 1218  
Db 365 LysMetAspAsnLeuAlaLeuProAsp---GlyTrpLeuTrpLysLeuSerAsnAspLeu 383  
QY 1219 GAGACTCCCTACTACTGCTGGTGGCGCGGAGGCCAGCTGGAGGAACAGCTCCGGCCAGAT 1278  
Db 384 ArgGlnHisTyr----- 387  
QY 1279 GACAACTGCAGCAGCAGCAGCGAGGCCAACCGGACGGGCTGGAGCTGTGGCGGCCCG 1338  
Db 388 ---AsnIleProLeuSerAsnLysThrThr-----LeuValGlyGlyPro 401  
QY 1339 TCGCTGGCGCAGCGCTACATCACCTCCCTCTACTTCGCACCTCAGCAGCCTCACCAGCGTG 1398  
Db 402 SerArgThrSerAlaTyrIleSerSerLeuTyrTyrThrMetSerCysMetSerThrVal 421  
QY 1399 GCGTTTCGGCAACGTGTCCGCCAACACGCGACACCGAGATCTTCTCCATCTGCACCATG 1458  
Db 422 GlyPheGlyAsnIleAlaSerAsnThrAspAsnGluLysIlePheGlyValCysMetMet 441  
QY 1459 CTCATCGCGCGCTGATGCACGCGTGGTGTGTTGGAAACGTGACGGCCATCATCCAGCGC 1518  
Db 442 IleIleSerAlaLeuLeuTyrAlaAlaIlePheGlyHisMetThrThrIleIleGlnGln 461  
QY 1519 ATGTACGCCCGCGCTTCTGTACACAGCCGCGCAGCCTGCGCGACTACATCCGC 1578  
Db 462 MetThrSerSerThrValArgTyrHisGluMetIleSerAsnValArgGluPheIleLys 481  
QY 1579 ATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGTGTGAGTACTTCCAGGCCACCTGG 1638  
Db 482 LeuGlnGluIleProLysGluLeuAlaGluArgValMetAspTyrValValSerThrTrp 501  
QY 1639 GCGGTGAACAAATGGCATCGACACACCGAGCTGTGTGAGACCTCCCTGACGAGCTGCGC 1698  
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QY 1699 GCAGACATCGCCATGCACCTGCACAAAGGAGGTCTCT---CAGCTGCCACTGTTTGGCGC 1755  
Db 522 AlaAspIleCysValHisLeuAsnArgLysValPheAsnGluHisSerCysPheArgLeu 541  
QY 1756 GCCAGCCCGGCTGCTGCGGGCACTGTCTCTGCGCCCTGCGCGCCCGCTTCTGACCGCGC 1815  
Db 542 AlaSerAspGlyCysLeuArgSerLeuAlaMetPheLeuGluLeuAsnHisAlaAlaPro 561  
QY 1816 GGCAGTACCTCATCCACCAAGCGATGCCCTGCAGGCCCTCTACTTGTCTGTCTGCTGGC 1875  
Db 562 GlyAspLeuLeuTyrHisThrGlyGluSerValAlaAspAlaLeuTrpPheValValSerGly 581  
QY 1876 TCCATGGAGGTGCTCAAGGTGGCACCGTGTCTGCGCCATCCTAGGGAAGCGGACCTGATC 1935  
Db 582 SerLeuGluValIleGlnAspAspGluValValAlaIleLeuGlyLysGlyAspValPhe 601  
QY 1936 GGCTGTGAGCTGCCCGCGGAGCAGGTGGTAAAGGCCAAT----- 1977  
Db 602 Gly-----AspGluPheTrpLysAlaAsnGlySerThrGlyGlnSer 615  
QY 1978 ---GCCAGCTGAAGGGGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2034  
Db 616 AlaAlaAsnValArgAlaLeuThrTyrSerAspLeuHisMetIleLysLysAspLysLeu 635  
QY 2035 CACGACAGCTGCTGTACCCCGAGTTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCG 2094  
Db 636 MetAspValLeuAspPheTyrLysAlaPheAlaAlaAsnSerPheAlaArgAsnMet----- 653  
QY 2095 GAGCTCAGCTACAACCTGGTGTGCTGGGGAGGCTCTGTGAGAGGTGGACACGAGCTCCCTG 2154

Db 654 ThrLeuThrTyrAsnLeu-----ThrHisArg 662  
QY 2155 AGCGGGACAATACCTTATGTCCACGCTGGAGGAGAGAGACAGATGGGGAGCAG--- 2211  
Db 663 MetLysPheArgLysValAlaAspValLysArgGluLysGluLeuAspAlaLysArgLys 682  
QY 2211 ----- 2211  
Db 683 AsnGluLysLeuThrLeuProAsnAspHisProIleArgLysLeuLeuPheArgMetArg 702  
QY 2212 -----GGCCCCACGGTCTCCCCAGCCCCA-----GCTGATGAGCCCTCCAGCCCC 2256  
Db 703 GluArgHisGlyProArgIlePheProSerProMetPheAlaAsp----- 717  
QY 2257 CTGCTGTCCCTGGCTGCACCTCTCATCTCAGCTGCCAAGCTGTCTATCCACGTCGA 2316  
Db 718 ---IleGluLysGlyLeuLysLysSerThrGluLeuSerArgIleSerSerLeuHisSer 736  
QY 2317 ACAGCACCCCGGCTCGTCTAGGTGGCAGAGGAGGCCAGGCGAGGGGCTTTGAAG 2376  
Db 737 MetIle-----AspGluThrGlyGlyGlyGlySerSerTyr 748  
QY 2377 GCTGAGGCTGGCCCTCTGTCTCCCCACGGCCCTAGAGGGGCTACGGGCTGCCCCCATG 2436  
Db 749 ValLysSerProArgSerLysProLysArg----- 758  
QY 2437 CCATGGAATGTGCCCCACAGATCTGAGCCCCAGGGTAGTAGTGGCATTTGAGACGGCTGT 2496  
Db 759 -----ProLeuMetLysArgGlnThrValAsp-----GluAsp-AlaLe 772  
QY 2497 GGCTCGGACCCAGC-----CCAAGTTCTTTCCGCGTGGGCCAGTCTGGCCCGGAA 2547  
Db 772 uSerArgThrSerTrpGlyMetAspLysLysAspArgGluTrpSerSerLeuSerAsn-- 791  
QY 2548 TGTAGCAGCAGCCCTCCCTGGACCAGAGCGGCGCTGTCTACTGTTCCTCCCATGGGCC 2607  
Db 791 ----- 791  
QY 2608 AGCAGGCAAGAAACACAGACACACTGGACAAGCTTCGGCAGGCGG-----TGACA 2658  
Db 792 -IleLysThrGluMetLysSerLysPheAspIleIleGlyGluArgLeuThrIleIleG1 811  
QY 2659 GAGCTGTACAGCAGGCTGTGCAGATCGGGAAGGACTGCAGTCACTTCGCCAGGCTGTG 2718  
Db 811 uGlnIleAsnSerArg-LeuAlaLeuLeuGluArgValLeuIleGlyAsnAsnGly---- 829  
QY 2719 CAGCTTGTCTCGGCCGCCACAGGGAGGGTCCGTGCCCCCTCGGGCATCGGAGAGGGCCG 2778  
Db 830 -----GlyAlaAsnThrProSerThrMetProValGlySerP 842  
QY 2779 TGCCCCAGCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTGTGACACTGGGCATCTCC 2838  
Db 842 he-----SerAlaLeuAsnGluSerGlyAsn-----ArgLeuT 853  
QY 2839 TACTGCTGCAGCCCCCAGCTGGCTCTGTCTTGTAGTGG----- 2876  
Db 853 hrLeuAspAlaAlaProValAlaArgSerValSerTrpSerGluGlnHisGlnProHist 873  
QY 2877 -----GACTTGGCCCCACCCCTCGTCCGGGCGCTCTCCCTCCCTC-----ATG 2916  
Db 873 rpGlnArgPheValGluIleTyrSerGluThrSerThrVal-ProProLeuArgGluLeu 892  
QY 2917 GCACCTGGCCCTGGGGTCCCCCAGCGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCT 2976  
Db 893 GluAlaGlyGluTrpGluProProIleArgGluProThrProAsnPro----- 908  
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RESULT 10  
T19579  
hypothetical protein C30D11.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T19579  
R;Mortimore, B.  
submitted to the EMBL Data Library, August 1994  
A;Reference number: Z19145  
A;Accession: T19579  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-514 <WIL>  
A;Cross-references: EMBL:Z35596; PIDN:CAA84644.1; GSPDB:GN00021; CESP:C30D11.1  
A;Experimental source: clone C30D11  
C;Genetics:  
A;Gene: CESP:C30D11.1  
A;Map position: 3  
A;Introns: 49/3; 77/2; 151/3; 192/3; 244/2; 264/1; 366/3; 435/2; 479/1  
Alignment Scores:  
Pred. No.: 5,45e-46 Length: 514  
Score: 1029.50 Matches: 215  
Percent Similarity: 61.78% Conservative: 84  
Best Local Similarity: 44.42% Mismatches: 138  
Query Match: 16.91% Indels: 47  
DB: 2 Gaps: 10  
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QY 664 GCACTGAGAGCCACCTGGGATGGCTTCACTCTGCTGCCACACTCTATGCGCTGTCACT 723  
Db 78 ProPheLysAlaValTrpAspTrpIleIleLeuLeuValIleTyrThrAlaValPhe 97  
QY 724 GTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAG-----CCCAGT 765  
Db 98 ThrProTyr---ValAlaAlaPheLeuLeuArgGluLeuGlnAspThrAlaLysSer 116  
QY 766 GCCGCCCGCGCGCCAGCGTCTGTGACCTGGCCGTGGAGGTCTCTTTCATCTTTCATCTGAC 825  
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QY 826 ATTGTGCTGAATTCCGTACCACATTCGTGTCTCCAGTCGGG-----CAGGTGGTG 876  
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QY 877 TTTGCCCCCAAAGTCCATTTCCTCCACTACGTACCCACCTGCTGCTGCTGCTGCTGCTATC 936  
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QY 937 GCAGCGCTGCCCTTTGACCTGCTA-----CATGCTTCAAGGTCAACGTGTAC 984  
Db 177 AlaAlaValProPheAspLeuLeuValSerThrAsnSerAspGluThrThrLeu 196  
QY 985 TTGGGGCCCATCTGCTGAAGAGCGGTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1044  
Db 197 IleGly-----LeuLeuLysThrAlaArgLeuLeuArgValAlaArgLys 214  
QY 1045 CTGACCGGTACTCGCAGTACAGCGCGGTGGTGTGCTGACACTGCTCATGGCGGTGTTCCGCC 1104  
Db 215 LeuAspArgTyrSerGluTyrGlyAlaAlaValLeuLeuLeuMetAlaThrPheAla 234  
QY 1105 CTGCTCGGCACACTGGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1164  
Db 235 LeuIleAlaHisTrpLeuAlaCysIleTrpTyrAlaIleGlySerAlaGluLeuSerHis 254  
QY 1165 AGCGAATCCGAGCTGCCCTGAGATTGGCTGGTGCAGAGCTGGCCCGGAGTGGAGACT 1224  
Db 255 Lys-----GluTyrThrTrpLeuHisGlnLeuSerLysGlnLeuAlaGln 269  
QY 1225 CCCTACTACTGTTGGTGGCCGAGGCGCAGCTGGAGGAAACAGCTCCGGCCAGAGTGAACAAC 1284

Db 270 ProTyr----- 271

QY 1285 TGCAGCAGCAGCAGGAGCCAAACGGGACGGGCTGGAGCTGCTGGGGCGCCCGTCGCTG 1344

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QY 1345 CGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTCACCAGCGTGGGCTTC 1404

Db 286 LysSerArgTyrValThrSerLeuTyrPheThrLeuSerThrIleThrSerIleGlyPhe 305

QY 1405 GGCAACGTGTCCGCCAACACGACACCGACCGAGAGATCTTCTCCATCTGCACCATGCTCATC 1464

Db 306 GlyAsnValSerAlaThrThrAspSerGluLysIlePheThrIleIleMetMetIleLeu 325

QY 1465 GCGGCCCTGATGACCGCGGTGGTGTGGGAACGTGACGGCCATCATCCAGCGCATGTAC 1524

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QY 1525 GCGCGCGCTTCTGTACCACAGCCGACCGCGACCTGCGGCACTACATCCGATCCAC 1584

Db 346 SerGlyThrAlaArgTyrHisThrGluMetSerArgLeuArgGluPheIleArgPheHis 365

QY 1585 CGTATCCCAAGCCCTCAAGCAGCGCATGTCTGAGTACTTCCAGGCCACTGGGCGGTG 1644

Db 366 GlnIleProAsnProLeuArgGlnArgLeuGluTyrPheGlnHisAlaTrpSerTyr 385

QY 1645 AACATGGCATCGACACACCGAGCTGTGTCAGAGCCTCCCTGACGAGCTGCGCGCAGAC 1704

Db 386 ThrAsnGlyIleAspMetAsnLeuValLeuLysGlyPheProAspCysLeuGlnAlaAsp 405

QY 1705 ATCGCCATGCACCTGCACAAGGAGGTCTCTGCAG---CTGCCACTGTTTGAGGCGGCCAGC 1761

Db 406 IleCysLeuHisLeuAsnArgAsnLeuLeuSerGlyCysAlaAlaPheAlaGlySerThr 425

QY 1762 CGCGGCTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCCCGCTTCTGCACCGCGGCGAG 1821

Db 426 ProGlyCysLeuArgAlaLeuSerMetArgPheArgThrThrHisSerProGlyAsp 445

QY 1822 TACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTTACTTTGTCTGCTCTGGCTCCATG 1881

Db 446 ThrLeuValHisArgGlyAspIleLeuThrGlyLeuTyrPheIleAlaArgGlySerVal 465

QY 1882 GAGTGCTCAAG---GGTGGCACCGTGTCTGCCATCTAGGGAAGGCGCACCTGATCGGC 1938

Db 466 GluIleLeuAsnAspAspAsnThrValMetGlyIleLeuGlyLysAspAspIlePheGly 485

QY 1939 TGTGAGTGTCCCGGGAGCAGGTGGTAAAGGCCAATCCGACGTGAAGGGGCTGACG 1998

Db 486 GluAsnProLeuTyrAspGluValGlyLysSerSerCysAsnValArgAlaLeuThr 505

QY 1999 TACTGCGTCTG 2010

Db 506 TyrCysAspLeu 509

RESULT 11

A55251

cyclic nucleotide-gated Ca++ channel protein CNG-3 - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 13-Aug-1999

C;Accession: A55251; S43976

R;Biel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockerzi, V. Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994

A;Title: Another member of the cyclic nucleotide-gated channel family, expressed in testis

A;Reference number: A55251; MUID:94224768; PMID:8170936

A;Accession: A55251

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-706 <BIE>

A;Cross-references: GB:X76485; NID:9488728; PIDN:CAA54023.1; PID:9488729

A;Experimental source: kidney

R;Weyand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.; Nature 368, 859-863, 1994

A;Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from man

A;Reference number: S43976; MUID:94211295; PMID:7512693

A;Accession: S43976

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-706 <WEY>

A;Cross-references: GB:X89600; NID:908823; PIDN:CAA61759.1; PID:908824

A;Experimental source: testis

C;Genetics:

A;Gene: CNG3

C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-gated channel; ion channel; ion transport; membrane protein

C;Keywords: cGMP binding; ion channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

F;501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Alignment Scores:

Pred. No.:	2.2e-15	Length:	706
Score:	439.00	Matches:	145
Percent Similarity:	42.56%	Conservative:	101
Best Local Similarity:	25.09%	Mismatches:	208
Query Match:	7.21%	Indels:	124
DB:	2	Gaps:	19

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x A55251 (1-706)

QY 424 CCCGACAGATGGAAGGAGACAGGTGGTGGCGGCGCCGATATGGCCGGGACGATCCAAA 483

Db 127 ProAspArg-----GlyArgSerAlaTrpProLeuAlaArgAsnAsn 140

QY 484 GGCCTCAATGCCAACCGGCGGAGCGCGCGCTGTCTACCACCTGTCCGGGCACCTG 543

Db 141 ThrAsnThrCysAsnAsnSerGluLys-----AspAspLysAla 153

QY 544 CAGAAGCAGCCCAAGGCAAGCAAGCTCAATAAGGGGTGTTGGGGAGAAACCAAAC 603

Db 154 LysLysGluGluLysGluLysGluLysLys-----GluAsnProLys 169

QY 604 TTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCCCTTCATCTGTTCACCTGTGGG 663

Db 170 LysGluGluLysLysAspSerValValMetAspProSerSerAsnMetTyrTyrHis 189

QY 664 GCACTGAGAGCCACCTGGGATGGCTTCATCTCTGCTCGCCACACTCTATGTGGTGTCT 723

Db 190 TrpLeuThrVal-----IleAlaValPro 197

QY 724 GTGCCCTACAGCGTGTGTGTGACACAGCACAGCAGCGGAGCCAGTCCGCGCGGCC 783

Db 198 ValPheTyrAsnTrpCysLeuValCysArg----- 208

QY 784 AGCGTCTGT-----GACCTG 798

Db 209 ---AlaCysPheAspGluLeuGlnSerGluHisLeuMetLeuTrpLeuValLeuAspTyr 227

QY 799 GCCGTGGAGGTCTCTTCATCTTGACATTGTGTGATTTCCGTACCATTCGTGTCC 858

Db 228 SerAlaAspIleLeuTyrGlyMetAspMetLeuValArgAlaArgThrGlyPheLeu--- 246

QY 859 AAGTCGGGCCAGGTGGTGGTGGCCCAAGTCCATTGGCTCCACTACGTC---ACCACC 915

Db 247 GluGlnGlyLeuMetValMetAspAlaSerArgLeuTrpLysHisTyrThrGlnThrLeu 266

QY 916 TGTTCTCTGTGGATGTCATCGCAGCGTGCCTTTGACTGCTACATGCCTTCAAGTTC 975

Db 267 HisPheLysLeuAspValLeuSerLeuValProThrAspLeuAlaTyr---PheLysLeu 285

QY 976 AACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCGCTGCTGCGCTGCGCTG 1035

Db 286 GlyMetAsnTyrProGlu-----LeuArgPheAsnArgLeuLeuLysLeuAlaArgLeu 303

QY 1036 CTTCCGGCGCTGGACCGGTACTCG-----CAGTACAGC 1068

Db 304 PheGluPhePheAspArgThrGluThrArgThrAsnTyrProAsnMetPheArgIleGly 323

QY 1069 GCCGTGGTGTGACACTGTCTCATGCGCGTGTTCGCCCTGTCTCGGCACCTGGTTCG 1128



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Db      324 AsnLeuValLeuTyrIleLeu-----IleIleIleHisTrpAsnAlaCys 338
QY      1129 GTCTGTTTACATTGGCCAGCGGAGATCGAGAGCAGCAATCCGAGCTGCCTGAGATT 1188
Db      339 IleTyrPheAlaIleSerLys-----PheIle 347
QY      1189 GGCTGGCTGCAGGAGCTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGCCGGAGG 1248
Db      348 GlyPhe----- 349
QY      1249 CCAGCTGGAGGGAACAGCTCCGGCCAGAGTGACAACACTGCAGCAGCAGCAGGAGGCCAAC 1308
Db      350 -----GlyThrAspSerTrpValTyrProAsnValSerAsnProGluTyrGlyArg 366
QY      1309 GGGACGGGCTGGAGCTGCTGGGCGGCCGCTGCGCTGCGCAGCGCCCTACATCACCTCCCTC 1368
Db      367 -----LeuSerArgLysTyrIleTyrSerLeu 375
QY      1369 TACTTCGCACTCAGCAGCCTCACAGCGTGGGCTTCGGCAACAGTGTCCGCCAACACGGAC 1428
Db      376 TyrTrpSerThrLeuThrLeuThrIleGly---GluThrProProValLysAsp 394
QY      1429 ACCGAGAAGATCTTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGTGGTG 1488
Db      395 GluGluTyrLeuPheValValIleAspPheLeuValGlyValLeuIlePheAlaThrIle 414
QY      1489 TTTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTCTGTACCACAGC 1548
Db      415 ValGlyAsnValGlySerMetIleSerAsnMetAsnAlaSerArgAlaGluPheGlnAla 434
QY      1549 CGCACGGCGGACCTGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAG 1608
Db      435 LysIleAspSerIleLysGlnTyrMetGlnPheArgLysValThrLysAspLeuGluThr 454
QY      1609 CGCATGCTGGAGTACTTCCAGGCCACTGGGCGGTGAACAATGGCATCGACACCCGAG 1668
Db      455 ArgValIleArgTrpPheAspTyrLeuTrpAlaAsnLysLysThrValAspGluLysGlu 474
QY      1669 CTGTGCAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAG 1728
Db      475 ValLeuLysSerLeuProAspLysLeuLysAlaGluIleAlaIleAsnValHisLeuAsp 494
QY      1729 GTCCTG--CAGCTGCCACTGTTTGAGCGCGCCAGCCGCGCTGCTGCGGCGACTGTCT 1785
Db      495 ThrLeuArgLysValArgIlePheGlnAspCysGluAlaGlyLeuLeuValGluLeuVal 514
QY      1786 CTGGCCCTGCGGCCCGCCTTCTGCACGCCCGCGGAGTACCTCATCCACCAGCGATGCC 1845
Db      515 LeuLysLeuArgProAlaValPheSerProGlyAspTyrIleCysLysLysGlyAspIle 534
QY      1846 CTGAGGCCCTCTACTTTGTCTGTCTGGCTCCATGGAGTGCTC-----AAGGTGGC 1899
Db      535 GlyArgGluMetTyrIleIleLysGluGlyLysLeuAlaValAlaGluAspGlyIle 554
QY      1900 ACCGTGCTCGCCATCCTAGGGAAGGGCGACCTGATCGGC-----TGTGAGCTG 1947
Db      555 ThrGlnPheValValLeuGlyAspGlySerTyrPheGlyGluIleSerIleLeuAsnIle 574
QY      1948 CCCCGGCGGAGCAGGTGGTAAAGGCCAATGCCGACGTGAAGGGGCTGACGTACTGCGTC 2007
Db      575 LysGlySerLysSerGlyAsnArgArgThrAlaAsnIleArgSerIleGlyTyrSerAsp 594
QY      2008 CTGCAGTGTCTGCAGCTGGCTGGCTGCACGACAGCCCTTGGCTGTACCCCGAG 2061
Db      595 LeuPheCysLeuSerLysAspAspLeuMetGluAlaLeuThrGluTyrProGlu 612

RESULT 12
I50630
alpha subunit of cone photoreceptor CNG-channel - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C/Accession: I50630
R;Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.B
```

Neuron 10, 865-877, 1993  
A;Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels  
A;Reference number: I50630; MUID:93264082; PMID:7684234  
A;Accession: I50630  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-735 <BON>  
A;Cross-references: EMBL:X89598; NID:g908850; PIDN:CAA61757.1; PID:g908851  
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>  
F;524-648/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Alignment Scores:  
Pred. No.: 1.4e-14 Length: 735  
Score: 423.50 Matches: 149  
Percent Similarity: 40.74% Conservative: 115  
Best Local Similarity: 22.99% Mismatches: 224  
Query Match: 6.96% Indels: 160  
DB: 2 Gaps: 22

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x I50630 (1-735)

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QY      363 GGAGTGGCTCTCTTCTTAGTCTCTCACAAAGGA----- 395
Db      67 GlyArgGlyAlaMetAlaArgLeuSerArgPheValSerLeuArgSerTrpAlaThr 86
QY      396 -----CATCAGCGAAACCAAGAACCG-----AGGGGGCCC 425
Db      87 ArgHisLeuHisHisGluAspGlnArgProAspSerPheLeuGluArgIleArgGlyPro 106
QY      426 CGACAGATGGA-----GGAGACAGGTGG 449
Db      107 GluLeuValGluValSerSerArgGlnSerAsnIleArgSerPheLeuGlyIleArgGlu 126
QY      450 TGGCCGCGCCGATA-----TGGCCGGGCACGATCCAAAGGCTTCAATGCCAAC-- 498
Db      127 GlnProGlyGlyValAsnGlyProTrpPro-----LeuAlaArg-PheAsnValAsnPh 144
QY      499 -----CGCGCGCGAGCGCGCGTGTCTTACCACCTGTC 533
Db      144 eSerAsnAsnThrAsnGluAspLysLysGluGluLysLysGluValLysGluLysLy 164
QY      534 CGGCACCTGCAGAAGCAGCCCAAGGCAAGCAAGCTCAATAAAGGGGTGTTTGGGGA 593
Db      164 sGluGluLysLysGluLysLysGluGluLysLysAspAspLysLysAspAspLysLy 184
QY      594 GAAACCAAACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTGTT 653
Db      184 sAspAspLysLysAspAspLysLysLysGluGluGlnLysLysGluValPheValIleAs 204
QY      654 GCACGTGTGGGCACCTGAGAGCCACCTGGATGGCTTCATCTCTCGCCACACTCTATGT 713
Db      204 pProSerSerAsnMetTyrTyrAsnTrp-----LeuThrIleIl 217
QY      714 GGCTGTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCAGCGGAGCCAGTCCGCCCG 773
Db      217 eAlaAlaProValPheTyrAsnTrpCysMetLeuIleCysArg----- 231
QY      774 CGGCCCGCCAGCGTCTGT----- 792
Db      232 -----AlaCysPheAspGluLeuGlnIleAspHisIleLysLeuTrpLeuPh 247
QY      793 ---GACCTGGCCGTGGAGTCTCTTCATCCTTGACATTTGTCTGAATTTCCGTACCAC 848
Db      247 eLeuAspTyrCysSerAspIleIleTyrValPheAspMetPheValArgPheArgThrGl 267
QY      849 ATTCGTGTCCAAAGTCGGGCCAGGTGGTGTGTGCCCCCAAGTCCATTTGCCTCCACTACGT 908
Db      267 yPheLeu---GluGlnGlyLeuLeuValLysAspGluLysLysLeuArgAspHisTyrTh 286
QY      909 C---ACCACCTGGTTCCTGCTGGATGTTCATCGCAGCGCTGCCCTTTGACCTGCTACATGC 965
Db      286 rGlnThrValGlnPheLysLeuAspValLeuSerLeuLeuProThrAspLeuAlaTyr-- 305
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QY 966 CTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGGCCTGCTGGCCT 1025  
Db 306 -LeuLysLeuGlyLeuAsnTyrProGlu-----LeuArgPheAsnArgLeuLeuArgI 323  
QY 1026 GCTGGCTGCTTCCGGCGGTGGACCGGTACTCG----- 1059  
Db 323 eAlaArgLeuPheGluPhePheAspArgThrGluThrArgThrAsnTyrProAsnMetPh 343  
QY 1060 -CAGTACAGCGCGGTGGTGTGACACTGCTCATGGCCGTGTTGCGCCTGCTCGCGCACTG 1118  
Db 343 eArgIleGlyAsnLeuValLeuTyrIleLeu-----IleIleIleHisTr 358  
QY 1119 GGTCGCCTGCTGCTGTTTACATTGCCAGCGGAGATCGAGAGCAGCAATCC----- 1173  
Db 358 pAsnAlaCysIleTyrPheAlaIleSerLysValIleGlyPheGlyThrAspSerTrpVa 378  
QY 1174 -----GAGCTGCCTGAGATTGGCTGGCTGCAGGAGCTGGCCCGCCGACTGGA 1220  
Db 378 lTyrProAsnValSerIleProGluTyrGly-----ArgLeuSerArgLys----- 393  
QY 1221 GACTCCCTACTACTGTTGGCGCGGAGCCAGCTGGAGGGAACAGTCCGGCCAGAGTGA 1280  
Db 393 ----- 393  
QY 1281 CAACTGCAGCAGCAGCAGCGAGGCGCAACGGGACGGGCTGGAGTGTGGCGGCCGTC 1340  
Db 393 ----- 393  
QY 1341 GCTGCGCAGCGCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTCACCGGTGG 1400  
Db 394 -----TyrIleTyrSerLeuTyrTrpSerThrLeuThrLeuThrIleG 409  
QY 1401 CTTCGGCAACGTGTCCGCCAACACACGACACCGGAGAGATCTTCTCCATCTGCACCATGCT 1460  
Db 409 y---GluThrProProValLysAspGluGluTyrLeuPheValValIleAspPheLe 428  
QY 1461 CATCGCGCGCTGATGCACGCGGTGTTGGGAACGTGACGGCCATCATCCAGCGCAT 1520  
Db 428 uValGlyValLeuIlePheAlaThrIleValGlyAsnValGlySerMetIleSerAsnMe 448  
QY 1521 GTACGCGCGCGCTTCTGTACCACAGCCGCGCGACCTGCGGCACTACATCCGCAT 1580  
Db 448 tAsnAlaSerArgAlaGluPheGlnAlaLysValAspSerIleLysGlnTyrMetHisPh 468  
QY 1581 CCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGGC 1640  
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QY 1758 CAGCCGCGGCTGCTGCGGCACTGTCTCTGCGCCCTGCGGCGCCCTTCTGCACGCGCGG 1817  
Db 528 sGluAlaGlyLeuLeuIleGluLeuValLeuLysLeuLysProThrValPheSerProGl 548  
QY 1818 CGAGTACCTCATCCAAAGCGCATGCCCTGAGGCCCTCTACTTTGTCTGCTCTGGCTC 1877  
Db 548 yAspTyrIleCysLysLysGlyAspIleGlyArgGluMetTyrIleIleLysGluGlyLy 568  
QY 1878 CATGGAGGTGCTC-----AAGGTGGCACCGTGTGCTGCCATCTTAGGGAAGGCGCACCT 1931  
Db 568 sLeuAlaValValAlaAspAspGlyIleThrGlnPheValValLeuSerAspGlySerTy 588  
QY 1932 GATCGGC-----TGTGAGCTGCCCCGGGGGAGCAGGTGGTAAAGGCCAATGC 1979  
Db 588 rPheGlyGluIleSerIleLeuAsnIleLysGlySerLysSerGlyAsnArgArgThrAl 608  
QY 1980 CGACGTGAAGGGGCTGACGTACTGCGTCTCTGCAGTGTCTGCAGCTGGCTGGCCTGCACGA 2039

Db 608 aAsnIleArgSerIleGlyTyrSerAspLeuPheCysLeuSerLysAspLeuMetGl 628  
QY 2040 CAGCCTTGGCTGTACCCCGAG 2061  
Db 628 uAlaLeuThrGluTyrProGlu 635  
RESULT 13  
S52072  
DmCNGC protein - fruit fly (Drosophila sp.)  
C:Species: Drosophila sp.  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Jul-1999  
C:Accession: S52072  
R:Baumann, A.; Frings, S.; Godde, M.; Seifert, R.; Kaupp, U.B.  
EMBO J. 13, 5040-5050, 1994  
A:Title: Primary structure and functional expression of a Drosophila cyclic nucleotide-  
A:Reference number: S52072; MUID:95045396; PMID:7957070  
A:Accession: S52072  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-665 <BAU>  
C:Genetics:  
A:Gene: FlyBase:Cng  
A:Cross-references: FlyBase:FBgn0014462  
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-  
F:429-553/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>  
Alignment Scores:  
Pred. No.: 1.77e-14 Length: 665  
Score: 421.50 Matches: 155  
Percent Similarity: 43.27% Conservative: 102  
Best local Similarity: 26.09% Mismatches: 227  
Query Match: 6.92% Indels: 110  
DB: 2 Gaps: 23  
US-09-965-830-1\_COPY\_6\_3257 (1-3252) x S52072 (1-665)  
QY 393 GGACATCAGCGAAACCAAGAACCCAGAACCCAGAGGGGGCCCCGACAGATGGAAGAGACAGGTGGTGG 452  
Db 20 GlyGlnGlnThrAspAlaGluPro-----SerLysArgSerLys 32  
QY 453 CCGGCGCGATATGGCGGGCACGATCCAAAGGCTTCAATGCCAACCGCGCGGAGCGG 512  
Db 33 ProSerAlaLeu--ArgArgThrLeuGlnAlaLeuArg---GlnArgLeuThrLysArg 50  
QY 513 GGCGGTGCTCTACACCTGTCCGGGCACCTGCAGAAG-----CAGCCCAAGGCAAGCA 566  
Db 51 AsnArgProLysProPro-AspTrpPheLeuGluLysPheSerAsnThrThrAsnThrAs 70  
QY 567 CAAGCTCAATAAGGGGTGTTTGGGGAGAAACCAACTTGCCTGAGTACAAAGTAGCCGC 626  
Db 70 pLysIleArgLysGlyCys-----ProAlaMetGluAspAlaAlaLeuSerSe 86  
QY 627 CATCCGGAAGTCGCCCTTCATCCTGTTCACCTGTGGGGCAGTGCAGAGCC----- 675  
Db 86 rGluIleArgGlySerSerValLeu-----CysAsnArgLeuSerValAspProThrLe 104  
QY 676 -----ACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGTGTAC 722  
Db 104 uGlnSerHisTyrArgTrpLeuAlaIleValSerLeuAlaValLeuTyrAsnIleIlePh 124  
QY 723 TGTGCCCTACAGCGTGTGTGTGAGCACAGACAGCGGAGCCAGTGCAGCGCGCGGCCGCC 782  
Db 124 eVal-----ValGlyArgAlaValPheTrpGluIleAsnLysSerAlaPr 139  
QY 783 CAGC-----GTCTGTGACCTGGCGCGTGGAGGTCTCTTTCATCTTGACATGTGTCT 833  
Db 139 oAlaPheTrpTyrThrLeuAspTyrLeuCysAspPheIleTyrLeuLeuAspThrLeuVa 159  
QY 834 GAATTTCCGTACCACATTCGTGTCCCAAGTCGGGCCAGGTGGTGTGTTTGTCCCAAGTCCAT 893  
Db 159 lHisMetHisGluGlyPheLeuAspGln---GlyLeuLeuValArgAspAlaPheArgLe 178





Db 210 TyrLeuLeuAspMetPheValArgThrArgThrGlyTyrLeuGluGlnGlyLeuLeuVal 229  
QY 874 GTGTTTGGCCCAAGTCCATTGCTGCCTCCACTAGCTACCACTGGTTCCTGCTGGATGTC 933  
Db 230 ArgGluGluAlaLysLeuIleGluLysTyrLysSerAsnLeuGlnPheLysLeuAspPhe 249  
QY 934 ATCGCAGCGTGCCTTTGACCTGTCTACATGCTTCAAGGTCAAC---GTGTACTTCGGG 990  
Db 250 LeuSerValIleProThrAspLeuLeuArgIleSerArgMetPheGluPhePheGlnArgThrGlu 268  
QY 991 GCCCATCTGTGAAGACGGTGCCTGCTGCGCTGTCTGCGCTGTCTTCGCGGCTGGAC 1050  
Db 269 IleArgLeuAsnArgLeuLeuArgIleSerArgMetPheGluPhePheGlnArgThrGlu 288  
QY 1051 CGGTACTCGCAGTACAGCGCCGTGGTG---CTGACACTGCTCATGGCCGTGTTTCGCCCTG 1107  
Db 289 ThrArgThrAsnTyrProAsnIlePheArgIleSerAsnLeuValMetTyrIleValIle 308  
QY 1108 CTCGCGCACCTGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1167  
Db 309 IleIleHisTrpAsnAlaCysValTyrPheSerIleSerLysAlaIleGlyPheGlyAsn 328  
QY 1168 GAATCCGAGCTG-----CCTGAGATTGGTGGCTGTCAGGAGCTGGCC 1209  
Db 329 AspThrTrpValTyrProAspValAsnAspProGluPheGly-----ArgLeuAla 345  
QY 1210 CGCCGACTGGAGACTCCCTACTACCTGGTGGCCGAGGCCAGCTGGAGGAAACAGCTCC 1269  
Db 346 ArgLys----- 347  
QY 1270 GGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTGGAGCTGCTG 1329  
Db 347 ----- 347  
QY 1330 GGCGGCGCGTGCCTGCGCAGCGCTACATCACCTCCCTCTACTTCGCACTCAGCAGCCTC 1389  
Db 348 -----TyrValTyrSerLeuTyrTrpSerThrLeuThrLeu 359  
QY 1390 ACCAGCGTGGGTTGCGCAACGTGTCCGCCAACACGACACCGAGAGATCTTCTCCATC 1449  
Db 360 ThrThrIleGly---GluThrProProValArgAspSerGluTyrValPheValVal 378  
QY 1450 TGCACCATGCTCATCGGCGCCCTGTATGACCGCGGTGGTGTGTTGGAACTGACGGCCATC 1509  
Db 379 ValAspPheLeuIleGlyValLeuIlePheAlaThrIleValGlyAsnIleGlySerMet 398  
QY 1510 ATCCAGCGCATGTACGCCCGCGCTTCTGTACACAGCCGACCGCGACCTGCGCGAC 1569  
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QY 1570 TACATCCGCATCCACCGTATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAG 1629  
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QY 1630 GCCACCTGGCGGTGAACAATGGCATCGACACCAACCGAGCTGCTGCAGAGCCTCCCTGAC 1689  
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QY 1690 GAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGTCCCTG---CAGCTGCCACTG 1746  
Db 459 LysLeuArgAlaGluIleAlaIleAsnValHisLeuAspThrLeuLysLysValArgIle 478  
QY 1747 TTTGAGGCGGCCAGCGCGGTGCTGCTGCGGGCACTGTCTCTGGCCCTGCGGCCCGCCTTC 1806  
Db 479 PheAlaAspCysGluAlaGlyLeuLeuValGluLeuValLeuLysLeuGlnProGlnVal 498  
QY 1807 TGCACGCGCGCGAGTACCTCATCCACCAAGCGATGCCCTGCAGGCGCCTCTACTTTGTC 1866  
Db 499 TyrSerProGlyAspTyrIleCysLysLysGlyAspIleGlyArgGluMetTyrIleIle 518  
QY 1867 TGCTCTGGCTCCATGGAGGTGCTC-----AAGGTGGCACCGTGTCTGCTCGCCATCCTAGGG 1920  
Db 519 LysGluGlyLysLeuAlaValAlaAspAspGlyIleThrGlnPheValValLeuSer 538

QY 1921 AAGGGCGACCTGATCGGC-----TGTGAGCTGCCCCGGGCGAGCAGGTGGTA 1968  
Db 539 AspGlySerTyrPheGlyGluIleSerIleLeuAsnIleLysGlySerLysAlaGlyAsn 558  
QY 1969 AAGGCCAATCCGACGTGAAGGGCTGACGTACTCGTCTCGAGTGTCTGCACTGGCT 2028  
Db 559 ArgArgThrAlaAsnIleLysSerIleGlyTyrSerAspLeuPheCysLeuSerLysAsp 578  
QY 2029 GGCTGACACAGCCTTGGCTGTACCCGAGTTTCCCGCGCTTACGTGTCGCTC 2088  
Db 579 AspLeuMetGluAlaLeuThrGluTyrProAsp-----AlaLysThrMet 593  
QY 2089 CGAGGGAGCTCAGCTACAACCTGGTGGTGGGAGGCTCTGCAGAGTGGACACCAGC 2148  
Db 594 LeuGluGluLysGlyLysGlnIleLeuMetLysAspGlyLeuLeuAspIleAsnIleAla 613  
QY 2149 TCCCTGAGCGCGACAATACCCCTTATGTCCACGCTGGAGGAGAGAGACA 2199  
Db 614 AsnAlaGlySerAsp-----ProLysAspLeuGluGluLysValThr 627  
RESULT 15  
S74179  
cyclic nucleotide-gated channel protein - human  
C;Species: Homo sapiens (man)  
C;Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 16-Jul-1999  
C;Accession: S74179  
R;Yu, W.P.; Grunwald, M.E.; Yau, K.W.  
FEBS Lett. 393, 211-215, 1996  
A;Title: Molecular cloning, functional expression and chromosomal localization of a human cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-gated channel; ion channel; ion transport; membrane protein  
C;Keywords: ion channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>  
F;482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>  
Alignment Scores:  
Pred. No.: 2.12e-14 Length: 695  
Score: 420.00 Matches: 141  
Percent Similarity: 42.25% Conservative: 96  
Best Local Similarity: 25.13% Mismatches: 218  
Query Match: 6.90% Indels: 106  
DB: 2 Gaps: 17  
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QY 787 GTCTGTGACCTGGCGCTGGAGGTCTCTTTCATCTTGACATTGTGCTGAATTCGTACC 846  
Db 205 ValLeuAspTyrSerAlaAspValLeuTyrValLeuAspValLeuValArgAlaArgThr 224  
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Db 264 ---LeuLysValGlyThrAsnTyrProGlu-----ValArgPheAsnArgLeuLys 280  
QY 1024 CTGCTGGCGCTGCTTCCGCGGCTGGACCGGTACTCG----- 1059  
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Db 316 TrpAsnAlaCysIleTyrPheAlaIleSerLys----- 326  
Qy 1177 CTGCCTGAGATTGGCTGGCTGCAGGAGTGGCCCGCCGACTGGAGACTCCCTACTACCTG 1236  
Db 327 -----PheIleGlyPhe----- 330  
Qy 1237 GTGGGCCGAGGCCAGCTGGAGGGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGC 1296  
Db 331 -----GlyThrAspSerTrpValTyrProAsnIleSerIlePro 343  
Qy 1297 AGCGAGGCCAACGGGACGGGGCTGGAGCTGCTGGGCGGCCCTCGCTGGCAGCGCCTAC 1356  
Db 344 GluHisGlyArg-----LeuSerArgLysTyr 352  
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Qy 1834 CAAGGCGATGCCCTGCAGGCCCTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTC--- 1890  
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Qy 1891 ---AAGGTGGCACCGTGTCTCGCCATCCTAGGGAAGGCGACCTGATCGGC----- 1938  
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Db 627 LeuGluGluLysValGluGlnLeuGlySerSerLeuAspThrLeuGlnThrArgPheAla 646  
Qy 2296 AAGCTGCTATCCCCACGTCGAACAGCACCC-----CGGCTCGTCTA----- 2337  
Db 647 ArgLeuLeuAlaGluTyrAsnAlaThrGlnMetLysMetLysGlnArgLeuSerGlnLeu 666  
Qy 2338 -----GGTGGCAGAGGGAGGCCAGGCAGGCAGGGGCTTTGAAGGCTGAG 2382  
Db 667 GluSerGlnValLysGlyGlyAspLysProLeuAlaAspGlyGluValProGlyAsp 686  
Qy 2383 GCT 2385  
Db 687 Ala 687

Search completed: September 1, 2004, 15:40:30  
Job time : 225.5 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2004, 14:38:36 ; Search time 5277 Seconds  
(without alignments)  
18402.845 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257  
Perfect score: 3252  
Sequence: 1 atgcgcgcacatcgccggcct.....aagaaggcacaggggtctga 3252

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	844.4	26.0	1114	14 U69184	U69184 U69184 Soar
2	802.4	24.7	896	12 BM452074	BM452074 AGENCOURT
3	783.4	24.1	4015	11 AK048629	AK048629 Mus muscu
4	675.6	20.8	862	13 BU187340	BU187340 AGENCOURT

5	662.8	20.4	766	10	BE795800	BE795800 601590834
6	658.4	20.2	714	10	BE778330	BE778330 601463723
7	608.6	18.7	617	10	AW249035	AW249035 2820908.5
8	582.4	17.9	704	14	CD354565	CD354565 UI-M-GM0-
9	550.6	16.9	651	9	AL134774	AL134774 DKFZp547I
10	492	15.1	501	10	AW249298	AW249298 2821074.5
11	477	14.7	865	14	CD106245	CD106245 AGENCOURT
12	470	14.5	482	10	BE266788	BE266788 601190482
13	424	13.0	424	9	AI272282	AI272282 ap23c04.x
14	369.8	11.4	682	13	BQ444229	BQ444229 UI-M-EX0-
15	361	11.1	522	12	BI975332	BI975332 483675 MA
16	345	10.6	710	12	BQ045257	BQ045257 UI-CF-EN1
17	337.4	10.4	387	14	R35526	R35526 YG64e08.r1
18	328.4	10.1	463	14	R73353	R73353 Yl10e04.r1
19	315.6	9.7	572	14	CB055396	CB055396 NISC_jj03
20	313	9.6	391	14	R13511	R13511 Yf59c02.r1
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22	305.6	9.4	328	9	AA325048	AA325048 EST27976
23	301.4	9.3	1076	12	BM561167	BM561167 AGENCOURT
24	294.4	9.1	1115	12	BM547060	BM547060 AGENCOURT
25	284.2	8.7	351	14	R35105	R35105 YG59f09.r1
26	278.8	8.6	839	12	BI737339	BI737339 603357994
27	271.4	8.3	438	14	CB751495	CB751495 AMGNNUC:N
28	261.8	8.1	337	10	BF449484	BF449484 maa43d03.
29	259.8	8.0	909	13	BM391570	BM391570 BX391570
30	258.8	8.0	924	14	CA454037	CA454037 AGENCOURT
31	256	7.9	878	13	BU170580	BU170580 AGENCOURT
32	255.8	7.9	615	14	CB579755	CB579755 AMGNNUC:N
33	250.2	7.7	438	29	CG479581	CG479581 OST10634
34	246.6	7.6	635	10	BF589083	BF589083 nac29h08.
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38	242.2	7.4	784	13	BU707166	BU707166 UI-M-FR0-
39	239.6	7.4	815	12	BM948237	BM948237 UI-M-EG0P
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41	234	7.2	558	9	AI450906	AI450906 ms26e01.x
42	232.6	7.2	315	13	BY363096	BY363096 BY363096
43	228	7.0	926	13	BX327696	BX327696 BX327696
44	227.8	7.0	475	9	AW082228	AW082228 xb64c03.x
45	227.4	7.0	2894	29	AY409916	AY409916 Mus muscu

ALIGNMENTS

RESULT 1	U69184	U69184	1114 bp	mRNA	linear	EST 27-OCT-1999
LOCUS	U69184	Soares	infant brain	INIB	Homo sapiens	cDNA clone 37299, mRNA
DEFINITION	U69184	sequence.				
ACCESSION	U69184	U69184.1	GI:2739408			
VERSION	U69184.1	GI:2739408				
KEYWORDS	EST.					
SOURCE	Homo sapiens	(human)				
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 1114)				
AUTHORS	Volorio,S., Simon,G., Repetto,M., Cucciard,M., Banfi,S., Borsani,G., Ballabio,A. and Zollo,M.					
TITLE	Sequencing analysis of forty-eight human image cDNA clones similar to drosophila mutant protein					
JOURNAL	DNA Seq. 9	(5-6), 307-315	(1998)			
MEDLINE	99452388					
PUBMED	10524757					
COMMENT	Contact: Zollo, Massimo Telethon Institute of Genetics and Medicine Via Olgettina 58, Milan, MI 20132, Italy Email: zollo@tigem.it. Location/Qualifiers 1. .1114 /organism="Homo sapiens"					
FEATURES	source					



QY 532 TCCGGGCACCTGTCAGAAAGCAGCCCAAGGGCAAGCACAAAGCTCAATAAGGGGTGTTTGGG 591  
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RESULT 3  
AK048629  
LOCUS AK048629 4015 bp mRNA linear HTC 20-SEP-2003  
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30090D05 product:ELK CHANNEL 3 (FRAGMENT) homolog [Rattus norvegicus], full insert sequence.  
ACCESSION AK048629  
VERSION AK048629.1 GI:26339459  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6 (bases 1 to 4015)  
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.  
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Db	1828	GGAGCAAAATTATCAATTAAAGACCAAGTGATCAAGACCAACGCTGATGTGAAGGCGCTG	1887
Qy	1996	ACGTACTGCGTCTGTCAGTGTCTGCAGCTGGCTGGCCTGCACGACAGCCTTGCGCTGTAC	2055
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Db	1948	CCAGAGTATGCACACAAATTCGTAGAAGACATCCAGCACGACCTCACATACAACCTTCGA	2007
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Db	2008	GAAGG 2012	
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DEFINITION			
5', mRNA sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 763; Conservative			
Qy			
Db			

Qy	605	TGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGG	664
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Db	361	ACGTACCACTGGTTCCTGCTGGATGTCTATCGCAGCGCTGCCCTTTGACCTGCTACATG	420
Qy	965	CCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCGCCCTGCTGGCC	1024
Db	421	CCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCGCCCTGCTGGCC	480
Qy	1025	TGCTGCGCTGCTTCCGCGGTGGACCGGTACTCGCAGTACAGCG-CCGTGGTGTGACA	1083
Db	481	TGCTGCGCTGCTTCCGCGGTGGACCGGTACTCGCANACAGCGCCGTGGTGTGCTGACA	540
Qy	1084	CTGCTCATGGCCGTGTTTCGCCCTGCTCGGCACCTGGGTGCGCTTGGTGTGTTTACAT	1142
Db	541	CTGCTCATGGCCGTGTTTCGCCCTGCTCGGCACCTGGGTGCGCTTGGTGTGTTTACAT	600
Qy	1143	TGGCCAGC-GGGAGATCGAGAGCAGCAATCCGAGCTGCCCT-GAGATTGGCTGGCTGCAG	1200
Db	601	TGGCCAGCNGGGAGATCGAGAGCAGCAATCCGAGCTGCCCTGCTGAGAGCTGGCTGCAG	660
Qy	1201	GAGTGGCCCGCCGACTGGAGACTCCCTACTACCTTGGTGGG--CCGGAGCCAGCTGGAG	1258
Db	661	GAGTGGCCCGCCGACTGGAGACTCTANTTTACTGGGGGGGGCCGGAGCCAGCCTGGAG	720
Qy	1259	GGAACAGC-TCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGCCAAACGGGACGGG	1317
Db	721	GGAACAGCTTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGCGGCAACCGGACGGG	780
Qy	1318	CTGGAGCTGCTGGGCGGCCCGCTGCTG 1344	
Db	781	GGCTGGAACCTGCTGGGCGGGGCCCCCG 807	
RESULT 5			
BE795800			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 763; Conservative			
Qy			
Db			

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: LLCMB02 row: d column: 10  
 High quality sequence start: 5  
 High quality sequence stop: 763.

## ORIGIN

Query Match	20.4%;	Score 662.8;	DB 10;	Length 766;
Best Local Similarity	96.4%;	Pred. No. 1.3e-97;		
Matches 744;	Conservative	0;	Mismatches 17;	Indels 11;
				Gaps 6;

[illegible]

Qy 2279 CCTCATCTCAGTGCCAAAGCTGCTATCCCCACGTCGAACAGACCCCCGGCCTCGTCTAG 2338

Db 64 CCTCATCTCAGTGCCAAAGCTGCTATCCCCACGTCGAACAGACCCCCGGCCTCGTCTAG 123

Qy	2339	GTGGCAGAGGAGGCAGGCAGGCAGGGCTTTGAAGCGCTGAGGCTGGCCCCCTCGCTC	2398
Db	124	GTGGCAGAGGAGGCAGGCAGGCAGGGCTTTGAAGCGCTGAGGCTGGCCCCCTCGCTC	183

Qy	Db
2399	184
CCCCACGGGCCCTAGAGGGGCTACGGCTGCCCGCCCATGCCATGGAATGTGCCCGCAGATC	CCCCACGGGCCCTAGAGGGGCTACGGCTGCCCGCCCATGCCATGGAATGTGCCCGCAGATC
2458	243

[illegible]

Qy	db
2519	CTTTCCGCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCCTCCCTCGACACAGAGA 2578
303	CTTTCCGCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCCTCCCTCGACACAGAGA 362

[illegible]

QY 2639 AGCTTCGGCAGGCGGTGACAGAGCTGTTCAGAGCAGGTGCTGCAGATCGCGGAAGGACTGC 2698

Db 423 AGCTTCGGCAGGCGGTGACAGAGCTGTTCAGAGCAGGTGCTGCAGATCGCGGAAGGACTGC 482

Qy	2699	AGTCAC	TTGGCC	AGGCTG	TGCAGC	TTGTCT	CTGGCG	CCCCCA	CAGGGAG	GGTCCG	TGCCCC	TC	2758
Db	483	AGTCAC	TTGGCC	AGGCTG	TGCAGC	TTGTCT	CTGGCG	CCCCCA	CAGGGAG	GGTCCG	TGCCCC	TC	542

QY	2759	GGGCATCGGAGAGGGGGCCGTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCCTCTGTGTG	2818
Db	543	GGGCATCGGAGAGGGGGCCGTGCCAGCCAGCACCTCCGGGCTTCTGCAGCCCTCTGTGTG	602

Qy 2819 TGGACACTGGGCATCCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTTGAGTGGGA 2878

Db	603	TGGACACTGGGGCATCTCCTACTGCCTGCAG-CCCCAGCTGGCTCTGTCTTGAGTGGGA	661
QY	2879	CTTGGCCCCACCCTCGTCGCGGGGCCCTCCTCCCTCATGGCACCCCTGGCCCCCTGGGGTCCCC	2938
Dd	662	CTTGG-CCCACCCCTCGTCGCGGGGCCCTCCTCCC-----TCATGCACCTGGCCTGGGGT-CCC	715
QY	2939	CAGCGTCTCAGAGCTCCCCCTGGCCCTCGAGCCACAGCTTTCTGGACCTCCAC	2990
Dd	716	CAGCGTCTCAGAGCTCGCCTGGCTCGAG---CACAGCTTTCTGGACTTCCAC	764

RESULT	6
BE778330	
LOCUS	
DEFINITION	714 bp mRNA linear EST 20-OCT-2000 601463723F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867076 5', mRNA sequence.
ACCESSION	BE778330
VERSION	BE778330.1 GI:10199528
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

# FEATURES

## ORIGIN

Query Match	20.2%	Score 658.4;	DB 10;	Length 714;
Best Local Similarity	99.3%	Pred. No. 6.4e-97;		
Matches 703; Conservative	0;	Mismatches 1;	Indels 4;	Gaps 4;

Oy	377	TCCTAGTCTCTCAAGAAGACATCAGCGAAACCAAGAACCGAGGGGCCCCGACAGATGGA	436
Dd	1	TCCTAGTCTCTCAAGAAGACATCAGCGAAACCAAGAACCGAGGGGCCCCGACAGATGGA	60

Qy 437 AGGAGACAGGTGGTGGCCGGCGCCGGATATGGCCGGGCACGATCAAAGGCTTCAATGCCA 496

Db 61 AGGAGACAGGTGGTGGCCGGCGCCGGATATGGCCGGGCACGATCAAAGGCTTCAATGCCA 120

Qy	Db
497	121

QY 557 AGGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCAAACTTGCCTGAGTACA 616

Db 181 AGGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCAAACTTGCCTGAGTACA 240



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QY 617 AAGTAGCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACCTGTGGGGCACTGAGAGCCA 676
    |||||||
Db 241 AAGTAGCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACCTGTGGGGCACTGAGAGCCA 300

QY 677 CTTGGGATGGCTTCATCCTGCTGCGCACACTCTATGTGGCTGTCACTGTGCCCTACAGCG 736
    |||||||
Db 301 CTTGGGATGGCTTCATCCTGCTGCGCACACTCTATGTGGCTGTCACTGTGCCCTACAGCG 360

QY 737 TGTGTGTGAGCACAGCACGGGAGCCAGTCGCCCGCGCGCCCGCCAGCGTCTGTGACC 796
    |||||||
Db 361 TGTGTGTGAGCACAGCACGGGAGCCAGTCGCCCGCGCGCCCGCCAGCGTCTGTGACC 420

QY 797 TGGCGGTGG-AGGTCCTCTTCATCCTTGACATTTGCTGAATTTCCGTACCACATTCGTG 855
    |||||||
Db 421 TGGCGGTGGCAGGTCCTCTTCATCCTTGACATTTGCTGAATTTCCGTACCACATTCGTG 480

QY 856 TCCAAGTCGGGCCAGGTGGTGTGTTGCCCCAAAGTCCATTTGCCCTCCACTACGTCACCACC 915
    |||||||
Db 481 TCCAAGTCGGGCCAGGTGGTGTGTTGCCCCAAAGTCCATTTGCCCTCCACTACGTCACCACC 540

QY 916 TGGTTCCTGCTGGATGTCATCGAGCGCTGCCCTTTGACCTGTACATGCTTCAAGGTC 975
    |||||||
Db 541 TGGTTCCTGCTGGATGTCATCGAGCGCTGCCCTTTGACCTGTACATGCTTCAAGGTC 600

QY 976 AACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCTGCTGCGCCTGCTGCGCCTG 1035
    |||||||
Db 601 AACGTGTACTTCGGGG-CCATCTGCTGAAGACGGTGCCTGCTGCGCCTGCTGCGCCTG 659

QY 1036 CTTCCGCGGCTGGACCGGTACTCGCAGTA-CAGCGCGGTGGTGTGAC 1082
    |||||||
Db 660 CTTACGCGG-TGGACCGGTACTCGCAGTACCAGCGCGGTGGTGTGAC 706
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```
RESULT 7
AW249035
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 617)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2820908.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu
Plate: LLCM5 row: G column: 21
High quality sequence stop: 569.
Location/Qualifiers
1..617
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820908"
/tissue_type="small cell carcinoma"
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
ORIGIN
Query Match 18.7%; Score 608.6; DB 10; Length 617;
Best Local Similarity 99.3%; Pred. No. 7.5e-89;
Matches 611; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2431 CCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCCAGGGTAGTAGATGGCATTGAAGAC 2490
    |||||||
Db 3 CACGAGGCATGGAATGTGCCCCCAGATCTGAGCCCCAGGGTAGTAGATGGCATTGAAGAC 62

QY 2491 GGCTGTGGCTCGGACCAAGTCTCTTTCCGCGTGGGCCAGTCTGGCCCCGGAATGT 2550
    |||||||
Db 63 GGCTGTGGCTCGGACCAAGTCTCTTTCCGCGTGGGCCAGTCTGGCCCCGGAATGT 122

QY 2551 AGCAGAGCCCCCTCCCTGGACCAAGAGCGGCTGCTACCTGTTCCCCATGGGCCCAGC 2610
    |||||||
Db 123 AGCAGAGCCCCCTCCCTGGACCAAGAGCGGCTGCTACCTGTTCCCCATGGGCCCAGC 182

QY 2611 GAGGCAAGGAACACAGACACACTGGACAAAGCTTCGGCAGGCGGTGACAGAGCTGTGAG 2670
    |||||||
Db 183 GAGGCAAGGAACACAGACACACTGGACAAAGCTTCGGCAGGCGGTGACAGAGCTGTGAG 242

QY 2671 CAGGTGCTGCAGATCGGGAAGGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTG 2730
    |||||||
Db 243 CAGGTGCTGCAGATCGGGAAGGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTG 302

QY 2731 GCGCCCCACAGGAGGGTCCGTGCCCTCGGGCATCGGGAGAGGGGCGTGTGCCCGCCAGC 2790
    |||||||
Db 303 GCGCCCCACAGGAGGGTCCGTGCCCTCGGGCATCGGGAGAGGGGCGTGTGCCCGCCAGC 362

QY 2791 ACCTCCGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGGCATCTCTACTGCTGCAG 2850
    |||||||
Db 363 ACCTCCGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGGCATCTCTACTGCTGCAG 422

QY 2851 CCCCCAGCTGGCTCTGTCTTGTAGTGGACTTGGCCCCACCCCTGTCGGGGCCCTCTCCC 2910
    |||||||
Db 423 CCCCCAGCTGGCTCTGTCTTGTAGTGGACTTGGCCCCACCCCTGTCGGGGCCCTCTCCC 482

QY 2911 CTCATGGCACCCCTGGCCCTGGGTCGCCCGAGCGTCTCAGAGCTCCCGCTGGCGCTCGAGCC 2970
    |||||||
Db 483 CTCATGGCACCCCTGGCCCTGGGTCGCCCGAGCGTCTCAGAGCTCCCGCTGGCGCTCGAGCC 542

QY 2971 ACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGCTCT 3030
    |||||||
Db 543 ACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCAGGAGACCTCTGCTCT 602

QY 3031 GAGCCCCAGCACCCCT 3045
    |||||||
Db 603 GAGCCCCAGCACCCCT 617
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RESULT 8
CD354565
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CD354565
UI-M-GMO-c9d-j-01-0-UI.r1 NIH_BMAP_GMO Mus musculus cDNA clone
IMAGE:30361272 5', mRNA sequence.
CD354565
CD354565.1 GI:31147066
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 704)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pyX-5.

FEATURES  
source

Location/Qualifiers

1..704  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30361272"  
/tissue\_type="whole brain"  
/dev\_stage="1, 5 and 15 days newborn"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP\_GMO"  
/note="Organ: Brain; Vector: pyX- Asc; Site\_1: Ecor I;  
Site 2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was size  
selected according to mRNA size fraction, ligated with Ecor  
I adaptor, digested with NotI and then cloned  
directionally into pyX-Aec vector. The library tag  
sequence located between the Not I site and the polyA tail  
is CGAAGTGAAT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

ORIGIN

Query Match 17.9%; Score 582.4; DB 14; Length 704;  
Best Local Similarity 89.2%; Pred. No. 1.4e-84;  
Matches 628; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1661 CCACGAGCTGTCGAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGGCATGCACCTGC 1720  
Db |||||  
1 CCACTGAGCTGTCGAGAGCCTCCCGGATGAGCTTCGTGCAGACATCGGCATGCACCTGC 60  
QY 1721 ACAAGGAGTCCCTGCAGCTGCCACTGTTTGAGGCGGCCAGCGCGCTGCCTGCGGGCAC 1780  
Db |||||  
61 ACAAGGAAGTCTGCAGCTGCCGCTGTTTCGAGGCCGCCAGCCGTGGCTGCCTGCGGGCGC 120  
QY 1781 TGTCTCTGGCCCTGCGGCCGCTTCTGACGCGCGGCGAGTACCTCATCCACCAAGGCG 1840  
Db |||||  
121 TGTCCCTGGCCCTGAGGCGCGCCTTCTGACGCGCGGCGAGTACCTCATTCACCAAGGCG 180  
QY 1841 ATGCCCTGCAGGCCCTCTACTTTTGTCTGCTTGGCTCCATGGAGGTGCTCAAGGGTGGCA 1900  
Db |||||  
181 ATGCTCTCCAGGCCCTCTATTTTGTCTGCTCGGGTTCATGGAGGTCTCAAAGGTGGCA 240  
QY 1901 CCGTGTCCCATCTAGGGAAGGCGACCTGATCGGCTGTGAGCTGCCCGCGGGGAGC 1960  
Db |||||  
241 CCGTGTCCCATCTAGGGAAGGGTGACCTGATCGGCTGCGAGCTGCCCGCAGCGGGAAC 300  
QY 1961 AGGTGGTAAAGCCAATGCCGACGTGAAGGGGTGACGTACTGCTGCTGTCAGTGTCTGC 2020  
Db |||||  
301 AAGTAGTAGGCAATGCAGCGTGAAGGGGTGACATACTGCGTCTCTACAGTGTCTGC 360  
QY 2021 AGCTGGCTGGCCTGCACGACAGCCTTGGCTGTACCCCGAGTTTGGCCCGCGCTTCAGTC 2080

Db 361 AGTTGGCTGGGCTGCATGAGAGCCTTGCTCTGTACCCCTGAGTTTGCCCCACGCTTAGCC 420  
QY 2081 GTGGCCTCCGAGGGAGCTCAGCTACAACCTTGGGTGCTGGGGAGGCTCTGCAGAGGTGG 2140  
Db |||||  
421 GTGGCCTCCGAGGGAGCTCAGCTACAACCTTGGGAGCTGGTGGAGTCTCTGCGAGGTGG 480  
QY 2141 ACACCAGCTCCTGAGCGGGGACAATACCTTATGTCCACGCTGGAGGAGGAGACAG 2200  
Db |||||  
481 ATACCAGCTCCTGAGTGGTGACAACACCTCATGTCCACACTGGAGGAGGAGACAG 540  
QY 2201 ATGGGAGAGCGGCCCTCAGGTCTCCCGAGCCCCCAGCTGATGAGCCCTCCAGCCCCCTGC 2260  
Db |||||  
541 ATGGGAGAGCAGGACACACGCTCTCACAGCCCCCAGCAGATGAGCCCTCCAGTCCCTGC 600  
QY 2261 TGTCCCTGGTGCACCTCCTCATCTCAGCTGCCAAGCTGCTATCCACAGTCGAACAG 2320  
Db |||||  
601 TGTGCGCCCGCTGTACCTCCTCCTCAGCGGCCAACTACTCTCCCGACGTCGAACAG 660  
QY 2321 CACCCCGGCTCGTCTAGGTGGCAGAGGAGGCCAGGCGGCA 2364  
Db |||||  
661 CGCCTCGGCCGAGGTGGGTGGCAGAGGCGGCCAAGTAGGGCA 704

RESULT 9

AL134774

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL134774 651 bp mRNA linear EST 04-SEP-2003  
DKFZp547I2290 rl 547 (synonym: hfbrl) Homo sapiens cDNA clone  
DKFZp547I2290 5', mRNA sequence.  
AL134774  
AL134774.1 GI:6602961  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 651)  
Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).  
EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and  
Wiemann, S.)  
Unpublished (1999)  
Contact: MIPS  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email [s.wiemann@dkfz-heidelberg.de](mailto:s.wiemann@dkfz-heidelberg.de);  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp547I2290) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: [clone@rzpd.de](mailto:clone@rzpd.de).

FEATURES

source

1..651  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp547I2290"  
/tissue\_type="brain"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_lib="547 (synonym: hfbrl)"  
/note="Vector: pAMP1; Site\_1: NotI; Site\_2: SalI"

ORIGIN

Query Match 16.9%; Score 550.6; DB 9; Length 651;  
Best Local Similarity 98.8%; Pred. No. 2.1e-79;  
Matches 553; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 272 AGGAGTCAAGGCTGAGCTGATCTCTGTCAGGAGCGGGCTCCGTTCTGTGTCTCC 331  
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Db 1 AGGAGTTCAAGGCTGAGCTGATCCTGTACCGGAAGAGCGGGCTCCCGTTCTCGTGTCTCC 60

QY 332 TGGATGTGATACCCATAAAGATGAGAAAGGGGAGGTGGCTCTCTTCTTAGTCTCTCACA 391

Db 61 TGGATGTGATACCCATAAAGATGAGAAAGGGGAGGTGGCTCTCTTCTTAGTCTCTCACA 120

QY 392 AGGACATCAGCGAAACCAAGAACCGAGGGGCCCCGACAGATGGAAGGAGACAGGTGGTG 451

Db 121 AGGACATCAGCGAAACCAAGAACCGAGGGGCCCCGACAGATGGAAGGAGACAGGTGGTG 180

QY 452 GCCGGCGCGATATGGCCGGCACGATCCAAAGGCTTCAATGCCAACCGGGCGGAGGCC 511

Db 181 GCCGGCGCGATATGGCCGGCACGATCCAAAGGCTTCAATGCCAACCGGGCGGAGGCC 240

QY 512 GGGCCGTGCTCTACCACTGTCCGGGCACCTGCAGAAAGCAGGCCCAAGGGCAAGCACAAGC 571

Db 241 GGGCCGTGCTCTACCACTGTCCGGGCACCTGCAGAAAGCAGNCCAAGGGCAAGCACAAGC 300

QY 572 TCAATAAGGGGTGTTTGGGAGAAAACCAACTTGCCTGAGTACAAAGTAGCCGCCATCC 631

Db 301 TCAATAAGGGGTGTTTGGGAGAAAACCAACTTGCCTGAGTACAAAGTAGCCGCCATCC 360

QY 632 GGAAGTCGCCCTTCACTCTGTCACCTGTGGGCACTGAGAGCCACCTGGGATGGCTTCA 691

Db 361 GGAAGTCGCCCTTCACTCTGTCACCTGTGGGCACTGAGAGCCACCTGGGATGGCTTCA 420

QY 692 TCCTGCTGCCACACTCTATGTGGTGTCACTGTGCCCTACAGCGTGTGTGAGCACAG 751

Db 421 TCCTGCTGCCACACTCTATGTGGTGTCACTGTGCCCTACAGCGTGTGTGAGCACAG 480

QY 752 CACGGAGCCCAGTGCCGCCCGCGGCCCGCCAGCGTCTGTGACCTGGCCGTGGAGGTCC 811

Db 481 CACGGAGCCCAGTGCCGNCCCGGTCCGCCAGNGTCTGTGACCTGGCCGTGGAGGTCC 540

QY 812 TCCTCATCCTTGACATTGTG 831

Db 541 TCCTCATCCTTGTTACTGTG 560

RESULT 10

AW249298

LOCUS

DEFINITION

AW249298

AW249298.1 GI:6592291

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW249298

2821074.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821074 5',

mRNA sequence.

AW249298

AW249298.1 GI:6592291

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 501)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other\_ESTs: 2821074.3prime

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu>

Plate: LLCM5 row: N column: 19

High quality sequence stop: 500.

Location/Qualifiers

1. .501

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2821074"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 15.1%; Score 492; DB 10; Length 501;

Best Local Similarity 100.0%; Pred. No. 6.3e-70;

Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1263 CAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCAACGGGAGCTGGA 1322

Db 10 CAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCAACGGGAGCTGGA 69

QY 1323 GCTGTGGCGGGCCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAG 1382

Db 70 GCTGTGGCGGGCCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTCAG 129

QY 1383 CAGCCTCACCAGCGTGGGCTTCGGCAACGTTGCCCAACGTTGCCCAACGAGATCTT 1442

Db 130 CAGCCTCACCAGCGTGGGCTTCGGCAACGTTGCCCAACGAGATCTT 189

QY 1443 CTCCATCTGCACCATGCTCATCGCGCCCTGATGCAACGCGTGGTGTGGAAACGTGAC 1502

Db 190 CTCCATCTGCACCATGCTCATCGCGCCCTGATGCAACGCGTGGTGTGGAAACGTGAC 249

QY 1503 GGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCAAGCCGACCGCGACCT 1562

Db 250 GGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCAAGCCGACCGCGACCT 309

QY 1563 GCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTA 1622

Db 310 GCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCGCATGCTGGAGTA 369

QY 1623 CTTCCAGCCACCTGGCGGTGAACAATGGCATCGACACCAAGCGAGTGTGCAGAGCCT 1682

Db 370 CTTCCAGCCACCTGGCGGTGAACAATGGCATCGACACCAAGCGAGTGTGCAGAGCCT 429

QY 1683 CCCTGACGAGCTGGCGGAGACATCGCCATGCACCTGCACAAGGAGTCTTCGAGCTGCC 1742

Db 430 CCCTGACGAGCTGGCGGAGACATCGCCATGCACCTGCACAAGGAGTCTTCGAGCTGCC 489

QY 1743 ACTGTTTGAGGC 1754

Db 490 ACTGTTTGAGGC 501

RESULT 11

CD106245

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

CD106245

AGENCOURT\_13980050 NIH\_MGC\_179 Homo sapiens cDNA clone

IMAGE:30368984 5', mRNA sequence.

CD106245

CD106245.1 GI:30759419

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 865)

NIH-MGC <http://mgc.nci.nih.gov/>.



TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM432 row: k column: 09  
High quality sequence stop: 548.  
Location/Qualifiers  
1. .865  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30368984"  
/tissue\_type="Pituitary"  
/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances) "  
/clone\_lib="NIH\_MGC\_179"  
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site\_1: EcoRV  
(destroyed); Site\_2: NotI; Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.1 kb. Library was  
constructed by (Invitrogen). Note: this is a NIH\_MGC  
Library."

ORIGIN

Query Match 14.7%; Score 477; DB 14; Length 865;  
Best Local Similarity 100.0%; Pred. No. 2.1e-67;  
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2776 CCGTGGCCAGCCAGCACCTCCGGGCTTCTGGCAGCCTCTGTGTGGACACTGGGGCATCC 2835  
Db |||||  
1 CCGTGGCCAGCCAGCACCTCCGGGCTTCTGGCAGCCTCTGTGTGGACACTGGGGCATCC 60

QY 2836 TCCTACTGCTGCAGCCCCCAGCTGGCTCTGTCTTGTAGTGGGACTTGGCCCCACCCCTCGT 2895  
Db |||||  
61 TCCTACTGCTGCAGCCCCCAGCTGGCTCTGTCTTGTAGTGGGACTTGGCCCCACCCCTCGT 120

QY 2896 CCGGGGCTCTCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCAGCGTCTCAGAGCTCC 2955  
Db |||||  
121 CCGGGGCTCTCTCCCTCATGGCACCCCTGGCCCTGGGGTCCCCAGCGTCTCAGAGCTCC 180

QY 2956 CCCTGGCTTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCA 3015  
Db |||||  
181 CCCTGGCTTCGAGCCACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCCTCA 240

QY 3016 GGAGACCTCTGCTGTAGCCCCAGCACCCCTGCCTCCCTCCCTCTCTGAGGAAGGGCT 3075  
Db |||||  
241 GGAGACCTCTGCTGTAGCCCCAGCACCCCTGCCTCCCTCCCTCTCTGAGGAAGGGCT 300

QY 3076 AGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCCAGCACTGGAGAGCCCCCA 3135  
Db |||||  
301 AGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCCAGCACTGGAGAGCCCCCA 360

QY 3136 CCAGGFTCAGGGGGCCTGGCCCTTGCCCTGGGACCCCCACAGCCTGGAGATGGTCTTATT 3195  
Db |||||  
361 CCAGGFTCAGGGGGCCTGGCCCTTGCCCTGGGACCCCCACAGCCTGGAGATGGTCTTATT 420

QY 3196 GGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGCACAGGGGTCTGA 3252  
Db |||||  
421 GGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGCACAGGGGTCTGA 477

RESULT 12  
BE266788  
LOCUS 601190482F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3534309 5',  
DEFINITION mRNA sequence.  
ACCESSION BE266788

VERSION BE266788.1 GI:9140371  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 482)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Plate: LLCM213 row: d column: 22  
High quality sequence stop: 482.  
Location/Qualifiers  
1. .482  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3534309"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant) "  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 14.5%; Score 470; DB 10; Length 482;  
Best Local Similarity 99.8%; Pred. No. 2.3e-66;  
Matches 481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2456 ATCTGAGCCCCAGGGTAGTAGATGGCATGAAGACGGCTGTGGCTCGGACCAAGT 2515  
Db |||||  
1 ATCTGAGCCCCAGGGTAGTAGATGGCATGAAGACGGCTGTGGCTCGGACCAAGT 60

QY 2516 TCTCTTTCCGCGTGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAG 2575  
Db |||||  
61 TCTCTTTCCGCGTGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCTCCCTGGACCAG 120

QY 2576 AGAGCGGCTGCTCACTGTTCCCATGGCCAGCGAGGCAAGAAACACAGACACTGG 2635  
Db |||||  
121 AGAGCGGCTGCTCACTGTTCCCATGGCCAGCGAGGCAAGAAACACAGACACTGG 180

QY 2636 ACAAGCTTCGGCAGGCGGTGACAGAGCTGTGACAGCAGGTGCTGCAGATCGGGAGGAC 2695  
Db |||||  
181 ACAAGCTTCGGCAGGCGGTGACAGAGCTGTGACAGCAGGTGCTGCAGATCGGGAGGAC 240

QY 2696 TGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTGGCGCCCCACAGGGAGGGTCC-GTGC 2754  
Db |||||  
241 TGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCTCTGGCGCCCCACAGGGAGGGTCTCTGTGC 300

QY 2755 CCTCGGCGATCGGGAGAGGGGCGCTGCCAGCTTGTCTCGGGCTTCTGCAGCCTCTG 2814  
Db |||||  
301 CCTCGGCGATCGGGAGAGGGGCGCTGCCAGCTTGTCTCGGGCTTCTGCAGCCTCTG 360

QY 2815 TGTGTGGACACTGGGGCATCTCTCTACTGCTGCAGCCCGCAGCTGGCTCTGTCTTGA 2874  
Db |||||  
361 TGTGTGGACACTGGGGCATCTCTCTACTGCTGCAGCCCGCAGCTGGCTCTGTCTTGA 420

QY 2875 GGGACTTGGCCCCACCCCTCGTCGGGGGCTCTCTCCCTCATGGCACCCCTGGCCCTGGGGT 2934  
Db |||||  
421 GGGACTTGGCCCCACCCCTCGTCGGGGGCTCTCTCCCTCATGGCACCCCTGGCCCTGGGGT 480

QY 2935 CC 2936  
Db ||

481 CC 482

```
RESULT 13
AI272282
LOCUS
DEFINITION
  AI272282 424 bp mRNA linear EST 18-NOV-1998
  ap23c04.x1 Schiller oligodendroglioma Homo sapiens cDNA clone
  IMAGE:1956198 3' similar to TR:Q23974 Q23974 PUTATIVE POTASSIUM
  CHANNEL SUBUNIT. ;, mRNA sequence.
ACCESSION
VERSION
  AI272282.1 GI:3894553
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 424)
AUTHORS
  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
  Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
  Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
  Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  WashU-NCI human EST Project
  Unpublished (1997)
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  This clone is available royalty-free through LLNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Possible reversed clone: similarity on wrong strand
  Possible reversed clone: polyT not found
  Seq primer: -40UP from Gibco
  High quality sequence stop: 401.
  Location/Qualifiers
    1..424
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      /clone="IMAGE:1956198"
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      /dev_stage="44 years"
      /lab_host="SOLR"
      /clone_lib="Schiller oligodendroglioma"
      /note="Organ: brain; Vector: pBluescript SK- (Stratagene);
  Site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was
  prepared from human oligodendroglioma using primer
  5'-GAGAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An EcoRI
  adaptor was used on the 5' end of the cDNA as follows:
  5'-AATCGGCACGAG-3'. The library was size-selected and
  went through one round of amplification. Average insert
  size is 1.7 kb, with a range from 0.4-12 kb. Tumor
  identification by consensus pathology; contains
  chromosome 1p and 19q deletion as determined by CGH. This
  library was constructed by Dr. Martin Schiller (Johns
  Hopkins University)."
```

ORIGIN

```
Query Match 13.0%; Score 424; DB 9; Length 424;
Best Local Similarity 100.0%; Pred. No. 6.7e-59;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1348 AGCGCCTACATCACCTCCCTCTACTTCGCACCTCAGCAGCCTCACCAGCGTGGCTTCGGC 1407
Db |||||||
1 AGCGCCTACATCACCTCCCTCTACTTCGCACCTCAGCAGCCTCACCAGCGTGGCTTCGGC 60

QY 1408 AACGTGTCCGCCAACACGACACCGAGAGATCTTCTCCATCTGCACCATGCTCATCGGC 1467
Db |||||||
61 AACGTGTCCGCCAACACGACACCGAGAGATCTTCTCCATCTGCACCATGCTCATCGGC 120

QY 1468 GCCCTGATGCACGCGGTGGTGTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCC 1527
|||||
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```
Db 121 GCCCTGATGCACGCGGTGGTGTGGGAACGTGACGGCCATCATCCAGCGCATGTACGCC 180

QY 1528 CGCCGCTTTCTGTACCACAGCCGACGGCGACCTGGCGGACTACATCCGCATCCACCGT 1587
|||||
Db 181 CGCCGCTTTCTGTACCACAGCCGACGGCGACCTGGCGGACTACATCCGCATCCACCGT 240

QY 1588 ATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGCGGTGAAC 1647
|||||
Db 241 ATCCCAAGCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCACCTGGCGGTGAAC 300

QY 1648 AATGGCATCGACACCAACCGAGCTGCTGCAGAGCCCTCCCTGACGAGCTGCGCGACATC 1707
|||||
Db 301 AATGGCATCGACACCAACCGAGCTGCTGCAGAGCCCTCCCTGACGAGCTGCGCGACATC 360

QY 1708 GCCATGCACCTGCACAAGGAGTCTCTGCAGCTGCCACTGTTTGAGGGCGCCAGCGCGGC 1767
|||||
Db 361 GCCATGCACCTGCACAAGGAGTCTCTGCAGCTGCCACTGTTTGAGGGCGCCAGCGCGGC 420

QY 1768 TGCC 1771
|||||
Db 421 TGCC 424
```

RESULT 14

```
BQ444229
LOCUS
DEFINITION
  BQ444229 682 bp mRNA linear EST 29-MAY-2002
  UI-M-EX0-bxk-c-05-0-UI.r1 NIH BMAP_EX0 Mus musculus cDNA clone
  IMAGE:5709244 5', mRNA sequence.
ACCESSION
VERSION
  BQ444229.1 GI:21247341
KEYWORDS
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
  1 (bases 1 to 682)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Dr. James Lin, Univeristy of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
```

FEATURES

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source
  1..682
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="IMAGE:5709244"
    /tissue_type="whole brain"
    /dev_stage="embryo 15.5 dpc"
    /lab_host="DH10B (T1 phage resistant)"
    /clone_lib="NIH_BMAP_EX0"
    /note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
  Site 2: Not I; The library was constructed according to
  Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
  1996. Denatured mRNA was size fractionated on a 1% agarose
  gel. First strand cDNA synthesis was primed with an
  oligo-dT primer containing a Not I site. Double stranded
  cDNA was size selected according to mRNA size fraction,
  ligated with EcoR I adaptor, digested with Not I, and then
  cloned directionally into pYX-Asc vector. The library tag
  sequence located between the Not I site and the polyA
  tail, is GTGCGTGGAA. This library was created for the
```

